Virus and host determinants of HIV-1 infection and AIDS pathogenesis
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Chapter 3

'Susceptibility of in vitro stimulated PBMC to infection with NSI HIV-1 is associated with levels of CCR5 expression and β-chemokine production'

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Cell with lower susceptibility, the expression of alleles one of HIV-1-induced transmembrane in order to undergo apoptosis, which would otherwise spread the longest (many of CCR5, CCR2a, and CCR2b were found to be inferior to the relatively silent one)[1].

In an additional investigation, CCR5 'X3E' heterozygotes, TNF-α and TNF-α receptors, and TNF-α and TNF-α receptors in wild-type CCR5 and wild-type CCR5 heterozygous blood donors, measured their dependence on CCR5 for efficient replication, excluding the dysfunctioning of other receptors as a likely explanation for reduced susceptibility of the ANVAG from individuals with a wild-type CCR5 genotype. Whether there are additional independent influences for HIV-1 that determine differences in HIV-1 infection and HIV-1 susceptibility will be the subject of future research.

From these transmembrane and from one extracellular, virus variants that replicated and/or CCR5 X3E heterozygous blood donors using PBMC were evaluated. This finding might be explained by an inability of these variants to infect these individuals. Interestingly, some of these individuals had a heterozygous CCR5 X3E genotype themselves which may have been the reason for their low infection. Infection with wild-type CCR5 and CCR5 heterozygous individuals also has been reported. This finding supports the hypothesis that CCR5 heterozygosity is a contributing factor for reduced susceptibility to HIV-1 and suggests that future investigations should be directed to the role of CCR5 heterozygosity in the susceptibility of HIV-1 to infection.

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References


Susceptibility of in vitro stimulated PBMC to infection with NSI HIV-1 is associated with levels of CCR5 expression and β-chemokine production

Susceptibility of phytohemagglutinin and recombinant interleukin-2 (PHA/rIL-2)-stimulated peripheral blood mononuclear cells (PBMC) from 14 healthy blood donors to non-syncytium-inducing (NSI) human immunodeficiency virus type 1 (HIV-1) infection was analyzed in relation to CCR5 expression and β-chemokine production. After 1 week of culture in the presence of rIL-2, but not at the moment of inoculation, CCR5 surface expression was positively and β-chemokine production inversely associated with susceptibility to NSI HIV-1 infection. Surprisingly, no association was observed between CCR5 genotype and in vitro NSI HIV-1 susceptibility, which was in agreement with similar levels of CCR5 surface expression and β-chemokine production in CCR5A32/+ and CCR5 +/A PBMC after PHA/rIL-2 stimulation. In contrast to what was observed in vitro, CCR5 genotype did associate with CCR5 surface expression levels in vivo in resting as well as in activated CD4+ T cell populations that were identified by the expression of CD45RO, CD27, HLA-DR and CD69. The association between CCR5 expression and susceptibility to infection by NSI HIV-1 in vitro, likely explains the in vivo observed protective effect of CCR5 polymorphisms that influence CCR5 expression on disease progression. Additionally, genetically based differences in the level of β-chemokine production may enhance the effect of CCR5 mutations and contribute to slow disease progression also in individuals with a wild-type CCR5 genotype.

Non-syncytium-inducing (NSI) variants of human immunodeficiency virus type-1 (HIV-1) use the β-chemokine receptor CCR5 as a cofactor for entry of target cells. The relevance of this receptor in HIV-1 infection and AIDS pathogenesis has become clear by virtue of genetic polymorphisms influencing its expression levels. In the human Caucasian population, the most prevalent polymorphism in the coding region of CCR5 is a 32-bp deletion (CCR5Δ32). Individuals homozygous for CCR5Δ32 (CCR5Δ32/Δ32), who consequently lack CCR5 cell surface expression, are protected from HIV-1 infection. However, the existence of HIV-1-infected CCR5Δ32/Δ32 individuals showed that this protection is not absolute, which might be explained by transmission of viruses that use CXCR4 as a coreceptor. CCR5Δ32 heterozygous individuals (CCR5Δ32+/Δ32) were shown not to be protected from infection, but CCR5Δ32 heterozygosity has been associated with a mean elongated AIDS-free survival period compared to individuals with the wild-type CCR5 genotype (CCR5 +/A). More recently, also other polymorphisms in the coding region and the promoter region of CCR5 have been shown to be associated with disease progression. In line with the in vivo observations, peripheral blood mononuclear cells (PBMC) from CCR5Δ32+/Δ32 individuals were shown to be less susceptible to NSI HIV-1 in vitro and in vivo in PBL-SCID mice compared to PBMC from CCR5+/+ individuals. The on average lower proportion of CCR5-expressing CD4+ T cells and lower CCR5 surface expression levels on PBMC and in PBL-SCID mice, may result in slower spread of the virus and hence explain reduced NSI HIV-1 susceptibility of PBMC and slower disease progression in CCR5Δ32+/Δ32 individuals.

An additional factor influencing HIV-1 replication is the presence of the natural ligands of CCR5: RANTES, MIP-1α, and MIP-1β. These ligands were shown to inhibit NSI replication in vitro and in vivo, and high endogenous production by PBMC and/or CD4+ T lymphocytes was associated with protection from HIV-1 infection in vivo and protection from HIV-1 disease progression. The inhibitory effect of β-chemokines is proposed to act through blocking of the coreceptor as well as through down-regulation of CCR5 on the cell surface. The relevance of β-chemokine production in HIV-1...
disease progression was recently supported by the identification of a polymorphism in the RANTES promoter that associates with reduced RANTES secretion and concomitantly with reduced CD4+ T cell decline.[296]

We here analyzed CCR5 expression levels and β-chemokine production of total PBMC and PBMC depleted of CD8+ T cells, after in vitro stimulation with PHA and rIL-2. In parallel, the susceptibility for a panel of primary NSI variants was determined and the relation with CCR5 and β-chemokine levels was studied.

MATERIALS AND METHODS

Cells and viruses. Peripheral blood mononuclear cells (PBMC) were isolated from buffy coats from 14 healthy plasmapheresis donors by ficoll-paque isolation. PBMC were stored in liquid nitrogen until usage. Three days prior to infection (t=-3) thawed PBMC (5.10^6/ml) were stimulated with phytohemagglutinin (PHA; 1 μg/ml). At the day of infection (t=0), PHA-supplemented medium was removed and replaced by fresh rIL-2-supplemented medium. At day 7, virus production was determined with an in-house dose-dilution of each virus stock and cultures were maintained for 14 days. At day 7, 1/3 of the medium was removed and replaced by fresh rIL-2-supplemented medium. At day 14, virus production was determined with an in-house p24 ELISA[394] and the 50% tissue culture infectious dose (TCID50) per ml of virus stock was determined. For each donor, the average TCID50 of 7 NSI viruses was used as a measure of NSI HIV-1 susceptibility of their PBMC and CD8+ PBMC.

CCR5 genotyping. Genomic DNA was isolated from fresh PBMC (Qiagen; Westburg, Hilden, Germany). CCR5 genotyping was performed by PCR analysis using primers flanking the 32-bp deletion in CCR5[395].

FACS analysis. Prior to stimulation (t=-3), after PHA stimulation, (i.e., just before inoculation; t=0), and after 6 days of mock-infection in the presence of rIL-2 (t=6), cells were stained with a combination of monoclonal antibodies (mAbs) directed against CD4 (-TC; Caltag, Burlingam, CA) and CCR5 (5G7-FITC; Pharmingen, San Diego, CA). Since after 1 week of culture the proportion of viable CD4+ T cells decreases rapidly (unpublished observation), and hence most of the viral spread through the culture will occur during the first week, no analysis was performed on cells during the second week of the culture period. To monitor the efficiency of CD8 depletion, cells were stained with a combination of mAbs directed against CD3 (-PE), CD8 (-FITC), and CD4 (-TC) (all mAbs from Caltag, Burlingam, CA).

In order to determine CCR5 expression levels on in vivo activated CD4+ T cells, cryopreserved, unstimulated PBMC were stained with a combination of 1: CD4 (-PERCP; Becton Dickinson, San Jose, CA), CD45RO (-APC; Becton Dickinson), HLA-DR (-PE; Caltag), and CCR5 (5G7-FITC; Pharmingen), 2: CD4 (-PERCP; Becton Dickinson), CD45RO (-PE; DAKO, Glostrup, Denmark), CD69 (-APC; Becton Dickinson), and CCR5 (5G7-FITC; Pharmingen); 3: CD4 (-PERCP; Becton Dickinson), CD45RO (-APC; Becton Dickinson), CD27 (-FITC; CLB, Amsterdam, Netherlands), and CCR5 (5G7-PE; Pharmingen). All incubation steps were performed for 20 min at 4°C. Expression of the markers was analyzed with a FACSscan or a FACS caliber (both from Becton Dickinson).

β-Chemokine production. At t=0 and t=6, 200 μl of cell-free culture supernatant was sampled and stored at -20°C until analysis. The presence of MIP-1α, MIP-1β, and RANTES in the supernatant was determined by ELISA (R&D systems; Minneapolis, MN).

Statistical analyses. Comparisons between cells with the CCR5+/- and CCR5Δ32/Δ32 genotype, between cells with high and low susceptibility, and between total PBMC and CD8+ PBMC were made with the Student's t-test. In the cases of comparisons of β-chemokine levels, statistics were performed on the log-transformed values. The correlation between CCR5 expression and the log-transformed values of RANTES was determined with the Pearson's correlation coefficient (r). Normality of the samples was determined by the Shapiro-Wilk W test for normality. All statistical analyses were performed by the use of SPSS 7.5 for windows.
Chapter 3

Susceptibility of total PBMC and CD8+ PBMC.

Three-day PHA-stimulated PBMC and CD8+ PBMC derived from 14 healthy donors were inoculated with a panel of 7 primary NSI variants, and further cultured in the presence of rIL-2. The donors were selected based on their CCR5 genotype: 7 had the CCR5 Δ32/+ and 7 had the CCR5 +/+ genotype. After 14 days of culture, the TCID50 was determined for each virus-donor combination. Since cells from each donor were inoculated with the same stock of each virus, the differences in the virus titers are a reflection of differences in NSI HIV-1 susceptibility of the cells. Paired analysis of PBMC and CD8+PBMC showed that the susceptibility was similar in 11/14 cases (Fig. 1). For one donor the susceptibility of PBMC was higher than that of CD8+ PBMC (donor 1: average TCID50: 10^4.60 versus 10^4.22, respectively; P = 0.028). For two donors the inverse was observed, with reduced susceptible PBMC compared to CD8+PBMC (donor 7: average TCID50: 10^4.05 versus 10^4.30, respectively; P = 0.058; donor 10: average TCID50: 10^3.40 versus 10^4.25, respectively; P = 0.002). Although inter-individual differences in susceptibility were observed, these differences were not related to differences in CCR5 genotype (Fig. 1).

Correlates of NSI HIV-1 susceptibility.

For the PBMC of each donor, the average TCID50 of 7 NSI variants was used as a measure for NSI HIV-1 susceptibility. In order to classify the relative NSI susceptibility of the PBMC from each of the 14 donors, the median of the 14 average TCID50 values was determined. PBMC with an average TCID50 below that of the group median were defined as having relatively low NSI HIV-1 susceptibility. PBMC with an average TCID50 equaling or above that of the group median were defined as having relatively high NSI HIV-1 susceptibility. Thus, 7 donors with less and 7 donors with more susceptible PBMC could be identified. For these 2 groups of donors, CCR5 expression prior to stimulation (t=-3) and CCR5 expression and β-chemokine production after 3 days of PHA stimulation (i.e., just prior to inoculation; t=0) were compared. In parallel cultures that were mock-infected, the CCR5 expression and β-chemokine production after further propagation in

Fig. 2. CCR5 expression on cells with high and low susceptibility for primary NSI HIV-1 infection. (a) The percentage of CCR5-expressing CD4+ T cells and (b) the mean fluorescence intensity of the CD4+ T cell population was compared for PBMC with high (●) and low (□) susceptibility. CCR5 expression was analyzed prior to stimulation and infection (t=-3), after 3 days of PHA stimulation (t=0) and after 6 days mock-infection in the presence of rIL-2 (t=6). Error bars represent the standard error of the mean. Differences were analyzed with the Student's t-test, statistical significance is indicated by * (P < 0.05).
In vitro susceptibility to NSI HIV-1 infection

Production of MIP-1α, MIP-1β, and RANTES between PBMC with relatively high and relatively low NSI HIV-1 susceptibility (Fig. 3a). After 6 days of mock-infection, the mean level of each β-chemokine was higher in the cell cultures with the lowest susceptibility (mean values: MIP-1α: 10.6 versus 2.7 ng/ml; P = 0.025; MIP-1β: 5.5 versus 2.3 ng/ml; P = 0.042; RANTES: 6.4 versus 0.6 ng/ml; P = 0.010; Fig. 3b).

Similar to what we observed for PBMC, the NSI HIV-1 susceptibility of CD8 PBMC was associated with the levels of CCR5 surface expression and β-chemokine production at t=6 (data not shown).

Association between CCR5 surface expression and β-chemokine production. Both high CCR5 surface expression and low β-chemokine production after PHA/rIL-2 stimulation (i.e., at t=6) were associated with high in vitro NSI HIV-1 susceptibility. Since it was shown previously that low CCR5 cell surface expression is associated with high β-chemokine levels, which is likely due to internalization of the receptor after chemokine binding, we analyzed the correlation between β-chemokine production and CCR5 expression, in relation to susceptibility. No (or a weak) correlation was observed between the

the presence of rIL-2 (t=6) were analyzed.

The percentage of CCR5+ cells and the mean fluorescence intensity (MFI_{CCR5}) in the CD4+ T cell population prior to stimulation and at the moment of inoculation did not differ between donors with relatively low and donors with relatively high in vitro NSI HIV-1 susceptibility (Fig. 2). However, in vitro susceptibility of PBMC was highly associated with the levels of CCR5 expression observed after 6 days of mock-infection (42 and 20% CCR5+ CD4+ T cells in PBMC with high and low susceptibility, respectively; P = 0.002; MFI_{CCR5} of 25 and 14 in PBMC with high and low susceptibility, respectively; P = 0.013; Fig. 2).

Similarly, at the end of 3-day PHA stimulation, no difference was observed in the mean production of MIP-1α, MIP-1β, and RANTES between PBMC with relatively high and relatively low NSI HIV-1 susceptibility (Fig. 3a). After 6 days of mock-infection, the mean level of each β-chemokine was higher in the cell cultures with the lowest susceptibility (mean values: MIP-1α: 10.6 versus 2.7 ng/ml; P = 0.025; MIP-1β: 5.5 versus 2.3 ng/ml; P = 0.042; RANTES: 6.4 versus 0.6 ng/ml; P = 0.010; Fig. 3b).

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percentages of CCR5* CD4* T cells and the log-transformed values of levels MIP-1α and MIP-1β after PHA/rIL-2 stimulation ($r_p = -0.455, P = 0.10$; and $r_p = -0.301, P = 0.30$, respectively; not shown). A strong inverse correlation was observed however, for the percentages of CCR5-expressing CD4* T cells and the level of RANTES production ($r_p = -0.630, P = 0.016$; Fig. 4). It is clear from Figure 4 that the PBMC with low susceptibility have both a relatively low proportion of CCR5-expressing CD4* T cells and a relatively high level of RANTES production.

**CCR5 genotype and in vitro NSI HIV-1 susceptibility.** In contrast to what was found previously by some, but in agreement with others, we did not observe that susceptibility to NSI HIV-1 infection in vitro was associated with the CCR5 genotype (Fig. 1). In order to understand the basis of this dissociation, we analyzed the association of CCR5 genotype with in vitro induced CCR5 surface expression and β-chemokine production after PHA/rIL-2 stimulation. As it was shown previously, the percentage of CCR5-expressing CD4* T cells was associated with the CCR5 genotype prior to stimulation (24% in CCR5 +/- and 14% in CCR5 Δ32/+, $P = 0.006$; Fig. 5a). However, after PHA/rIL-2 stimulation this association was lost (31% CCR5-expressing CD4* T cells both in CCR5 +/- and CCR5 Δ32/+) PBMC, $P = 0.96$; Fig. 5b).

The similar CCR5 expression levels in CCR5 +/- and CCR5 Δ32/+ cells after stimulation could be explained by an average higher up-regulation in CCR5 Δ32/+ (on average: +17%; range: +2 to +40%) compared to CCR5 +/- (on average: +7%; range: -16 to +31%) cells. Similar observations were made for CCR5 expression as measured by the MFI (not shown). In addition, no CCR5 genotype-related differences in β-chemokine production were observed after PHA/rIL-2 stimulation (mean values of 22.1 and 6.0 ng/ml for CCR5 +/- and CCR5 Δ32/+ PBMC, respectively; $P = 0.13$; Fig. 5c).

**CCR5 genotype and CCR5 surface expression on in vivo activated cells.** The absence of an association between CCR5 genotype and CCR5 expression after in vitro stimulation prompted us to study the association between CCR5 genotype and CCR5 surface expression on in vivo activated cells. To this purpose, CCR5 expression was analyzed on resting and activated CD4* T cells in unstimulated PBMC from the 14 healthy blood donors. In vivo activation was identified by cellular expression of CD45RO in the absence of CD27 expression or in combination with either HLA-DR or CD69 expression. The proportion of CCR5-expressing cells was very low within the naive CD4* T cell population (average values:
Fig. 6. Ex vivo CCR5 surface expression on resting and activated CD4+ T cell subsets. (a) The average percentage of CCR5-expressing cells in total CD4+ T cells (hatched bar) and in naive (CD), resting memory (■), and activated memory (▲) CD4+ T cells was determined. (b and c) For the resting CD4+ memory (b) and the activated CD4+ memory (c) T cells, the expression levels on CCR5 Δ32/+ and CCR5 +/+ PBMC were analyzed separately. The subsets were defined as indicated in the figures. Vertical bars (a) represent the standard error of the mean, and horizontal bars (b, c) indicate the average percentage of CCR5+ CD4+ T cells within each CD4+ T cell subset and the standard deviation. Differences were analyzed with the Student's t test.

CD45RO+/HLA-DR*: 7%, CD45RO+/CD69*: 3%; CD45RO+/CD27*: 0.7%; Fig. 6a), and not statistically different between CCR5 +/+ and CCR5 Δ32/+ PBMC (not shown). The proportion of CCR5-expressing cells was highest in the activated memory CD4+ T cells (average values: CD45RO+/HLA-DR*: 50%, CD45RO+/CD69*: 62%, CD45RO+/CD27*: 60%, fig 6a), and intermediate in the resting memory CD4+ T cells (average values: CD45RO+/HLA-DR*: 29%, CD45RO+/CD69*: 25%, CD45RO+/CD27*: 22%; Fig. 6a). The association between the level of CCR5 expression and activation status of the cells is in agreement with previous observations.

Both in the resting and in the activated memory CD4+ T cell populations, the proportion of CCR5-expressing cells (Fig. 6b and c) and CCR5 expression as measured by MFI (not shown) were on average lower in CCR5 Δ32/+ compared to CCR5 +/+ PBMC.

DISCUSSION

Susceptibility of PBMC and PBMC depleted of CD8+ T cells for in vitro NSI HIV-1 infection was associated with the expression of the coreceptor for NSI variants, CCR5, and the levels of its natural ligands, the β-chemokines, produced during culture. This association was only observed for 3-day PHA stimulated PBMC that had subsequently been cultured for 6 days in the presence of rIL-2, paralleling 6 days of infection. The absence of an association of HIV-1 susceptibility with CCR5 surface expression and β-chemokine levels immediately after 3-day PHA stimulation, so at the moment of inoculation, suggests that under the presently used conditions virus production is determined by the capacity of the virus to spread through culture, rather than by the efficiency of the initial inoculation.

In HIV-1-infected individuals in general, a correlation has been demonstrated between a CCR5Δ32 heterozygous genotype and a more benign clinical course of HIV-1 infection. This was attributed to a reduced percentage of CCR5-expressing cells, the target cells for NSI HIV-1. Indeed, early in infection the mean viral load in CCR5Δ32 heterozygotes was shown to be lower than in CCR5+/+ individuals, indicative of impaired virus replication. Here, we did not observe a correlation between CCR5 genotype and in vitro NSI HIV-1 susceptibility. This by itself was in
good agreement with the equal CCR5 surface expression in CCR5Δ32/+ and CCR5+/+ PBMC after PHA/rIL-2 stimulation. The equal CCR5 surface expression in the two genotypic groups and the absent difference in NSI HIV-1 susceptibility may however be an in vitro artefact. Indeed, in the PBL-SCID mouse model, replication of NSI HIV-1 was significantly lower in mice repopulated with PBMC from a CCR5Δ32 heterozygous donor compared to mice repopulated with CCR5+/+ PBMC. Also, as we demonstrate here, ex vivo CCR5 expression is generally lower on cells from CCR5Δ32 heterozygotes, even on CD4+ T cells with an activated phenotype, that were activated in vivo under more physiological conditions. Although the CCR5 surface expression on cells from CCR5Δ32/+ individuals is generally lower, there is a large overlap with the expression on cells from CCR5+/+ individuals. This indicates that the CCR5 surface expression is not only influenced by the CCR5Δ32 genotype but under control of multiple mechanisms. Indeed, polymorphisms in the CCR5 promotor region have been demonstrated that might influence expression levels. In addition, the natural ligands are able to down-modulate their receptor and high β-chemokine levels may consequently result in reduced CCR5 expression. In agreement with this is the inverse correlation we here observed between RANTES production and CCR5 surface expression. The down-modulation of CCR5 by RANTES may explain the association between β-chemokine production and reduced susceptibility for NSI HIV-1. In addition the β-chemokines may directly interfere with HIV-1 entry.

Our data indicate that the CCR5 expression level, and not CCR5 genotype perse, is an important determinant for NSI HIV-1 susceptibility in vitro. In agreement, we previously demonstrated that among individuals with a CCR5 +/+ genotype, a reduced CCR5 surface expression correlated with a better prognosis of HIV-1 infection. Even though CCR5 Δ32/+ individuals are generally not protected from infection, a higher frequency of CCR5Δ32/+ individuals and reduced in vitro susceptibility to HIV-1 infection was observed in uninfected monogamous sexual partners of infected individuals. This suggests that reduced susceptibility may tip the balance in favor of the exposed individuals under certain conditions. In addition, susceptibility of cells is likely to be of importance during acute infection. Individuals that subsequently progressed to AIDS had already higher CCR5 surface expression levels pre-seroconversion compared with individuals that did not progress to AIDS in the same infection period. Thus, lower CCR5 surface expression and reduced susceptibility may result in a less severe viremia early in infection and consequently in a lower viral set-point, which is associated with a better prognosis.

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Both in the resting and in the activated memory CD4+ T cell populations, the proportion of CD38-expressing cells (Fig. 5b and c) and CD27 expression as measured by MFI (not shown) were on average lower in CD95+ T cells compared to CD95- T cells.

DISCUSSION

Susceptibility of PBL and PBMC depleted of CD8+ T cells in vitro to HIV-1 infection is not associated with the expression of the CD95 or CD95L molecules.