Blood T cell receptor diversity decreases during the course of HIV infection but the potential for a diverse repertoire persists

Running Title: Impact of HIV infection on blood TCR diversity

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Scientific Category: Immunobiology
Abstract

HIV infection results in a decrease in circulating CD4\(^+\) T cell and naïve T cell numbers. If such losses were associated with an erosion of T cell receptor (TCR) repertoire diversity in the peripheral T cell pool, this might exacerbate the state of persistent immunodeficiency. Existing methods for the analysis of the TCR repertoire have demonstrated skewed distributions of TCR genes in HIV-infected subjects but cannot directly measure TCR diversity. Here, we used AmpliCot, a quantitative assay based on DNA hybridization kinetics, to measure TCR diversity in a cross-sectional comparison of 19 HIV-infected individuals to 18 HIV-uninfected controls. HIV-infected individuals had a 10-fold decrease in total TCR repertoire diversity in 1.5 mL of blood compared to uninfected controls, with decreased diversity correlating most closely with a lower CD4\(^+\) T cell percentage. Nonetheless, the TCR repertoire diversity of sort-purified T cell subpopulations in HIV-infected and HIV-uninfected subjects was comparable. These observations suggest that the TCR repertoire diversity changes in whole blood during HIV disease progression are due primarily to changes in the number and proportion of T cell subpopulations and that most HIV-infected individuals may retain a sufficiently diverse TCR repertoire to permit immune reconstitution with antiretroviral therapy alone, without thymopoiesis.
Introduction

Since CD4+ T cells are progressively lost in most HIV-infected individuals, the absolute CD4+ T cell count has proven useful for staging the degree of immunosuppression and for predicting the risk of opportunistic infections and cancers in these patients1-3. Hidden within the absolute count, however, is a range of features that are critical for the function of the immune system, including the relative proportion of thymically derived naïve T cells and peripherally-expanded memory/effector subpopulations, and the repertoire of T cell receptors found within each of these subpopulations. Clearly, substantial changes in the composition of the T cell compartment occur during disease progression, with loss of naïve T cells and expansion of memory/effector cells4. Less well understood is the impact of HIV infection on the TCR repertoire of the total CD4+ and CD8+ T cell compartments and of their constituent subpopulations.

Previous studies have found that HIV disease alters the normal distribution of TCRs in the repertoire5. Moreover, analysis of patients who had recurrent opportunistic infections even after effective antiretroviral therapy demonstrated that these patients had lost antigen-specific responses, despite having high CD4+ T cell counts6. Data such as these raised the possibility that the immunodeficiency of HIV disease might be due, at least in part, to loss of TCR repertoire diversity, resulting in patients lacking the optimal TCR specificities for recognizing and responding to pathogens5,6. There was concern that TCR specificities might be permanently lost, especially in patients whose HIV had not been treated until late-stage AIDS. To address this concern, efforts were made to monitor thymic activity in HIV-infected patients7-9 and to boost thymic function (e.g., with
growth hormone or interleukin-7)\(^{10-13}\) so that naive T cells with a diverse TCR repertoire might be made anew.

However, evidence supporting the hypothesis that HIV causes a reduction in TCR diversity is limited. Most investigations of the TCR repertoire in HIV disease have measured either Vβ gene usage (determined by flow cytometry or quantitative PCR) or the length distribution of VC rearrangements (analyzed with Spectratyping/Immunoscope)\(^{5,14-16}\). These studies have found a skewed distribution of circulating TCR clones in HIV-infected patients, with certain clones expanded relative to others. Unfortunately, these methods are both qualitative and insensitive, and cannot distinguish between two possible mechanisms of skewing: the expansion of selected clones versus the loss of others.

Here, we apply the quantitative AmpliCot method\(^{17-19}\) to a cross-sectional study of HIV-infected and -uninfected subjects to clarify the impact of HIV disease on the TCR repertoire. One challenge with quantitative measurements of TCR diversity is that they are dependent on the nature of the sample used. Three potential approaches are schematized in Figure 1. The “whole body repertoire” (Figure 1A) is, in theory, the frame of reference that defines whether clones are truly permanently lost. In practice, the repertoire of the estimated \(10^{11}\) T cells in the body is impossible to measure\(^{20}\). Even if it were possible to enumerate all TCR clones, rare clones may not be available at the required anatomic sites for immune responses or immune reconstitution. Figure 1B depicts what we will call the “whole-blood TCR repertoire,” or the number of unique
TCRs found in a fixed volume of whole blood (essentially, the operational definition of the repertoire most often used by clinical researchers). It reflects the absolute abundance of different T cell subpopulations in the blood and may define the current state of the immune system’s ability to recognize a pathogen. Finally, we measured the “subpopulation TCR repertoire,” or the number of unique TCRs found in a fixed number of cells from defined T cell subpopulations (Figure 1C). This more detailed examination may define the potential diversity that could be used to reconstitute the immune system if cells of these subpopulations were expanded.

We find that there is a significant decrease in the whole-blood TCR diversity in untreated HIV-infected subjects as opposed to well-matched HIV-uninfected subjects and argue that these defects may contribute to the immune deficits associated with untreated HIV disease. In contrast, the TCR repertoires of constituent naïve and memory/effector subpopulations, when analyzed on a per-cell basis, are largely indistinguishable between infected and uninfected subject, suggesting that that the decrease in whole-blood TCR diversity is largely due to changes in the relative representation of different T cell subpopulations. Consequently, it should be possible to reconstitute a T cell compartment with a diverse TCR repertoire in most HIV-infected subjects, even in the absence of thymic function.
Patients, Materials, and Methods

Subjects

HIV-infected subjects, recruited from the SCOPE cohort, were infected for over six months and had not received antiretroviral drugs in the six months before enrollment. HIV-uninfected subjects were recruited from the community to match the demographics and disease exposures of the HIV-infected participants and were also enrolled into the SCOPE cohort. Subjects were excluded from the study if they were born outside USA, Canada, or Western Europe; had known chronic HBV infection, or present or past HCV infection; had taken systemic corticosteroids or immunosuppressive drugs; had a history of disseminated malignancy, organ or bone marrow transplant, pregnancy, or hemophilia; or had used intravenous drugs within the previous six months. Subjects had their participation deferred for infections requiring systemic antibiotics, immunizations, or blood transfusions in the past month, fever, cough diarrhea, or travel to Asia, Africa or Latin America in the past week. Subjects provided demographic information and information on routine exposures via questionnaire. All human subject research was conducted under protocols approved by the University of California, San Francisco Committee on Human Research and all subjects gave written informed consent in accordance with the Declaration of Helsinki.

Blood samples

HIV-infected and HIV-uninfected subjects donated 40 mL and 100 mL blood, respectively. Samples were processed within six hours of donation. Leukocytes from 1.5 mL of blood were isolated by hypotonic lysis, followed by lysis of the leukocyte pellet in
buffer RLT (QiAmp RNA kit, Qiagen, Valencia, CA). The lysate was homogenized using shredding columns and then stored at -80°C before batch RNA isolation according to manufacturer’s instructions.

Plasma was isolated by centrifugation of blood (400xg for 10 minutes and 800xg for 10 minutes). Mononuclear cells were obtained by ficoll preparation of the remaining blood, and were stained for the markers CD3, CD4, CD8β, CD45RA, CCR7, and CD57 and sorted for the phenotypes described in Table 3. To measure the percentage of cells of each phenotype using particular Vβ families, required for calculations of absolute TCR diversity, two aliquots of cells were additionally stained with either Vβ1, Vβ3, Vβ4; or Vβ2, Vβ17, Vβ22.

Cell samples were sorted with a FACSaria (BD Biosciences, San Jose, CA) into chilled 1.5 mL collection tubes containing 250 μL of PBS + 2% FCS. Cell yields were determined from cytometer event counts, after verification using a hemocytometer. Viability and purity were assessed by re-analysis of propidium iodide-stained sorted cells. Viability was greater than 95% and purity (defined in terms of contamination with other T cell subpopulations) was greater than 98%. Cells were centrifuged at 4°C for 10 minutes at 3000 rpm and then lysed in buffer RLT.

AmpliCot and quantitative PCR

Total RNA was reverse transcribed and amplified for measuring VJ family sequence diversity, as described17,19. V primers for the most abundant Vβ gene families (V9, V20,
and V28) were used, corresponding to the Vβ1, Vβ2, and Vβ3 antibodies used for flow cytometry\textsuperscript{21}. J primers used were J2S1, J2S2, and J2S3. Measurements of up to nine VJ families were averaged to estimate total sample diversity. For whole blood samples, the diversity of the sample is expressed as the sum of the Cot\textsubscript{1/2} values for these VJ families. The Cot\textsubscript{1/2} value is the concentration x time product required for half of the sample to reanneal under stringent conditions and is proportional to the sequence diversity of the sample. For whole blood samples, the wide variation of clone frequency makes it difficult to translate Cot\textsubscript{1/2} values into an absolute number of sequences. For sorted T cell subpopulations, which have more uniformity in their clone frequency, the absolute number of sequences of a given VJ family in the sample was calculated using quantitative standards as described\textsuperscript{18}. This value was then used to estimate the total number of sequences in the sample by multiplication with measured parameters of VJ family usage as described in references 17 and 19. The error due to selection of individual VJ families was assessed by measuring the reproducibility of measurements of the same samples using different VJ families (Appendix, Supplemental Figure 3). This estimate of sequences per sample was more accurate for highly diverse cell types, such as CD4\textsuperscript{+} naïve T cells, than for low diversity cell subpopulations, such as CD8\textsuperscript{+} central memory T cells. More details of the AmpliCot method are available at http://amplicot.ucsf.edu.

Other measurements

Viral loads were measured by the SFGH Clinical Laboratory using the bDNA v3 Versant assay (Siemens, Tarrytown, NY). Complete blood counts were performed by the SFGH Clinical Laboratory. Transcription Mediated Amplification for hepatitis B and C viruses
was performed by Dr. Leslie Tobler of the Blood Systems Research Institute. Serological tests for HBV IgG, HCV IgG, *H. pylori* IgG, EBV VCA IgG, and CMV IgG used Bioquant EIA kits (San Diego, CA), following the manufacturer’s instructions.
**Results**

*Subjects*

We recruited HIV-infected subjects with a range of CD4⁺ T cell counts to reflect the spectrum of disease progression. Study participants were naïve to antiretroviral medications, except for two individuals who had been off treatment for at least six months. Because our goal was an internally valid study (to be followed by later generalizable studies) and because much remains to be learned about the factors that determine TCR repertoire diversity, strict enrollment criteria were used. As a matched comparator group, HIV-uninfected subjects were selected to have pre-specified characteristics that might impact upon the TCR repertoire. In addition to age and CMV serostatus, factors shown to affect repertoire diversity²²-²⁶, subject groups were also similar for gender, race, and prior exposure to HCV, HBV (Table 1). *H. pylori* seropositivity, a proxy for unmeasured socioeconomic variables affecting infectious disease exposure history²⁷, was similar in both groups (Table 1). Because the analysis of TCR repertoire diversity was carried out before the co-infection status could be ascertained, data were also gathered from subjects who did not meet all of the pre-specified characteristics. Data from these additional subjects, however, did not differ noticeably from that of the pre-defined subjects (see, for instance, open circles in Figure 2A) and are therefore included to increase the total number of data points. Little is known about the effects of acute exposures on the TCR repertoire; accordingly, a conservative list of exclusion criteria was applied and (as detailed in “Patients, Materials, and Methods”) potential subjects were excluded if they had a recent history of an acute infection, immunization, or travel.
**HIV disease associated with decreased whole-blood TCR repertoire diversity**

Previous studies using methods such as Immunoscope/Spectratyping have demonstrated that HIV disease is associated with a skewing of the T cell receptor repertoire, i.e., an increased representation of some clones relative to others\(^5,14\). While these data have been used to suggest that TCR specificities are lost from the repertoire during the course of HIV disease, they could simply reflect the preferential expansion of selected T cell clones in HIV-infected individuals. AmpliCot, an assay taking advantage of DNA hybridization kinetics and amenable to the evaluation of very large numbers of diverse sequences\(^17-19\), enabled the quantitative assessment of TCR repertoire diversity of human blood or cell samples. AmpliCot has been validated, using both oligonucleotide libraries and titrated naïve T cells, to make reproducible distinctions between samples with two-fold differences in diversity\(^17-19\). Interassay reproducibility for replicate samples collected in this study is shown in the Appendix. For samples containing single types of cells with relatively similar frequencies of TCR genes, it is possible to use standards to estimate the absolute number of unique TCR rearrangements in the sample. By contrast, because the whole blood repertoire contains a mixture of lymphocyte subtypes with an uneven distribution of TCR rearrangements, absolute counts are both technically difficult and less meaningful. For whole blood, we have accordingly expressed our diversity measurements in relative Cot units, which are proportional to the diversity of TCR rearrangements in a sample.

When whole blood was studied in this fashion, HIV disease was associated with a 10-fold reduction in TCR repertoire diversity of a 1.5 mL blood sample (Figure 2A). No other co-
infections or exposures were significantly associated with whole blood T cell diversity in the HIV-uninfected subjects (Table 2), but the small number of subjects limited our power to detect such associations. In particular, although large clonal expansions have been found in elderly individuals with CMV infection\textsuperscript{22-26}, we did not detect significantly decreased diversity in CMV-infected subjects with AmpliCot. Perhaps our subjects were not old enough to demonstrate this phenomenon. A less likely possibility is that AmpliCot, compared to the methods used in previous studies, may have more sensitivity for residual diversity in the presence of large clonal expansions. Although subjects had wide variability in the number of T cells contained in the 1.5 mL blood sample, there was no significant correlation between absolute T cell count and whole blood T cell diversity (Figure 2B).

We examined the relationship between T cell subpopulation counts and percentages and whole-blood TCR repertoire diversity. In HIV-infected subjects, the strongest correlation was between CD4\textsuperscript{+} T cell percentages and whole-blood TCR repertoire diversity (p=0.007, Figure 2C). CD4\textsuperscript{+} T cell absolute counts were also significantly correlated with whole-blood TCR repertoire diversity in the HIV-infected subjects if those with low viral loads (< 1000 RNA copies/mL) were excluded (p=0.01, Figure 2D). Focusing on naïve CD4\textsuperscript{+} T cells, as opposed to all CD4\textsuperscript{+} T cells, did not increase the strength of these correlations in HIV-infected subjects. By contrast, in HIV-uninfected subjects there was no significant correlation between CD4\textsuperscript{+} T cell percentages and counts and whole-blood TCR repertoire diversity. However, in the uninfected subjects there were significant correlations between naïve CD4\textsuperscript{+} T cell counts and percentages and whole-blood TCR
diversity (p=0.006, Figure 2E) as well as between naïve CD4+ T cell percentages and whole-blood TCR diversity (p=0.007).

The two patients with the lowest plasma HIV RNA levels (off therapy) had the highest whole-blood TCR repertoire diversity measurements (even overlapping with those observed in HIV-uninfected subjects) (see Figures 2C and 2E), but an inverse correlation trend between viral load and whole-blood TCR repertoire diversity was not significant for the HIV-infected group as a whole (Figure 2F). Since AmpliCot measurements, like all TCR repertoire diversity measurements, can be affected by large numbers of expanded clones, we were concerned that the whole-blood TCR diversity changes seen in HIV-infected subjects were solely an artifact of memory CD8+ T cell expansions seen in the context of HIV disease. Arguing against this possibility, there was no significant correlation between absolute memory CD8+ T cell counts and whole-blood TCR diversity in the HIV-infected or HIV-uninfected subjects (Figure 2G). There was, however, a significant correlation between the percentage of CD8+ cells that were of memory/effector phenotypes and the whole-blood TCR diversity in the HIV-infected subjects, largely driven by the two HIV+ outliers with low viral loads (Figure 2H).

*TCR repertoire diversity preserved within discrete T cell subpopulations*

Loss of whole-blood TCR repertoire diversity in HIV-infected subjects could be due to lower numbers of T cells per unit volume, perturbations in the proportions of different T cell subpopulations, and/or loss of TCR repertoire diversity within discrete T cell subpopulations. To address the latter possibility, various subpopulations of CD4+ and
CD8\(^+\) T cells were sort-purified (using the phenotypes shown in Table 3) and subjected to TCR repertoire analysis with AmpliCot. Because it is difficult to normalize diversity measurements to cell number, we selected samples containing equal numbers of cells of a given type for diversity comparisons. This led to the exclusion of some HIV-infected subjects whose very low numbers of certain subpopulations (particularly naïve CD4\(^+\) T cells) led to inadequate yields of sorted cells. An analysis plotting input cell number versus measured diversity that contained all patient samples, regardless of size, showed no evidence of a diversity difference between the HIV-infected and -uninfected subjects (Figure S1).

In healthy donors, and as expected, the greatest degree of diversity in the TCR repertoire was found to reside within naïve CD4\(^+\) and CD8\(^+\) T cells, and in central memory CD4\(^+\) T cells (Figure 3A) while much lower levels of TCR repertoire diversity were found in effector memory CD4\(^+\) and CD8\(^+\) T cells and central memory CD8\(^+\) T cells (Figure 3B). The relatively high diversity of central memory CD4\(^+\) T cells is corroborated by the results of sequencing studies\(^ {28,29}\). The number of unique TCRs found within the naïve T cell samples was less than the number of cells examined, a discrepancy likely due to bottlenecks resulting from the splitting of samples during the RT-PCR protocol (which limited the diversity in each V\(\beta\) PCR reaction).

The diversity of purified T cell subpopulations from HIV-infected and -uninfected subjects is compared in Figure 4. Surprisingly, when equal numbers of cells were analyzed, HIV-infected subjects did not appear to have significant changes in the
diversity of their CD4⁺ naïve T cells in the sample sizes examined. In fact, all T cell subpopulations examined had equal numbers of TCR sequences on a per cell basis in HIV-infected and -uninfected subjects, with one exception: central memory CD4⁺ T cells from HIV-infected subjects harbored a significantly more diverse TCR repertoire (p=0.007). The relatively high diversity of CD4⁺ central memory T cells in HIV-infected subjects may explain why whole-blood TCR diversity was no more strongly correlated with counts of naïve CD4⁺ T cells than with total CD4⁺ T cells in these subjects. This result suggests that HIV disease is associated with higher rates of naïve to central memory cell differentiation and/or changes in the turnover rate of central memory CD4⁺ T cells. Several features unique to HIV disease might contribute to these changes in the CD4⁺ central memory repertoire, including direct responses to HIV antigens, increased immune activation, and responses to unmeasured co-infections that are more prevalent in HIV-infected subjects.

Changes in whole-blood TCR repertoire diversity in HIV disease largely explained by changes in the numbers of T cell subpopulations

To integrate the above measurements of TCR repertoire diversity in whole blood and in sort-purified T cell subpopulations, we charted a representation of the component subpopulations in a 1.5 mL whole blood sample for the subjects in the pre-specified comparison groups. Two representative charts are shown in Figure 5, and charts for the remaining subjects are provided as supplementary material. The rectangles represent the number of cells of each subpopulation in 1.5 mL of blood (x axis) and the calculated
number of unique TCR sequences in that number of cells from that subpopulation (y axis; see figure legend for details). The rectangles are summated to reflect the total number of cells in the blood sample on the x axis and the estimated diversity in the blood sample on the y axis. For a given T cell subpopulation, cells from HIV-infected and HIV-uninfected subjects have similar TCR repertoire diversity when equal cell numbers are measured. However, the decreased number of cells from high diversity subpopulations in the peripheral blood (i.e., naive CD4$^+$ and CD8$^+$ T cells and, to a lesser extent, central memory CD4$^+$ T cells) results in a significant overall decrease in sum TCR repertoire diversity in whole blood samples from HIV-infected subjects.

We also used these data to test whether varying distributions of T cell subpopulations might have affected the accuracy of our whole-blood TCR diversity measurements. Figure 5C shows a plot of the total TCR diversity in 1.5 mL of blood estimated from the summation of cell subpopulations versus the measured Cot values from 1.5 mL of whole blood from these subjects. While these two measurements have a linear relationship, the best-fit line does not go through the origin, indicating moderate error in absolute terms. This discrepancy is likely due to the effect of large clonal expansions, reducing the Cot values of whole blood AmpliCot measurements, but may also reflect overestimates in our modeling of the diversity of the subpopulations of T cells found in these samples.
Discussion

Association of HIV disease with reduced T cell receptor repertoire diversity per volume of blood

Here, we have used a novel quantitative assay and a cross-sectional study design to demonstrate that progressive HIV disease is associated with decreased whole-blood TCR diversity. The decreased diversity of available TCRs per volume of blood may impair pathogen recognition of pathogens, thereby contributing to the immune dysfunction associated with HIV infection. Despite the strong associations found, our cross-sectional study design makes it impossible to establish a causal relationship between HIV infection and TCR diversity loss. Due in part to this concern, we were careful in selecting our control population, so that we could minimize unmeasured confounding variables. We therefore only included subjects who were CMV seropositive and who lacked evidence of hepatitis B or C exposure. We also matched subjects based on demographics, and excluded individuals with recent infections and other conditions potentially affecting the immune system. Two lines of evidence that the observed diversity differences are likely attributable to HIV infection are that no other measured co-infection was significantly associated with TCR diversity, and that the relationship between HIV infection and reduced diversity was consistently seen, whether or not the study analysis was restricted to the pre-specified groups of participants. Because we only enrolled subjects without active opportunistic infections or cancers, it is possible that our HIV-infected subjects may have been biased towards those who are healthy, which would decrease the observed effects of HIV infection on immune repertoire diversity.
Clinical significance of TCR diversity

In HIV-infected subjects, we found that blood TCR diversity correlated with CD4⁺ T cell counts and percentages, which are important albeit imperfect predictors of the risk of opportunistic infections. Is TCR diversity independent of T cell numbers clinically significant? Certainly, HLA diversity is important for pathogen resistance on a population level.

In principle, at least some TCR diversity (per fixed volume of blood or tissue) is necessary for basic antigen recognition, but how much is necessary is not known. Current data are equivocal about the importance of TCR diversity, although recent studies of aging in animal models suggest that skewing of the TCR repertoire predicts vulnerability to infection. While we do not yet know the clinical significance of the 10-fold decrease in whole-blood TCR diversity associated with HIV infection, deficits of this magnitude exceed the physiologic reserve of most organ systems. Future studies will determine whether TCR diversity is a clinically relevant predictor of a patient’s risk of opportunistic infections or cancer, potentially complementing counts of T cell subpopulations.

Although the CD4⁺ T cell count is a well-validated and useful marker, it does not provide perfect stratification of patient risks of opportunistic infections and cancers. TCR diversity could potentially provide additional prognostic information to a CD4⁺ T cell count, perhaps explaining cases of opportunistic infections that occur in patients with high CD4⁺ T cell counts. While CD4⁺ T cell counts are associated with the loss of immune function during HIV disease progression, the relationship between CD4⁺ T cell count and reconstitution of immune function after treatment has begun is less well
substantiated\textsuperscript{35-37}. Part of the benefit of antiretroviral therapy might be mediated through improvements in T cell diversity (e.g., through increases in the CD8$^+$ naïve:memory ratio), not just CD4$^+$ T cell counts. More evidence that CD4$^+$ T cell counts alone may not fully measure immunocompetence is the finding that interleukin-2, which increases CD4$^+$ T cell counts without increasing repertoire diversity, provides no clinical benefit to HIV-infected patients\textsuperscript{37}.

The two HIV-infected subjects with low plasma HIV RNA levels also had higher whole-blood TCR diversity. Because HIV-specific T cells represent a small fraction of total T cells\textsuperscript{38}, this association is not likely to be a simple consequence of the low abundance of HIV antigen in these patients, but may be a result of HIV immunopathogenesis. This result, if corroborated, might provide an explanation for two clinical phenomena. First, in cohort studies, viral load and CD4 counts are independent factors that predict progression to AIDS\textsuperscript{39}. High viral loads might not simply lead to AIDS by depletion of CD4$^+$ T cell number, but also by reducing T cell diversity per volume of blood. Second, patients on antiretroviral therapy have improved clinical outcomes, even if their CD4$^+$ T cell counts are not restored. Longitudinal studies of individuals beginning antiretroviral therapy will best address the question of whether suppression of viremia can result in rapid increases in TCR diversity. Clonal expansions have been observed to decrease once ART is started\textsuperscript{16} and, if these cells are replaced by more diverse T cells, TCR diversity per volume of blood may therefore increase.
Preserved diversity of T cell subpopulations and the potential for immune reconstitution

Our analysis of T cell subpopulations did not detect significant changes in TCR diversity between HIV-uninfected and HIV-infected subjects, except for CD4+ central memory T cells, which surprisingly were significantly more diverse in individuals with HIV. We therefore did not find evidence that HIV infection was associated with permanent losses of TCR diversity in T cell subpopulations. Consonant with this finding, it is unusual for patients to contract opportunistic infections after T cell reconstitution with antiretroviral therapy, and prophylaxis regimens can be safely discontinued. The preservation of a significant reservoir of TCR repertoire diversity in the naïve cell populations might permit a TCR repertoire to be successfully reconstituted without de novo thymic activity. Interleukin-7 is a promising agent that might reconstitute the immune system in this way in patients who do not achieve reconstitution with antiretroviral therapy alone. Human trial data suggest it may increase TCR diversity per blood/tissue volume by selectively stimulating proliferation of high-diversity cell populations rather than by stimulating thymopoiesis.

Sampling considerations

We do not yet know what sample size for repertoire diversity measurements (i.e., the number of cells or the volume of blood or tissue) is most clinically relevant. On the one hand, the body must certainly contain more than a single cell of a given specificity for it to be useful in either immunocompetence or potential immune reconstitution, suggesting that a significantly smaller unit of examination would be appropriate. The fact that individual memory or effector clones are represented by thousands of cells in the body is
further evidence that the unit of examination should be smaller than the whole body. On the other hand, if the unit of examination is too small, clinically significant differences in TCR diversity might be masked.

While the optimal sample sizes of blood and cells remain to be determined, we must underscore that our results are a function of the sample sizes we collected. If we had sampled larger volumes of whole blood, we might have found an even larger diversity difference between HIV-infected and HIV-uninfected subjects. Similarly, our samples of naïve cells represented only a tiny fraction of those found in the body, and our data suggest that our sample size was limiting for these cells (as opposed to memory-effector subpopulations). Had we been able to examine larger samples of cells, we might have detected a greater difference in diversity between, for example, naïve CD4+ T cells and central memory CD4+ T cells. Moreover, the 1.2 million naïve CD4+ T cell samples we collected represent the cells found in an average of 5 mL of blood in the HIV-uninfected subjects, but an average of 27 mL of blood in the HIV-infected subjects. If we had been able to measure the total body naïve repertoires of our subjects, we might have found a significant reduction in diversity in our HIV-infected subjects, because they have fewer total body naïve cells. However, the importance of the total body naïve repertoire for immune reconstitution is unknown.

Our study has several limitations, including the cross-sectional nature described above. We only sampled blood, and the TCR diversity of the lymphoid tissues that contain the bulk of T cells was not directly measured, although the extent to which these repertoires
differ is unclear\textsuperscript{41}. The TCR\(\beta\) chain repertoire is likely related to but is not identical to the functional TCR repertoire: our measurements did not capture TCR\(\alpha\) diversity, binding specificity or cellular function beyond that suggested by phenotypic markers. Our method cannot discern whether a repertoire of a given diversity may be depleted or enriched for important clones\textsuperscript{42}. Finally, AmpliCot measurements, while rapid and economical, are prone to error due to unequal frequencies of TCRs in the sample, particularly if they are not evenly distributed across all VJ families. As more TCR sequencing data become available, it may be possible to model these frequency distributions to reduce this source of error. Further discussion of technical limitations of our procedure is included in the Appendix.

In conclusion, while HIV infection is associated with a quantitative reduction in TCR repertoire diversity per volume of peripheral blood, diversity seems to be preserved on a per-cell basis for individual subpopulations. Thus, although significant efforts have been made to increase the diversity of the TCR repertoire of HIV-infected patients (e.g., through stimulation of thymic function), our results suggest that this may not be necessary for the restoration of a diverse repertoire per volume of whole blood. While this study was necessarily small because it required well-defined subject groups for internal validity and involved large-volume cell sorting, future studies of whole-blood diversity in larger numbers of subjects will test the generalizability of our findings and permit multivariate analysis of variables such as age, gender and co-infections. Longitudinal studies of patients beginning antiretroviral therapy will help elucidate the possible relationship between viral load and blood TCR diversity. Our work provides a
clinically relevant example of the use of AmpliCot for the direct measurement of repertoire diversity. Our method for measuring TCR diversity may also have application in low-resource settings because it could permit the measurement of immunologic status and viral loads with the same nucleic acid amplification technology.
Acknowledgments

We thank study volunteers for their participation; Marcia Smith, and Joy Madamba for help with recruitment, questionnaires and sample collection; Leslie Tobler for nucleic acid testing of samples; Saunak Sen for statistical consultation; and McCune lab members for discussions and comments on the manuscript. This work was funded by grants from the National Institutes of Health (K23 AI 073100 to P.D.B., and R37 AI40312, and UO1 AI43864 to J.M.M.) and from the California HIV/AIDS Research Program (an IDEA Grant to P.D.B.). J.M.M. is a recipient of the NIH Director’s Pioneer Award Program, part of the NIH Roadmap for Medical Research, through grant DPI OD00329. This SCOPE cohort was supported in part by the NIAID (RO1 AI087145, K24AI069994), the UCSF CFAR (PO AI27763), the UCSF CTSI (UL1 RR024131), the Cleveland Immunopathogenesis Consortium (AI 76174) and CFAR Network of Integrated Systems (R24 AI067039).

Authorship Contributions

PDB and JMM designed the experiments; RH, SD and JM managed the SCOPE study; PDB, DS, and RH recruited study subjects; PDB performed flow analysis and sorting; PDB, JJY and QZ performed AmpliCot and quantitative PCR analyses; PDB and QZ performed ELISAs; MB performed viral NAT assays; PDB and JMM wrote the manuscript with assistance from all co-authors.

Conflict of Interest Disclosures

No competing financial interests.
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Table 1. Study subjects

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<td>MSM (ever)</td>
<td>14 (93%)</td>
<td>7 (78%)</td>
</tr>
<tr>
<td>IVDU (ever)</td>
<td>1 (7%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Pet at home</td>
<td>3 (20%)</td>
<td>3 (33%)</td>
</tr>
<tr>
<td>Child under age 10 at home</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>CD4 count/μL</td>
<td>260</td>
<td>1203</td>
</tr>
<tr>
<td>-------------------</td>
<td>----------</td>
<td>------------</td>
</tr>
<tr>
<td>HIV VL/mL</td>
<td>44000</td>
<td>--</td>
</tr>
<tr>
<td>(Median, range)</td>
<td>(135-382000)</td>
<td>(135-382000)</td>
</tr>
<tr>
<td>History of ART</td>
<td>2 (13%)</td>
<td>--</td>
</tr>
</tbody>
</table>

**Serologies**

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td>EBV VCA IgG⁺</td>
<td>8 (53%)</td>
<td>4 (44%)</td>
<td>10 (53%)</td>
<td>6 (33%)</td>
</tr>
<tr>
<td><em>H. pylori</em> IgG⁺</td>
<td>6 (40%)</td>
<td>5 (56%)</td>
<td>8 (42%)</td>
<td>11 (61%)</td>
</tr>
<tr>
<td>CMV IgG⁺</td>
<td>15 (100%)</td>
<td>9 (100%)</td>
<td>19 (100%)</td>
<td>12 (68%)*</td>
</tr>
<tr>
<td>HCV IgG⁺ with</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>1 (5%)</td>
<td>2 (11%)</td>
</tr>
<tr>
<td>negative HCV</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>viral load</td>
<td></td>
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</table>

**Nucleic Acid Tests**

<p>| | | | | |</p>
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</thead>
<tbody>
<tr>
<td>HCV</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>1 (6%)</td>
</tr>
<tr>
<td>HBV</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>3 (16%)</td>
<td>1 (6%)</td>
</tr>
</tbody>
</table>

*P<0.05
Table 2. Patient variables not significantly associated with whole-blood TCR diversity among 18 HIV- study subjects.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Number positive</th>
<th>Statistical test</th>
<th>P value</th>
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<tbody>
<tr>
<td>CMV IgG⁺</td>
<td>12</td>
<td>Mann-Whitney</td>
<td>0.89</td>
</tr>
<tr>
<td>EBV IgG⁺</td>
<td>6</td>
<td>Mann-Whitney</td>
<td>0.28</td>
</tr>
<tr>
<td><em>H. pylori</em> IgG⁺</td>
<td>11</td>
<td>Mann-Whitney</td>
<td>0.86</td>
</tr>
<tr>
<td>HBV⁺ (NAT) or HCV⁺ (antibody or NAT)</td>
<td>4</td>
<td>Mann-Whitney</td>
<td>0.87</td>
</tr>
<tr>
<td>Pet at home</td>
<td>4</td>
<td>Mann-Whitney</td>
<td>0.22</td>
</tr>
<tr>
<td>Age</td>
<td>--</td>
<td>Linear regression</td>
<td>0.08</td>
</tr>
<tr>
<td>Phenotype</td>
<td>Defining markers</td>
<td>Cell number goal</td>
<td></td>
</tr>
<tr>
<td>---------------------------</td>
<td>---------------------------------------</td>
<td>------------------</td>
<td></td>
</tr>
<tr>
<td>naïve CD4⁺</td>
<td>CD3⁺CD4⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>1.2x10^6</td>
<td></td>
</tr>
<tr>
<td>central memory CD4⁺</td>
<td>CD3⁺CD4⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>1.2x10^6</td>
<td></td>
</tr>
<tr>
<td>effector memory CD4⁺</td>
<td>CD3⁺CD4⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>1.2x10^6</td>
<td></td>
</tr>
<tr>
<td>naïve CD8⁺</td>
<td>CD3⁺CD8β⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>1.2x10^6</td>
<td></td>
</tr>
<tr>
<td>central memory CD8⁺</td>
<td>CD3⁺CD8β⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>0.4x10^6</td>
<td></td>
</tr>
<tr>
<td>effector memory CD8⁺</td>
<td>CD3⁺CD8β⁺CD45RA⁺CCR7⁺CD57⁻</td>
<td>0.4x10^6</td>
<td></td>
</tr>
</tbody>
</table>
Figure Legends

Figure 1. Frames of reference for TCR diversity measurements.

A-C. In this schematic, circles represent T cells, their shading represents their phenotype (e.g., naive CD4⁺ T cells), and their letter represents their TCR clonotype.

A. Total body TCR diversity (i.e., unique TCR sequences in the entire body). B. TCR diversity per fixed volume of blood or tissue (e.g., unique TCR sequences per 1.5 mL of whole blood). C. TCR diversity per fixed number of cells, often of a defined subpopulation (e.g., number of unique TCR sequences found in a sample of 1.2 million naive CD4⁺ cells).

Figure 2. Impact of HIV infection on TCR repertoire diversity in a fixed volume of whole blood.

In this figure, as well as those that follow, HIV⁻ subjects are represented as circles and HIV⁺ subjects are represented as squares.

A. Whole-blood TCR repertoire diversity compared for HIV-infected and -uninfected subjects. Diversity is expressed in relative Cot units (17). Solid symbols represent subjects meeting pre-specified criteria for comparison; hollow symbols represent subjects that did not meet these pre-specified criteria. Diversity values for HIV-infected subjects were significantly lower (p=0.0005; two-tailed Mann-Whitney test for pre-specified comparison groups). B. Absolute T cell count did not correlate with whole-blood TCR repertoire diversity (Spearman r=-.07; p=.79 for HIV⁻; Spearman r=-.26; p=.27 for HIV⁺; Spearman r=.25; p=.14 for all subjects). C. CD4⁺ T cell percentage and whole-blood TCR repertoire diversity measured for HIV-infected subjects. Solid symbols indicate
subjects with viral loads > 1000 copies/mL. Hollow symbols indicate subjects with viral loads < 1000 copies/mL. CD4% and sum TCR repertoire diversity were significantly correlated for all HIV-infected subjects (Spearman r=0.55; p=0.01); the strength of correlation increases if the two subjects with viral loads<1000 copies/mL are excluded (Spearman r=0.72; p=0.001). D. CD4+ T cell absolute counts and whole-blood TCR repertoire diversity measured for HIV-infected subjects. Solid symbols indicate subjects with viral loads > 1000 copies/mL. Open circles indicate subjects with viral loads < 1000 copies/mL. Absolute CD4 count and whole-blood TCR repertoire diversity were significantly correlated (Spearman r=0.46; p=0.048) but the strength of this correlation improved if the two subjects with viral loads<1000 copies/mL are excluded (Spearman r=0.61; p=0.01). E. Naïve CD4+ T cell absolute counts and whole-blood TCR repertoire diversity measured for HIV-uninfected subjects (Spearman r=0.61; p=0.008). F. HIV viral load and blood TCR diversity for HIV-infected subjects. The correlation was not significant (Spearman r=-.42, p=.07). G. Absolute memory CD8+ cell count and whole-blood TCR diversity. Memory cells were defined as in Table 3 (Spearman r=-.21, p=.41 for HIV-; Spearman r=-.27, p=.29 for HIV+). H. Percentage CD8 effector/memory cells of all CD8 cells and whole-blood TCR diversity in HIV+ subjects. Hollow symbols indicate subjects with viral loads < 1000 copies/mL. Memory and effector cells were defined as in Table 3 (Spearman r=-.52, p=.03).

Figure 3. Subpopulation diversity of purified T cells from HIV-uninfected subjects.
A. Diversity (TCR sequences measured per 1.2 million cells) of naïve CD4+ T cells (4N; CD3+CD4+CCR7+CD45RA+CD57), central memory CD4+ T cells (4CM;
CD3⁺CD4⁺CCR7⁺CD45RA⁻CD57⁻), and naive CD8⁺ T cells (8N; CD3⁺CD4⁺CCR7⁺CD45RA⁺CD57⁻) sort-purified from HIV-uninfected subjects.

B. Absolute diversity (TCR sequences measured per 0.4 million cells) of central memory CD8⁺ T cells (8CM; CD3⁺CD8⁺CCR7⁺CD45RA⁻CD57⁻), effector memory CD4⁺ T cells (4EM; CD3⁺CD4⁺CCR7⁻CD45RA⁺), and effector memory CD8⁺ T cells (8EM; CD3⁺CD4⁺CCR7⁻CD45RA⁺) sorted from HIV-uninfected subjects. One-way ANOVA for the six populations was significant (Kruskal-Wallis test p<.0001). The 4N and 8N populations did not have a significant difference in sequences per sample (Mann-Whitney test, p=.32), but the 4CM population had significantly less diversity than 4N and 8N, and significantly more diversity than 8CM (All comparisons with two-tailed Mann Whitney tests, p<.0001).

Figure 4. Subpopulation diversity of sort-purified T cells in HIV-uninfected versus -infected subjects.

Data are shown for those HIV-uninfected and -infected subjects (regardless of pre-specified comparison group) from whom the target number of cells (1.2 million cells or 0.4 million cells) could be collected. Abbreviations for cell subpopulations and the markers used to define them for flow cytometric purification are the same as in Figure 3. All diversity comparisons were non-significant, except that the TCR repertoire of the central memory CD4⁺ T cell subpopulation from HIV-infected subjects was significantly more diverse than that found in HIV-uninfected subjects (two-tailed Mann-Whitney test p=0.007).
Figure 5. TCR repertoire diversity maps in HIV-infected and -uninfected subjects.

A and B. Plots represent the T cells present in 1.5 mL of blood, with each color block representing a different subpopulation. The x axis shows numbers of cells. The y axis shows TCR repertoire diversity (number of unique sequences found in the cell sample). We calculated this using several simplifying assumptions. First, we assumed that all receptors were present at equal frequency within a given T cell subpopulation. Based on the results our diversity measurements of highly diverse naïve samples, we estimated that the maximal measurable diversity in a sample of n cells was n/2.5. Finally, we assumed that if the number of a specific subpopulation of cells in a 1.5 mL blood volume was close to the diversity of that population, that the actual diversity seen in 1.5 mL would be reduced due to sampling, according to the Poisson distribution. We therefore plotted the diversity of each subpopulation as the smallest of the three values n/2.5; d; or [(n/2.5)+d]/3, where n=number of cells of that subpopulation in a 1.5 mL blood volume, and d=maximum measured sequence diversity of that subpopulation in a sample of any size. Sequences within subpopulations are depicted as non-overlapping; sequencing experiments suggest that this is largely the case with clone nucleotide sequences (references 43-45) but was not directly verified in our study. Dashed lines indicate total cell number and total TCR repertoire diversity within the 1.5 mL blood sample. The two plots are for representative subjects from the pre-specified comparison group who are either HIV-uninfected (A) or HIV-infected (B). Plots for all subjects in the pre-specified comparison groups are available as Supplementary Material. All plots use identical scales for cell number and TCR diversity. C. Correlation between subpopulation and sum blood measurements. For all subjects in the pre-specified comparison group, the measured sum
TCR repertoire diversity in whole blood (expressed in relative Cot units, as in Figure 2) is shown on the x axis. Subpopulation TCR repertoire diversity values (sequences expected per 1.5 mL whole blood), plotted on the y axis, were calculated as the sum of each of the absolute values of the T cell subpopulations that could be evaluated. The r squared value was 0.72 (p<0.0001).
Figure 1
Figure 2
Figure 3
Figure 4
Figure 5 (Color version for internet)
Blood T cell receptor diversity decreases during the course of HIV infection but the potential for a diverse repertoire persists

Paul D. Baum, Jennifer J. Young, Diane Schmidt, Qianjun Zhang, Rebecca Hoh, Michael Busch, Jeffrey Martin, Steven Deeks and Joseph M. McCune

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