Peripheral Blood CCR4+CCR6+ and CXCR3 +CCR6+ CD4+ T Cells Are Highly Permissive to HIV-1 Infection

Annie Gosselin, Patricia Monteiro, Nicolas Chomont, Felipe Diaz-Griffero, Elias A. Said, Simone Fonseca, Vanessa Wacleche, Mohamed El-Far, Mohamed-Rachid Boulaskell, Jean-Pierre Routy, Rafick-Pierre Sekaly and Petronela Ancuta

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Supplementary Material

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References

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Peripheral Blood CCR4⁺CCR6⁺ and CXCR3⁺CCR6⁺ CD4⁺ T Cells Are Highly Permissive to HIV-1 Infection

Annie Gosselin,*,+,*‑1 Patricia Monteiro,*,+,*‑1 Nicolas Chomont,*,+,*‑1 Elias A. Said,*,+,*‑1 Simone Fonseca,*,+,*‑1 Vanessa Wacleche,*,+,*‑1 Mohamed El‑Far,*,+,*‑1 Jean‑Pierre Routy,*,+,*‑1 Rafick‑Pierre Sekaly,*,+,*‑1‡ and Petronela Ancuta*,+,*‑1‡

There is limited knowledge on the identity of primary CD4⁺ T cell subsets selectively targeted by HIV‑1 in vivo. In this study, we established a link between HIV permissiveness, phenotype/homing potential, and lineage commitment in primary CD4⁺ T cells. CCR4⁺CCR6⁺, CCR4⁺CCR6⁺, CXCR3⁺CCR6⁺, and CXCR3⁺CCR6⁺ T cells expressed cytokines and transcription factors specific for Th17, Th2, Th1Th17, and Th1 lineages, respectively. CCR4⁺CCR6⁺ and CXCR3⁺CCR6⁺ T cells expressed the HIV coreceptors CCR5 and CXCR4 and were permissive to R5 and X4 HIV replication. CCR4⁺CCR6⁺ T cells expressed CXCR4 but not CCR5 and were permissive to X4 HIV only. CXCR3⁺CCR6⁺ T cells expressed CCR5 and CXCR4 but were relatively resistant to R5 and X4 HIV in vitro. Total CCR6⁺ T cells compared with CCR6⁺ T cells harbored higher levels of integrated HIV DNA in treatment‑naive HIV‑infected subjects. The frequency of total CCR6⁺ T cells and those of CCR4⁺CCR6⁺ and CXCR3⁺CCR6⁺ T cells were diminished in chronically infected HIV‑positive subjects, despite viral‑suppressive therapy. A high‑throughput analysis of cytokine profiles identified CXCR3⁺CCR6⁺ T cells as a major source of TNF‑α and CCL20 and demonstrated a decreased TNF‑α/IL‑10 ratio in CXCR3⁺CCR6⁺ T cells. Finally, CCR4⁺CCR6⁺ and CXCR3⁺CCR6⁺ T cells exhibited gut‑ and lymph node‑homing potential. Thus, we identified CCR4⁺CCR6⁺ and CXCR3⁺CCR6⁺ T cells as highly permissive to HIV replication, with potential to infiltrate and recruit more CCR6⁺ T cells into anatomic sites of viral replication. It is necessary that new therapeutic strategies against HIV interfere with viral replication/persistence in discrete CCR6⁺ T cell subsets. The Journal of Immunology, 2010, 184: 1604‑1616.
T cells is HIV-specific, depleted, or both during HIV disease progression (15). Furthermore, CCR6+ T cells likely contribute to HIV dissemination from the portal site of entry, as demonstrated by the use of microbicides interfering with the CCL20-mediated recruitment of T cells into vaginal mucosal sites (16). Together, these lines of evidence suggest that the chemokine receptors CCR3, CCR4, and CCR6, which are differentially expressed on CD4+ T cells with Th1, Th2, Th17, and Th1T7 profiles (12, 14), might also identify subsets with distinct susceptibility to HIV infection and contribution to viral pathogenesis.

To gain insights into the phenotypic and functional characteristics of CD4+ T cell subsets permissive versus resistant to HIV, we investigated the susceptibility to HIV infection of T cell subsets with differential expression of the chemokine receptors CCR4, CCRX, and CCR6. We demonstrated that CCR4+CCR6−, CCR4+CCR6+, CCRX3+CCR6+, and CCRX3+CCR6− T cell subsets expressed cytokines and transcription factors specific for Th17, Th1, Th2, and Th1T7 profiles (12, 14), might also identify subsets with distinct susceptibility to HIV infection and contribution to viral pathogenesis.

Materials and Methods

Subjects

Subjects infected with HIV-1 (n = 42) and uninfected donors (n = 19) were recruited at the McGill University Health Centre, Royal Victoria Hospital, and the Saint-Luc Hospital, Montréal, Québec, Canada, through the Fonds de la Recherche en Santé Québec/AIDS-Infectious Diseases Network (Québec, Canada). Informed consent and Internal Review Board approval were obtained from all the participants. Tables I and II summarize immunological, virological, and clinical data for recently HIV-infected treatment-naïve (RI w/o ART) and chronically infected under long-term ART (CI on ART) subjects, respectively. Subjects treated with ART received antiretroviral therapy, and cell subsets were analyzed by flow cytometry. Sorted T cell subsets were on average >95% pure as 95% pure as determined by guest on June 2, 2017 http://www.jimmunol.org/ Downloaded from http://www.jimmunol.org/ on June 2, 2017

105 cells were used for real-time PCR under conditions of virus replication in discrete CCR6+ T cell subsets. The materials and methods section of the paper includes additional details on the specific methods used for isolating and analyzing T cell subsets.

Abs and polychromatic flow cytometry analysis

Fluorochrome-conjugated Abs used for polychromatic flow cytometry analysis were Cy5-CDC3-Pacific blue (UCHT1), Cy4-Alexa Fluor 700 (RPA-T4), CD45-PE (H100), CCR4-PECy7 (1G1), CCR6-PEcy5 (1G6), CCR5-FTTCy7 (2D7), CCR7-PEcy7 (11A9), and CCRX3-PEcy5 (12G5) (BD Pharmingen, San Diego, CA). CCR4X-FTTCy7 (12G5) and CCR7X-FTTCy7 (150503) (R&D Systems, Minneapolis, MN), mouse anti-human CD28-activated CD4+ T cells. Sorted CD4+ T cell subsets were activated with immobilized CD3 and soluble CD28 Abs (1 μg/ml; R&D Systems). Cell culture supernatants were harvested every 3 d, and HIV replication was measured by HIV p24 ELISA. In parallel, cells were harvested at days 3 or 12 postinfection, or both, and cell lysates were used for real-time RT-PCR quantification of HIV DNA.

Real-time RT-PCR quantification of HIV DNA

The quantification of integrated and total HIV DNA was performed, as previously described (8, 23). Briefly, T cells were digested in a proteinase K buffer (Invitrogen, Burlington, Ontario, Canada), and 105 cells/μl lysate were used per amplification. Integrated HIV DNA was amplified first (12 cycles) using two outward-facing Alu primers and one HIV long terminal repeat (LTR) primer tagged with a φλ sequence, and the CD3 gene was amplified in the same reaction (8). The HIV and CD3 amplicons were then amplified in separate reactions (LightCycler; Roche). The HIV DNA was amplified using a β-specific primer and an inner LTR primer in the presence of two fluorescent probes specific for HIV LTR (23). The CD3 DNA was amplified using inner primers and two fluorescent probes specific for CD3 (8). Amplification reactions were carried out with Jumpstart Taq Ready Mix (Sigma-Aldrich, St. Louis, MO) and Taq Polymerase (Invitrogen). The ACH2 cells carrying one copy of integrated HIV DNA per cell (The National Institutes of Health AIDS/L行业 Program) were used as a standard curve (8). A similar method was used to quantify total HIV DNA with the appropriate primers for HIV Gag and LTR (8).

Cytokine screening and quantification

Culture supernatants were screened for the expression of 120 soluble factors using the Cytokine Antibody Arrays VI and VII (RayBiotech, Norcross, GA). Cytokine levels were further quantified by ELISA assays specific for IL-2,
subsets, including CCR4 +CXCR3 used polychromatic flow cytometry to sort memory (CD45RA 
CD45RA, as previously described (11, 14, 24). In this study, we were identified as cells lacking the expression of naive T cell 
Whether CCR4, CXCR3, and CCR6 identify subsets with distinct 
A
t)(Fig. 1 
CD4+ T cell subsets: Th17 (CCR4 +CCR6+), Th2 (CCR4 +CCR6 
CCR6 (R6) are surface markers for functionally distinct memory 
Previous studies demonstrated that CCR4 (R4), CXCR3 (X3), and 
CCR4, CXCR3, and CCR6 identify CD4+ T cell subsets with 
regression. All of the statistical analyses were performed using Prism 5 
Comparison of paired samples) as specified in the figure legends. Associations 
T cells produced IL-17 and expressed the 
CCR4+CCR6+ T cells produced IL-17 and expressed the 
IFN- 
CD4+ T cell subsets with differential expression of CCR4, 
CCR4, CXCR3, and CCR6 using a gating strategy depicted in Fig. 1 
To determine whether CCR4, CXCR3, and CCR6 identify subsets 
In contrast, the HIV coreceptor 
CXCR4 was expressed at similar levels on the four T cell subsets (Fig. 
Thus, CCR4+CCR6+, CCR4+CCR6, CXCR3+CCR6, and 
CXCR3+CCR6+ T cell subsets were enriched in markers specific for Th17, Th2, Th1Th17, and Th1 lineages, respectively, but did not express the Treg marker FoxP3.

Results
CCR4, CXCR3, and CCR6 identify CD4+ T cell subsets with distinct lineage commitment and expression of the HIV coreceptor CCR5

Previous studies demonstrated that CCR4 (R4), CXCR3 (X3), and CCR6 (R6) are surface markers for functionally distinct memory CD4+ T cell subsets: Th17 (CCR4+CCR6+), Th2 (CCR4+CCR6), Th1Th17 (CXCR3+CCR6+), and Th1 (CXCR3+CCR6+) (14). Whether CCR4, CXCR3, and CCR6 identify subsets with distinct susceptibility to HIV infection remains unknown. Memory T cells were identified as cells lacking the expression of naive T cell CD45RA, as previously described (11, 14, 24). In this study, we used polychromatic flow cytometry to sort memory (CD45RA-) CD4+ T cell subsets with differential expression of CCR4, CXCR3, and CCR6 using a gating strategy depicted in Fig. 1A and 1B. The CCR4 and CXCR3 expression distinguished four memory subsets, including CCR4+CXCR3- and CCR4+CXCR3+ subsets (Fig. 1A). The expression of CCR6 further identified CCR4+CCR6, CCR4+CCR6-, CXCR3+CCR6-, and CXCR3+CCR6- T cell subsets (Fig. 1B). Highly pure T cell subsets (Supplemental Fig. 1) were assessed for the expression of lineage-specific cytokines and transcription factors upon CD3/CD28 triggering in vitro. The CCR4+CCR6+ T cells produced IL-17 and expressed the mRNA for the Th17-specific transcription factor RORC. The CCR4+CCR6- T cells produced IL-5 and expressed the mRNA for the Th2-specific transcription factor GATA3. The CXCR3+ 

Table I. Clinical parameters of RI w/o ART subjects

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*HIV RNA copies per milliliter of plasma.
DNA were higher in CCR4+CCR6+ and CXCR3+CCR6+ T cells compared with those in CXCR3+CCR6− T cells at day 3 post-infection (Fig. 3D). Consistent with their expression of CCR4, CCR4+CCR6− T cells were highly permissive to infection with X4 HIV (Fig. 3C, 3D). Of particular interest, CXCR3+CCR6+ T cells were relatively resistant to both R5 and X4 HIV replication (Fig. 3A-D), and levels of integrated R5 and X4 HIV DNA were significantly lower compared with those of CXCR3+CCR6− T cells at days 3 and 12 postinfection (Fig. 3E, 3F) (paired t test p values < 0.05, CXCR3+CCR6+ versus CXCR3+CCR6− T cells). This difference was observed despite the fact that CXCR3+CCR6− T cells expressed moderate levels of CCR5 and CXCR4 ex vivo (Fig. 2). Also, there was no difference in CCR5 and CXCR4 expression between CXCR3+CCR6− and CXCR3+CCR6+ T cells at day 3 post-stimulation (Supplemental Fig. 2). Moreover, T cell proliferation in culture was similar in the four T cell subsets as shown by a CFSE proliferation assay (Supplemental Fig. 3). In other studies, CXCR3+ T cells were infected with two other HIV molecular clones (i.e., R5 YU2 and X4 NDK strains) and results confirmed preferential HIV replication in CXCR3+CCR6+ T cells (data not shown). These results demonstrate the following: 1) CCR4+CCR6+ and CXCR3+CCR6+ T cells were highly permissive to R5 and X4 HIV replication, 2) CCR4+CCR6− T cells are permissive to X4 but not R5 HIV strains, and 3) CXCR3+CCR6− T cells are relatively resistant to both R5 and X4 HIV replication in vitro. Considering the critical role of R5 HIV strains during natural HIV transmission (1), CCR4+CCR6+ and CXCR3+CCR6− T cells may contribute significantly to HIV disease pathogenesis in vivo.

CCR6+ T cells harbor high levels of integrated HIV DNA, and their frequency is diminished in HIV-infected subjects under ART

Previous studies demonstrated that CCR6+ T cells disappeared from the peripheral blood of HIV-infected patients as the disease progressed (15). Depletion of CCR6+ T cells in HIV-infected subjects (15) may be a consequence of their selective infection by HIV in vivo. To test this hypothesis, we quantified integrated HIV DNA levels in memory CCR6+ and CCR6− T cells and analyzed the frequency of these cells in HIV-infected and uninfected individuals. Two HIV-infected patient cohorts were available for this study: 1) RI w/o ART (n = 19) (Table I) and 2) CI on ART (n = 23) (Table II). Levels of integrated HIV DNA were quantified by real-time PCR in matched naive (CD45RA+) and memory (CD45RA−) CCR6+ and CCR6− CD4+ T cell subsets from six RI w/o ART subjects (Fig. 4A, 4B). In six out of six HIV-infected subjects tested, levels of integrated HIV DNA were higher in memory CCR6+ compared with those in CCR6− T cells (Fig. 4A). Moreover, integrated HIV DNA levels were significantly higher in memory CCR6+ compared with those in naïve CD4+ T cells (Fig. 4B). Increased levels of integrated HIV DNA in memory CCR6+ T cells coincided with a significant decrease in the frequency of CCR6+ T cells in the peripheral blood of HIV-infected patients, both RI w/o ART and CI on ART, as compared with that in uninfected controls (Fig. 4C). These results demonstrate for the first time that circulating memory CCR6+ T cells are notable cellular sites for HIV integration in vivo and suggest that depletion of these cells may be related in part to their increased susceptibility to HIV replication.

Frequency of CCR4+CCR6+ and CXCR3+CCR6+ T cells is diminished in HIV-infected subjects under viral-suppressive therapy

To investigate a potential link between HIV infection in vitro and depletion in vivo, the frequencies of CCR4+CCR6+, CCR4+CCR6−, CXCR3+CCR6+, and CXCR3+CCR6− T cells were analyzed in RI w/o ART and CI on ART HIV-infected subjects (Tables I, II) and uninfected controls. The frequencies of CCR4+CCR6+ and CXCR3+CCR6− T cell subsets were slightly but significantly decreased in CI on ART but not

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**Table II. Clinical parameters of CI on ART subjects**

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*HIV RNA copies per milliliter of plasma.
3TC, Lamivudine; ABA/ABC, Abacavir; ATA, Atazanavir; AZT, Zidovudine; D4T, Stavudine; DEL, Delavirdine; EFV, Efavirenz; IND, Indinavir; KAL, Kaletra; LOP, Lopinavir; NA, not available; NEV, Nevirapine; RIT, Ritonavir; SAQ, Saquinar; TENO, Tenofovir.
RI w/o ART HIV-infected subjects compared with those in controls (Fig. 5A), indicating that this frequency alteration occurs only later during disease progression despite viral-suppressive therapy. In addition, a longitudinal follow-up in four CI on ART subjects demonstrated persistent reduced frequencies of circulating CCR4+CCR6+ and CXCR3+CCR6+ T cell subsets despite efficient control of HIV replication and CD4 counts within a normal range ($\geq 500$ cells per microliter) under ART (Supplemental Fig. 4). However, the frequency of CXCR3+CCR6+ T cells was significantly increased in both RI w/o ART and CI on ART HIV-infected subjects compared with those in controls (Fig. 5A) and the four CI on ART subjects followed up longitudinally (Supplemental Fig. 4), which was consistent with the relative resistance of these cells to HIV infection in vitro (Fig. 3).

Unexpectedly, the frequency of CCR4+CCR6+ T cells was significantly decreased in RI w/o ART HIV-infected subjects compared with that in controls but increased compared with that in CI on ART subjects (Fig. 5A). CCR4+CCR6+ and CXCR3+CCR6+ T cell counts positively correlated with CD4 counts in CI on ART HIV-positive subjects, whereas there was a weak or not significant correlation between CD4 counts and the number of circulating CCR4+CCR6+ and CXCR3+CCR6+ T cells (Fig. 5B). Thus, ART is associated with a tendency for normalization in the frequencies of CCR4+CCR6+ and CXCR3+CCR6+ T cells in HIV-infected patients, but not CCR4+CCR6+ and CXCR3+CCR6+ T cells. Very recent studies reported a Th17/T1 switch during HIV/SIV infection (5, 28). Consistent with these studies, the ratios between CCR4+CCR6+ (Th17 profile) and CXCR3+CCR6+ (Th1 profile)
T cells and between CXCR3+CCR6+ (Th1/Th17 profile) and CXCR3+CCR6+ T cells demonstrated a preponderance of the Th1 profile in both RI w/o ART and CI on ART HIV-infected subjects compared with that in controls (Fig. 5B). Together, these results demonstrate that the frequency of circulating CCR4+CCR6+ and CXCR3+CCR6+ T cell subsets is diminished in the peripheral blood of CI subjects, despite an efficient control of HIV replication and preservation of CD4 counts under ART. Depletion of CCR4+CCR6+ and CXCR3+CCR6+ T cell subsets is likely due to their increased susceptibility to HIV infection. In contrast, depletion of CCR4+CCR6− T cells, which are infected with X4 but not R5 HIV in vitro, might be the consequence of a bystander mechanism of CD4+ T cell depletion in HIV-infected subjects, as previously documented (1, 29, 30).

CCR4+CCR6+, CCR4+CCR6−, CXCR3+CCR6+, and CXCR3+CCR6− T cells exhibit differential cytokine/chemokine profiles

To further characterize the potential roles of these four T cell subsets in HIV pathogenesis, cytokine/chemokine profiles were investigated. Culture supernatants were screened for the expression of 60 soluble factors using the Cytokine Antibody Array VI (RayBiotec) and demonstrated differential expression of IL-10, IL-5, CCL20/MIP-3a, CCL5/RANTES, and TNF-α (Fig. 6A). IL-10 was selectively produced by CCR4+CCR6− T cells, IL-5 was preferentially expressed by CCR4+CCR6− T cells, whereas IL-8 was preferentially expressed by CCR4+CCR6+ T cells (data not shown). Levels of IL-10, TNF-α, CCL3, and CCL5 were further quantified by ELISA or Cytometric Bead Array (Fig. 6B).

The production of IL-10 (a cytokine produced by different cell subsets including effector CD4+ T cells (31, 32) and a potent inhibitor of HIV replication (33–37)) was higher in CXCR3+CCR6− T cells, and TNF-α and CCL20 were produced at higher levels in CXCR3+CCR6+ T cells compared with those in the other three T cell subsets (Fig. 6A). The CCR5 binding chemokine CCL5 was expressed at high levels in CXCR3+CCR6+ and CXCR3+CCR6− T cells and low levels in CCR4+CCR6+ and CCR4+CCR6− T cells. Screening for 60 other soluble factors using the Cytokine Antibody Array VII demonstrated high production of the CCR5 ligands CCL3 and CCL4 by CXCR3+CCR6+ and CXCR3+CCR6− T cells, whereas IL-8 was preferentially expressed by CCR4+CCR6− T cells (data not shown). Levels of IL-10, TNF-α, CCL20, IL-2, CCL3, and CCL5 were further quantified by ELISA or Cytometric Bead Array (Fig. 6B).
T cells (Fig. 6C), suggesting that the balance between TNF-α and IL-10 may control the degree of permissiveness to HIV replication in these cells. CCL20 (a Th17 marker (39) and a CCR6 ligand (16, 40)) was produced at high and moderate levels by CXCR3+CCR6+ and CCR4+CCR6+ T cells, respectively, but not by CCR4+CCR6− and CXCR3+CCR6− T cells (Fig. 6B), suggesting the ability of CXCR3+CCR6+ and CCR4+CCR6+ T cells to attract other CCR6+ T cells to sites of inflammation. CCR5 binding chemokines CCL3, CCL4, and CCL5 were produced at similarly high levels by CXCR3+CCR6+ and CCR4+CCR6+ T cells but at low to undetectable levels by CCR4+CCR6− T cells to sites of inflammation. CCR5 binding chemokines CCL3, CCL4, and CCL5 were produced at similarly high levels by CXCR3+CCR6+ and CXCR3+CCR6− T cells but at low to undetectable levels by CCR4+CCR6+ and CCR4+CCR6− T cells (Fig. 6B; data not shown). Finally, IL-2 production was similarly high in CXCR3+CCR6+ and CXCR3+CCR6− T cells, and low to undetectable in CCR4+CCR6+ T cells, and low to undetectable in CXCR3+CCR6− T cells (Fig. 6B). Together, these results demonstrate distinct cytokine profiles in T cells with differential expression of CCR4, CXCR3, and CCR6 (Supplemental Fig. 5) with relevance for their role in HIV pathogenesis. These results suggest that high levels of TNF-α, CCL20, or both by CXCR3+CCR6+ and CCR4+CCR6+ T cells may contribute to the increased ability of these cells to support HIV replication and to attract other CCR6+ T cells at sites of HIV replication in vivo. In contrast, the relative resistance of CXCR3+CCR6− T cells to HIV replication might be linked to a decreased TNF-α/IL-10 ratio, a “self protection” mechanism against R5 HIV entry via autocrine production of CCR5 ligands, or both (41, 42).

**CCR4+CCR6− and CXCR3+CCR6− subsets exhibit gut- and lymph node-homing potential**

The gut and vaginal mucosa are major sites for HIV replication (43, 44). The CCR6+ T cells are attracted to these sites (40, 45) and play a critical role in HIV mucosal transmission (16, 46). In addition, recruitment of T cells into lymph nodes via CCR7 (47) significantly contributes to HIV pathogenesis (48). To further characterize the trafficking potential of CCR4+CCR6−, CCR4+CCR6+, CXCR3+CCR6+, and CXCR3+CCR6− T cells, the expression of the gut-homing α4β7 integrin (49) and the lymph node-homing chemokine receptor CCR7 (47) was analyzed on CD4+ T cell subsets from uninfected individuals. The α4 chain was similarly expressed at >95% on the four cell subsets (data not shown), whereas the β7 chain was expressed at relatively high levels on CXCR3+CCR6− T cells, moderate levels on CCR4+CCR6− and CXCR3+CCR6− T cells, and low levels on CCR4+CCR6+ T cells (Fig. 7A). CCR7 was expressed on the four cell subsets, with the highest levels detected on CCR4+CCR6− and CXCR3+CCR6− T cells (Fig. 7B). Collectively these results...
suggest that a large fraction of CXCR3+CCR6+ T cells (median of 20%) have the potential to be recruited into the gut and vaginal mucosa via 4β7 and that a considerable fraction of each of the four subsets (median 37%) are CCR7+ central memory T cells with the potential to be recruited into lymph nodes, which are major sites for HIV replication in vivo (43, 46).

**Discussion**

In this study, we revealed the distinct susceptibility to HIV infection of four CD4+ T cell subsets recently identified based on their differential expression of the homing receptors CCR4, CXCR3, and CCR6 and lineage-specific markers (Fig. 8). We demonstrated that CCR4+CCR6+ (Th17 profile) and CXCR3+CCR6+ T cells were highly permissive to R5 and X4 HIV infection, that CCR4+CCR6+ T cells (Th2 profile) were susceptible to X4 HIV replication only, and that CXCR3+CCR6+ T cells (Th1 profile) were relatively resistant to both R5 and X4 HIV replication in vitro. Circulating CCR6+ T cells harbored the highest levels of integrated HIV DNA in treatment-naive HIV-infected subjects. A high-throughput analysis of cytokine profiles identified CXCR3+CCR6+ T cells as a major source of TNF-α and CCL20 and demonstrated a low TNF-α/IL-10 ratio in CXCR3+CCR6+ T cells. Finally, we showed that CCR4+CCR6+ and CXCR3+CCR6+ T cells exhibited gut- and lymph node-homing potential. Collectively, our study identified circulating CCR4+CCR6+ and CXCR3+CCR6+ T cells as highly permissive and CXCR3+CCR6+ T cells as relatively resistant to HIV infection and demonstrated that the frequency of these subsets was significantly altered in HIV-infected subjects despite viral-suppressive ART.

Recent studies identified the chemokine receptors CCR4, CXCR3, and CCR6 as surface markers for CD4+ T cells with distinct cytokine profiles and lineage-specific transcription factor expression (12, 14, 50–52) and so established a link between CD4+ T cell trafficking potential and immunologic function. In the current study, we confirmed first that 1) CCR4+CCR6+ T cells produced IL-17 and expressed the Th17-specific transcription factor RORC, 2) CCR4+CCR6+ T cells produced IL-5 and expressed the Th2-specific transcription factor GATA3, 3) CXCR3+CCR6+ T cells produced IFN-γ and expressed the Th1-specific transcription factor T-bet, and 4) CXCR3+CCR6+ T cells produced IL-17 and IFN-γ and expressed the transcription factors T-bet and RORC. Our findings, together with those published by other groups (14, 50–52), support the idea that chemokine receptors are surface markers for CD4+ T cell subsets with distinct lineage-specific transcriptional programs.

Studies by us and others demonstrated that CCR4 expression is relatively high on T cells infected with X4 HIV in vitro (22) and that CXCR3+ T cells preferentially express the HIV coreceptor CCR5 (12). In this study, we report that CCR5 is expressed at high levels on CXCR3+CCR6+ T cells, moderate levels on CCR4+CCR6+ and CXCR3+CCR6+ T cells, and low to undetectable levels on CCR4+CCR6+ T cells. In contrast, CXCR4, the second major HIV coreceptor (25–27), was similarly expressed on these four subsets. Expression of CCR5 and CXCR4 on CCR4+CCR6+ and CXCR3+CCR6+ T cells was associated with permissiveness of these cells to R5 and X4 HIV replication in vitro, whereas CXCR4 but not CCR5 expression on CCR4+CCR6+ T cells was in line with their permissiveness to X4 but not R5 HIV strains. These

**FIGURE 4.** CCR6+ T cells harbor relatively high levels of integrated HIV DNA, and their frequency is diminished in HIV-infected subjects. A, B, Matched naive (CD45RA+) and memory (CD45RA−) CCR6+ and CCR6− T cell subsets were sorted by MACS and FACS from PBMCs of viremic treatment-naive HIV-infected subjects (Table I). Levels of integrated HIV DNA were quantified by real-time nested PCR. Shown are (A) integrated HIV DNA copy numbers per 10^6 CCR6+ and CCR6− T cells (mean ± SD of triplicate wells) and (B) relative integrated HIV DNA levels in naive and memory CCR6+ and CCR6− T cells (mean ± SD, n = 6). CD4 counts (cells per microliter), plasma viral loads (HIV RNA copies per milliliter), and paired t test p values are indicated in the figure. C, The frequency of memory CCR6+ T cells was analyzed in recently RI w/o ART (n = 18) and CI on ART (n = 20) individuals (Tables I and II) as compared with that in uninfected subjects (n = 13). Mann-Whitney U test p values are indicated in the figures. Horizontal lines indicate median values.
results are consistent with some but not all of the previous studies performed on Th2 clones (42, 53). Of particular interest, we identified CXCR3+CCR6+ T cells as relatively resistant to R5 and X4 HIV replication in vitro despite expression of both HIV coreceptors. A report identified a CCR5+CCR7+CD45RO+CD45RA+ T cell subset resistant to R5 but not to X4 HIV replication due to a postentry restriction mechanism (54). CCR5+CCR7+ T cells are phenotypically distinct from CXCR3+CCR6+ T cells, and to our best knowledge, our work is the first characterization of a primary CCR5+CXCR4+ T cell subset resistant to both R5 and X4 HIV infection. Infection by R5 HIV strains is a critical step in primary infection (44, 48, 55), whereas X4 strains emerge later during disease progression (1). Thus, CCR4+CCR6+ and CXCR3+CCR6+ T cells may contribute to the emergence of X4 HIV strains, whereas CCR4+CCR6+ and CXCR3+CCR6+ T cells may be major players during HIV infection in vivo because they are permissive to both R5 and X4 HIV strains.

The CCR6-CCL20 axis is essential for the maintenance of mucosal homeostasis (40, 56) and contributes to HIV/SIV pathogenesis (16, 28, 40, 45, 56–58). CCR6 might also mediate migration of the CCR4+CCR6+ and CXCR3+CCR6+ T cells into different peripheral tissues expressing CCL20, including the gut and vaginal mucosa, which are major sites for HIV replication in vivo (43, 59). In addition to expressing CCR6, we found that CCR4+CCR6+ and CXCR3+CCR6+ T cells selectively produce the CCR6 ligand CCL20, previously identified as a Th17 marker (39). Furthermore, we showed that CXCR3+CCR6+, CCR4+CCR6+, and CXCR3+CCR6+ T cells expressed high to moderate levels of the α4β7 integrin, which in addition to mediating gut-trafficking (60) binds R5 HIV gp120 (61). The expression of CCR5 and α4β7 integrin on CXCR3+CCR6+ T cells, and to a lesser extent on CCR4+CCR6+ T cells, may render these cells extremely prone to R5 HIV binding and subsequent replication. Thus, CCR4+CCR6+ and CXCR3+CCR6+ T cells, by their permissiveness to HIV infection and ability to produce CCL20, have the potential to recruit more CCR6+ T cells at anatomic sites of HIV replication (Fig. 8).

We demonstrated that CCR6+ T cells compared with CCR6− T cells harbored higher levels of integrated HIV DNA in HIV-infected subjects. In addition, we found that the frequency of CCR6+ T cells was significantly reduced in HIV-infected subjects, RI w/o ART and CI on ART subjects compared with that in uninfected subjects (n = 13). B. Shown are the correlations among the CCR4+CCR6+, CCR4+CCR6−, CXCR3+CCR6+, and CXCR3+CCR6− T cell counts and CD4 counts in CI on ART individuals (n = 20) (Table II). Spearman correlation p and r values and linear regression r2 values are indicated in the figure. C. The relative frequency of CCR4+CCR6+ (Th17 profile) and CXCR3+CCR6+ T cells (Th1Th17 profile) versus CXCR3+CCR6− T cells (Th1 profile) (percentage/percentage) was calculated in RI w/o ART and CI on ART HIV-infected subjects as compared with that in uninfected subjects. Mann-Whitney U test p values are indicated in the figure. Horizontal lines indicate median values.
were decreased in frequency in RI w/o ART patients compared with controls highlights the possibility that other CCR6+ T cell subsets (i.e., the yet uncharacterized CCR4+CXCR3+CCR6+ or CCR4+CXCR3+CCR6+ T cell subsets) are subject to depletion during HIV primary infection. However, a decreased frequency of circulating CCR4+CCR6+ and CXCR3+CCR6+ T cells is observed in CI subjects as reflected by our transversal and a longitudinal study. This may explain deficient immunity against M. tuberculosis (62) and C. albicans during HIV infection (63), because these T cell subsets are specific for these two pathogens (14). Also, both RI and CI HIV-positive subjects express significantly lower CCR4+CCR6+ (Th17 profile) versus CXCR3+CCR6+ (Th1 profile) and CXCR3+CCR6+ (Th1-Th17 profile) versus CXCR3+CCR6+ (Th1 profile) ratios when compared with controls, thus supporting earlier findings that CD4+ T cells in HIV-infected patients are skewed toward a Th1 phenotype to the detriment of Th17 cells (5, 28). A skewed Th17/Th1 response may lead to microbial translocation, which is a cause of chronic immune activation in HIV-infected patients (43, 59, 64).

The frequency of circulating CCR4+CCR6+ T cells was rapidly and notably decreased in HIV-infected subjects despite the fact that these cells were only permissive to X4 HIV strains that emerge later during disease progression (65). This phenomenon might be explained by either a bystander killing of CD4+ T cells in HIV-infected subjects (1, 29, 30) or a redistribution of these cells in peripheral tissues. Finally, we found an increased frequency of CXCR3+CCR6+ T cells in HIV-infected subjects compared with controls;

**FIGURE 6.** CCR4+CCR6+, CCR4+CCR6+, CXCR3+CXCR6+, and CXCR3+CCR6+ T cell subsets exhibit differential cytokine/chemokine profiles. Memory CCR4+CCR6+, CCR4+CCR6+, CXCR3+CCR6+, and CXCR3+CCR6+ T cells were stimulated via CD3/CD28 for 3 d. A, Culture supernatants were screened for 60 soluble factors using the Cytokine Antibody Array V1 (RayBiocyt). Shown are results from one experiment representative of experiments performed with cells from two different donors. B, Levels of IL-10 (n = 11), TNF-α (n = 14), CCL20/MIP-3α (n = 14), CCL3/MIP-1α (n = 6), and IL-2 (n = 12) were quantified by ELISA, whereas levels of CCL5/RANTES (n = 2) were quantified in cell supernatants by Cytometric Bead Array (mean ± SD). C, Shown are TNF-α/IL-10 ratios in CXCR3+CCR6+ and CXCR3+CCR6+ T cell subsets. Wilcoxon signed-rank test p values are indicated in the figure. Horizontal lines indicate median values.

**FIGURE 7.** CCR4+CCR6+ and CXCR3+CCR6+ T cell subsets exhibit gut- and lymph node-homing potential. Memory CCR4+CCR6+, CCR4+CCR6+, CXCR3+CCR6+, and CXCR3+CCR6+ T cells from uninfected individuals were analyzed for the expression of (A) the integrin β7 and (B) CCR7. Shown are expression values in n = 13 HIV-uninfected subjects. Wilcoxon signed-rank test p values are indicated in the figure. Horizontal lines indicate median values.
this is consistent with their resistance to R5 and X4 HIV replication in vivo. Whether CXCR3+CCR6+ T cells play a beneficial or deleterious role in HIV pathogenesis remains unknown. Overall, our findings reveal a profound alteration of CD4+ T cell heterogeneity in HIV-infected subjects despite viral-suppressive ART that might impact on the quality of T cell responses against HIV.

Successful HIV replication requires a large number of host genes (66), with cytokines and chemokines regulating the state of T cell susceptibility to HIV infection. Proinflammatory cytokines such as TNF-α trigger nuclear translocation of NF-κB, which is critical for the initiation of HIV LTR transcription (38, 67). In contrast, the immunosuppressive cytokine IL-10 negatively regulates HIV replication by interfering with CCR5 and CXCR4 expression and cell responsiveness to TCR triggering (33–36). The present study demonstrated that IFN-γ, IL-10, TNF-α, IL-2, CCL3, and CCL5 were mainly produced by CXCR3+CCR6+ and CXCR3+CCR6− T cells, whereas CCR4+CCR6+ and CCR4+CCR6− T cells were sources of IL-17 and IL-5, respectively (Supplemental Fig. 5). Of particular interest, CXCR3+CCR6− T cells were identified in this study as a major source of TNF-α, with a TNF-α/IL-10 ratio significantly higher compared with that of CXCR3+CCR6− T cells. Thus, permissiveness to HIV replication in CXCR3+CCR6+ versus CXCR3+CCR6− T cells might be controlled at least in part by the TNF-α/IL-10 balance. Other studies described a synergy between TNF-α and IL-10 (68), but its relevance for HIV replication in vivo remains unknown. Originally considered a Th2 cytokine, IL-10 is produced by a large number of cells, including Tregs (69) and Th1 and Th17 cells (31, 32, 69). The CXCR3+CCR6+ and CXCR3+CCR6− T cells lacked the expression of FoxP3 (14, 70), a transcription factor specific for Tregs. Therefore CXCR3+CCR6+ and CXCR3+CCR6− T cells resemble recently described Th1/IL-10 cells (31, 32, 69).

The CCR5 binding chemokines prevent R5 HIV gp120 binding on CCR5, therefore limiting subsequent HIV entry and replication in T cells (25, 41). Although both CXCR3+CCR6+ and CXCR3+CCR6− T cells produce CCR5 ligands, the existence of a preferential block in CCR5-mediated HIV entry (41) in CXCR3+CCR6− T cells cannot be excluded and needs to be investigated at the single-cell level. Of particular interest, CXCR3+CCR6+ and CXCR3+CCR6− T cells produced similar levels of IL-2 and exhibited a similar ability to proliferate, thus excluding the possibility that limited HIV replication in CXCR3+CCR6− T cells is related to deficient TCR engagement.

In summary, by using CCR4, CXCR3, and CXCR6 as surface markers, we identified four primary CD4+ T cell subsets as either permissive or resistant to HIV infection (Fig. 8) and revealed a profound and previously unrecognized alteration in CD4+ T cell heterogeneity in HIV-infected subjects despite undetectable viral loads and preserved CD4 cell counts under viral-suppressive ART. The CCR4+CCR6+ and CXCR3+CCR6− T cells have the potential to be recruited into the gut and vaginal mucosa as well as the brain via a CCR6-CCL20–dependent mechanism (16, 45, 71) and thus might significantly contribute to HIV dissemination and persistence by attracting other CCR6+ T cells at sites of viral replication in vivo. Our results open the path for future studies on the identification of new molecular determinants of HIV restriction in CXCR3+CCR6− T cells and may suggest new therapeutic strategies aimed at HIV eradication by interfering with HIV replication in CCR4+CCR6+ and CXCR3+CCR6− T cells.

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