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

Citation

Published Version
doi://10.1371/journal.pone.0016714

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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 multivariant 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 \textit{gag} and \textit{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 \cite{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 \cite{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: \textit{acute} HIV infection was defined as the period from viral transmission to seroconversion; \textit{recent} HIV infection was defined as the period from viral transmission to seroconversion.

### Table 1. Patient characteristics, time of sampling, and number of analyzed \textit{gag} and \textit{env} sequences

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<th>Age(^1)</th>
<th>HIV-1 RNA load(^2)</th>
<th>Proviral DNA load(^3)</th>
<th>CD4 count</th>
<th>Date(^4)</th>
<th>Days from estimated s/c(^5)</th>
<th>Fiebig stage(^6)</th>
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<td>10/22/2007</td>
<td>44</td>
<td>V</td>
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</table>

\(^1\)Years at the time of sampling.

\(^2\)log\(_{10}\) copies/ml.

\(^3\)log\(_{10}\) copies/10\(^6\) PBMC.

\(^4\)Date of sampling (first sampling for patients with dual dates of sampling).

\(^5\)Seroconversion.


\(^7\)Subjects A and B had viral sequences available at two time points within 50 days p/s. Both sets were included in analysis.

doi:10.1371/journal.pone.0016714.t001
until one year post; primary HIV infection included both the periods of acute and recent HIV infection. The time interval of 0–50 days post-infection 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.](https://example.com/figure1.png)

**Figure 1.** HIV-1 subtype C diversity within 50 days post-infection 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 post-infection. 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.

doi:10.1371/journal.pone.0016714.g002
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

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 1.23E-05 (95% CI 8.07E-06 – 1.64E-05) substitutions per site per day. The geometric mean evolutionary rate in HIV-1C env gp120 was estimated at 3.71E-05 (95% CI 1.97E-05 – 5.45E-05) substitutions per site per day. The estimated rate of gag and env gp120 evolution

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, HD to consensus; J: env sequences, HD to consensus; K: env sequences, ML to MRCA; L: env sequences, K2P to consensus.
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 Akaikie 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 five (20%) cases (subjects D, OG, OW, PK, and PP), undetermined multiplicity of transmission in five (20%) cases (subjects A, E, F, OJ, and QP), and transmission of a single viral variant in 15 (60%) cases.

Branching topology of env sequences

Branching topology and length of env sequences in both NJ (Fig. 3) and ML trees (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, 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-based 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.

Plasmodium knowlesi
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 pairwise distances; I: gag sequences, Hamming distances; J: env sequences, ML-corrected distances to MRCA; K: env sequences, K2P-corrected pairwise distances; L: env sequences, Hamming distances.
correlated 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.g006

with ML-corrected pairwise distances. It is likely that this congruence 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 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 3 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 concurrence 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, OJ, 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, OJ, PO, and QP. To resolve

| Table 2. Decision thresholds for transmission of single and multiple HIV-1 variants |
|-----------------------------------------|-------------------------------|-------------------------------|
| **Maximum distances**                  | **Mean distances**            |
| Analysis                                | gag                           | env                           |
|                                        | Multi | Single | Multi | Single | Multi | Single | Multi | Single |
| ML pairwise                             | >1.25% | <0.5%  | >5%   | <1%    | >0.5% | <0.125% | >2%   | <0.5%  |
| K2P pairwise                            | >1.25% | <0.5%  | >5%   | <1%    | >0.5% | <0.125% | >2%   | >0.5%  |
| Hamming pairwise                        | >15   | <8     | >50   | <10    | >5    | <2.5    | >20   | <6     |
| ML to MRCA                              | >1.2% | <1%    | >4%   | <2%    | >0.5% | <0.125% | >2%   | >0.5%  |
| K2P to consensus                        | >1%   | <0.5%  | >3%   | <1%    | >0.25%| <0.063% | >1%   | <0.25% |
| Hamming to consensus                    | >10   | <5     | >30   | <10    | >2.5  | <1.25   | >10   | <3     |

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.

doi:10.1371/journal.pone.0016714.t002
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 were analyzed (Fig. 9). In contrast to the previously described analysis that utilized only maximum and mean distances, all individual pairwise distances were included in the distribution analysis. Two subjects, A and PO, demonstrated distinct patterns for gag and env distance distribution, suggesting transmission of a single variant based on the gag distance distribution, but two viral variants were evident from the distribution of env distances. In contrast, three other subjects, D, OJ, and QP, showed congruence between gag and env, and the observed distribution patterns were consistent with transmission of multiple viral variants. Interestingly, gag ML-corrected distances to MRCA matched with other analyzed models in all 5 subjects. However, env ML distances to MRCA matched the distribution of other analyzed distances only in 3 subjects, A, OJ, and QP, although they were skewed in subjects D and PO.

Highlighter plots. The shape of highlighter plots (Fig. 10) was coherent with the branching topology of phylogenetic trees for gag (Figs. 1 and 2) and env (Figs. 3 and 4). The shape of the gag highlighter plots for subjects PO and QP did not provide clear answers, leaving open the possibility of either transmission of a single variant followed by early diversification due to immune escape, or transmission of multiple viral variants. Thus, the multiplicity of HIV-1C infection for subjects A, D, and OJ was inconclusive based on the gag highlighter plots alone. The shape of the env highlighter plots suggested transmission of multiple viral
variants in 4 of 5 subjects, and was rather inconclusive for subject PO. Taking into account only conclusive shapes, the combined results of the gag and env highlighter plots suggest transmission of a single viral variant in subject PO, and transmission of multiple viral variants in subjects A, D, OJ, and QP.

Recombination analysis. Analysis of gag sequences showed no evidence of a recombination signal in 4 of 5 subjects (Fig. 10). The potential recombination events were identified in two gag sequences from subject QP, sequences 04 and 11 (Fig. 10 and Table 3), supported by LARD and 3Seq analyses. Analysis of env sequences revealed the presence of recombinant sequences in 3 of 5 subjects (Fig. 10 and Table 3). Two env sequences with recombination signal in subject A were supported by MaxChi, SiScan, LARD, and 3Seq analyses (sequence 006_05), and SiScan and LARD (sequence 022_05). A single env sequence with recombination in subject OJ was supported by SiScan, LARD, and 3Seq analyses, while in subject QP the recombination signal was supported by BootScan, MaxChi, SiScan, LARD, and 3Seq analyses. We assumed that presence of recombinant sequences in the pool of viral quasispecies provides evidence for transmission of multiple viral variants, even if the source of recombination (parent sequence) has not been identified. Therefore, the recombination analysis supported transmission of multiple viral variants in 3 of 5 subjects: A, OJ, and QP.

Time to MRCA (tMRCA) was estimated for gag and env sequences using BEAST v.1.5.4 [33,40], and is shown in Table 4. The geometric means of tMRCA identified for both gag and env sequences were substantially outside the time of seroconversion estimated by Fiebig staging for all 5 subjects. The 95% lower and upper HPD parameters were in an extremely large range, which is not normally observed for transmission of a single viral variant. Although lower 95% HPD was within the time of seroconversion estimated by Fiebig staging for gag sequences in subjects OJ and PO, and for env sequences in subject QP, the obtained large ranges of HPD provide little justification for utilizing them as informative parameters for the analyzed set of sequences. Based on geometric means of the estimated tMRCA alone, transmission of multiple viral variants occurred in subjects A, D, OJ, PO, and QP.

Summary of detailed analysis. Due to some inconsistent results regarding multiplicity of HIV-1C transmission in 5 cases, we estimated how likely it is that transmission of multiple viral variants occurred based on the number of methods with conclusive results for each subject (Fig. 11). The results obtained in detailed analyses were weighted similarly to the summary table presented in Figure 7. As shown in Figure 11, all methods with conclusive results suggested transmission of multiple viral variants in subjects OJ and QP. In subjects A and D, five methods suggested transmission of multiple viruses, while one method (pairwise distances and recombination analysis for subjects A and D, respectively) argued for transmission of single virus. In subject PO, the cumulative results were split with three methods suggesting transmission of single virus, and three methods suggesting transmission of multiple viral variants. Therefore, the cumulative 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

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**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>Methods of recombination analysis, p-values</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>RDP</td>
</tr>
<tr>
<td>A(006_05)</td>
<td>env</td>
<td>-</td>
</tr>
<tr>
<td>A(022_05)</td>
<td>env</td>
<td>-</td>
</tr>
<tr>
<td>OJ (10)</td>
<td>env</td>
<td>-</td>
</tr>
<tr>
<td>QP (04)</td>
<td>gag</td>
<td>-</td>
</tr>
<tr>
<td>QP (11)</td>
<td>gag</td>
<td>-</td>
</tr>
<tr>
<td>QP (05)</td>
<td>env</td>
<td>-</td>
</tr>
</tbody>
</table>

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**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>geo mean (95% lower and upper HPD)(^3)</td>
<td>ESS(^4)</td>
</tr>
<tr>
<td>gag</td>
<td>env</td>
<td></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.

\(^4\) Geo mean: Geometric mean (95% lower and upper HPD)
leading to transmission of multiple viral variants could improve public health strategies aimed at containing and controlling 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


