Plasma cytokine levels during acute HIV-1 infection predict HIV disease progression

Lindi Roberts[a], Jo-Ann S. Passmore[a,b], Carolyn Williamson[a,c], Francesca Little[d], Lisa M. Bebell[c,e], Koleka Mlisana[c], Wendy A. Burgers[a], Francois van Loggerenberg[c], Gerhard Walzl[f], Joel F. Djoba Siawaya[f], Quarraisha Abdool Karim[c,e] and Salim S. Abdool Karim[c,e]

Background: Both T-cell activation during early HIV-1 infection and soluble markers of immune activation during chronic infection are predictive of HIV disease progression. Although the acute phase of HIV infection is associated with increased pro-inflammatory cytokine production, the relationship between cytokine concentrations and HIV pathogenesis is unknown.

Objectives: To identify cytokine biomarkers measurable in plasma during acute HIV-1 infection that predict HIV disease progression.

Design: Study including 40 South African women who became infected with HIV-1 and were followed longitudinally from the time of infection.

Methods: The concentrations of 30 cytokines in plasma from women with acute HIV-1 infection were measured and associations between cytokine levels and both viral load set point 12 months postinfection and time taken for CD4 cell counts to fall below 350 cells/μl were determined using multivariate and Cox proportional hazards regression.

Results: We found that the concentrations of five plasma cytokines, IL-12p40, IL-12p70, IFN-γ, IL-7 and IL-15 in women with acute infection predicted 66% of the variation in viral load set point 12 months postinfection. IL-12p40, IL-12p70 and IFN-γ were significantly associated with lower viral load, whereas IL-7 and IL-15 were associated with higher viral load. Plasma concentrations of IL-12p40 and granulocyte–macrophage colony-stimulating factor during acute infection were associated with maintenance of CD4 cell counts above 350 cells/μl, whereas IL-1α, eotaxin and IL-7 were associated with more rapid CD4 loss.

Conclusion: A small panel of plasma cytokines during acute HIV-1 infection was predictive of long-term HIV disease prognosis in this group of South African women.

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[a]Division of Medical Virology, Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, [b]National Health Laboratory Services, Cape Town, [c]Centre for the AIDS Programme of Research in South Africa, University of KwaZulu Natal, Durban, [d]Department of Statistical Sciences, University of Cape Town, Cape Town, South Africa, [e]Columbia University, New York, New York, USA, and [f]Division of Molecular Biology and Human Genetics, Stellenbosch University, Stellenbosch, South Africa.

Correspondence to Dr Jo-Ann S. Passmore, Institute of Infectious Diseases and Molecular Medicine, University of Cape Town Medical School, Anzio Road, Observatory, 7925 Cape Town, South Africa.

Tel: +27 21 406 6089; fax: +27 21 406 6681; e-mail: Jo-ann.Passmore@uct.ac.za
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Introduction

Early immune events during HIV infection are associated with the rate of subsequent disease progression [1]. Peak viremia is accompanied by immune activation and $CD4^+$ T-cell depletion, particularly from the gastrointestinal tract [2–4]. Although viral load subsequently declines, immune activation persists, viral replication continues and $CD4^+$ T cells are progressively lost [1,5]. Immune activation during HIV infection involves activation and proliferation of most immune cells, including T cells, B cells, natural killer (NK) cells and macrophages [6–9]. It also includes increased production of pro-inflammatory cytokines [4,10,11]. In the blood of acutely infected individuals, an intense pro-inflammatory cytokine 'storm' is followed by immunoregulatory cytokine production [4]. Pro-inflammatory cytokines enhance HIV replication and $CD4^+$ T-cell loss by directly promoting proviral transcription, by recruiting and activating $CD4^+$ T-cell targets for HIV infection, and by activation-induced apoptosis of bystander T cells [12–14].

Although T-cell activation during early HIV infection is known to influence subsequent disease progression [1], the relationship between plasma cytokine production during acute infection and disease prognosis has not been investigated. Biomarkers that can be used to predict the rate of HIV disease progression could be useful in the clinical management of infected individuals and for the evaluation of candidate HIV vaccines or microbicides aimed at reducing the rate of disease progression, rather than preventing infection [15,16]. Blood CD4 cell counts and viral load measurements during primary, chronic and advanced HIV infection are strongly predictive of subsequent disease progression [16–19]. However, it has been argued that coupling CD4 cell counts and viral load measurements with estimates of T-cell proliferation and activation during acute and/or chronic HIV infection could provide significantly increased predictive power [1,5,20,21]. Soluble markers of immune activation, such as tumour necrosis factor-α receptor II p75 (TNF-RII), neopterin and β_2-microglobulin, are more easily measurable in plasma samples than cellular activation and have been found to predict HIV disease progression with comparable efficiency to that with CD4 cell counts and viral load measurements [17,22,23]. Although the benefits of being able to predict, and possibly modify, disease course during early HIV infection would be substantial, the predictive value of immune activation biomarkers has largely been investigated during chronic HIV infection.

Here we have investigated the association between plasma cytokine concentrations during acute infection and established markers of long-term HIV disease progression such as CD4 cell counts and viral load measurements. We describe two models based on the easily measurable concentrations of a small number of plasma cytokines that can be used during acute infection to predict HIV disease progression.

Patients and methods

Study participants

Consenting women, recently infected with HIV-1 subtype C were recruited from HIV-negative cohorts which were screened either monthly or 3 monthly for HIV-1 infection as part of the CAPRISA 002 Acute Infection Study [24]. Time of infection was defined as the midpoint between the last HIV antibody negative test and the first HIV antibody positive test or as 14 days prior to a positive RNA PCR assay on the same day as a negative HIV enzyme immunoassay. Plasma samples from 40 women at a median of 6 weeks postinfection (range 1–12) and from 14 of these 40 women 25.5 weeks preinfection (range 2–66) were available for analysis and were included in this study. This study was approved by the University of KwaZulu Natal and the University of Cape Town Ethics Committees.

Markers of HIV-1 disease progression

Absolute blood $CD4^+$ T-cell counts (cells/μl) were measured using a FACSCalibur (BD, Franklin Lakes, New Jersey, USA) flow cytometer at regular intervals during HIV-1 infection (weekly for a month following HIV-1 infection, fortnightly for 2 months, monthly for 9 months and quarterly thereafter). Plasma HIV-1 RNA concentrations (copies/ml) were quantified using the COBAS Amplicor HIV-1 Monitor version 1.5 or COBAS Ampliprep/COBAS TaqMan 48 Analyser (Roche Diagnostics, Branchburg, New Jersey, USA). Viral load and CD4 cell count set points were defined as the average $CD4^+$ T-cell or viral load measurements of three consecutive visits between medians of 47 and 55 weeks postinfection (range 37–69 weeks) overlying the 12-month postinfection time point.

Measurement of plasma cytokines

Thirty cytokines were measured in plasma from HIV-uninfected and HIV-infected women using high-sensitivity and human cytokine LINCO*plex* kits (LINCO Research, St. Charles, Missouri, USA): interleukin (IL)-1α, IL-1β, IL-1 receptor agonist (ra), IL-2, IL-4, IL-5, IL-6, IL-7, IL-8, IL-10, IL-12p40, IL-12p70, IL-13, IL-15, IL-17, epidermal growth factor (EGF), eotaxin, fractalkine, granulocyte colony-stimulating factor (G-CSF), granulocyte–macrophage (GM)-CSF, interferon (IFN)-γ, IFN-γ-induced protein (IP)-10, monocyte chemotactic protein (MCP)-1, macrophage inflammatory protein (MIP)-1α, MIP-1β, RANTES, soluble CD40 ligand (sCD40L), transforming growth factor (TGF)-α, TNF-α and vascular endothelial growth factor (VEGF) [25]. The sensitivity of these kits ranged between

0.01 and 27 pg/ml for each of the cytokines measured. All samples were assayed concurrently, on the same plates, in order to avoid intra-assay variability. Each sample was assayed twice using separate high-sensitivity kits, and the average cytokine concentrations of the two assays were used for all analyses. Data were collected using a Bio-Plex Suspension Array Reader (Bio-Rad Laboratories Inc., Hercules, California, USA). Cytokine concentrations below the lower limits of detection were reported as the midpoint between the lowest concentration for each cytokine measured and zero [11].

Statistical analyses

Univariate analyses were performed using GraphPad Prism 5 (GraphPad Software, San Diego, California, USA). Mann–Whitney *U*-test and Wilcoxon signed rank test were used for unmatched and matched comparisons, respectively. Spearman rank tests were used to test for correlations. *P* values less than 0.05 were considered significant. *P* values were adjusted using a false discovery rate (FDR) step-down procedure [26] in order to reduce false-positive results when multiple comparisons were made.

Multivariate analyses were performed using Stata (Stata Corp., College Station, Texas, USA). A multivariate regression model was used to determine the cytokines that best predicted 12-month viral load set points. Log-transformed viral loads and cytokine concentrations were used, except for IL-12p40, which was not normalized following log transformation and was therefore included as a categorical variable [response (1) versus no response (0)]. Using univariate regression as a starting point, cytokines that were significantly associated with viral load set point, while controlling for each of the cytokines already included, were added to the model in a stepwise manner. Likelihood ratio tests were used to compare nested models. Due to the relatively small size of the study group, the sample of individuals used to develop the model included all women who were followed for at least 12 months postinfection with complete cytokine datasets ($n = 31$). Model performance evaluation was conducted by repeatedly and randomly sampling subsets ($n = 10$) consisting of three-quarters of the developmental sample and reapplying the model. The validity of the assumptions underlying the model was evaluated and outliers and influential data points were determined using an analysis of residuals. Predicted viral load set points were calculated for each study participant using the standardized β-coefficients of each of the cytokines included in the model and the observed concentrations or response of each cytokine in the following regression equation:

$$\log_{10}\lambda_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \cdots + \beta_\rho X_{\rho i}$$

where λ_i is the predicted viral load set point of the ith patient whose log-transformed cytokine concentrations or response were X_{1i}, X_{2i},..., $X_{\rho i}$.

A Cox proportional hazards model was used to determine the cytokines significantly associated with the time taken for study participant CD4 cell counts to fall below 350 cells/μl for two or more consecutive visits (survival time). Log-transformed cytokine concentrations were used, except in the case of IL-12p40. Following univariate analysis, cytokines that were significantly associated with survival time, while controlling for each of the cytokines already included, were added to the model in a stepwise manner. The likelihood ratio test was used to compare nested models and nonnested models were compared using Aikaike's information criterion (AIC), with the lowest AIC indicating the best model in terms of fit. The sample for model development included all women for whom complete cytokine datasets were obtained ($n = 35$). Model performance evaluation was conducted by repeatedly sampling three-quarter subsets ($n = 10$) of the developmental sample and reapplying the model. The validity of the assumptions underlying the model was evaluated and outliers and influential data points were determined by an analysis of residuals.

Risk scores were calculated for each participant using the β-coefficients of the Cox proportional hazards model [27] and observed concentrations or response of cytokines included in the model according to the following equation:

$$\lambda_i = \beta_1 X_{1i} + \beta_2 X_{2i} + \cdots + \beta_\rho X_{\rho i}$$

where λ_i is the risk score of the ith patient whose log-transformed cytokine concentrations or response are X_{1i}, X_{2i},..., $X_{\rho i}$. The study group was divided into three groups based on the risk scores: low risk (0–15), medium risk (15–20) and high risk (20–25).

Results

Description of study participants

Forty black women from Durban, South Africa, recently infected with HIV-1 were recruited into this study (Table 1). Most of the women were unmarried (97.5%), 20% reported having more than one partner and 35% were using injectable hormonal contraception at the time of HIV infection. Sexually transmitted infections (STIs) were common in this cohort, with 94.5% of women having been diagnosed with at least one active infection or bacterial vaginosis. The median acute infection CD4 cell count and viral load in this group of women were 477 cells/μl and 76 200 copies/ml, respectively (Table 2). The median CD4 cell count and viral load set points of women who were followed for at least 12 months postinfection were 415 cells/μl and 39 783 copies/ml, respectively.

Table 1. Demographic characteristics and prevalence of sexually transmitted infections in HIV-infected study participants.

Characteristics	Value
Number of participants	40
Age in years [median (IQR)]	25 (21–37)
Marital status [*N*/total (% of women married)]	1/40 (2.5)
Number with >1 partner [*N*/total (% of women with >1 partner)]	8/40 (20)
Contraception use [*N*/total (% of women using contraception)]	14/40 (35)
Prevalence of STIs [*N*/total (% of women with lab diagnosed STI)]	37/39 (94.5)
Prevalence of multiple STIs [*N*/total (% of women with laboratory-diagnosed multiple STIs)]	31/36 (86.1)
Trichomonas vaginalis [*N*/total (% of women PCR positive for *T. vaginalis*)]	4/36 (11.1)
Chlamydia trachomatis [*N*/total (% of women PCR positive for *C. trachomatis*)]	6/36 (16.7)
Neisseria gonorrhoea [*N*/total (% of women PCR positive for *N. gonorrhoea*)]	6/36 (16.7)
Treponema pallidum [*N*/total (% of women with detectable *T. pallidum* antibody)]	2/40 (5.0)
Shedding HSV-2 [*N*/total (% of women PCR positive for HSV-2)]	1/36 (2.8)
HSV-2 IgG [*N*/total (% of women with detectable HSV-2 antibody)]	37/40 (92.5)
Bacterial vaginosis [*N*/total (% of women gram stain positive for BV)]	27/36 (75.0)

BV, bacterial vaginosis; HSV-2, herpes simplex virus type 2; IQR, interquartile range; STI, sexually transmitted infection.

Plasma inflammatory cytokine concentrations are elevated during acute HIV-1 infection and are associated with peak viremia

Cytokine concentrations in plasma from HIV-uninfected women (median of 25.5 weeks preinfection; $n = 14$) were compared with samples from the same women recently infected with HIV-1 (median of 6 weeks postinfection; Fig. 1). Plasma concentrations of several pro-inflammatory cytokines (IL-1α, IL-1β, IL-6, TNF-α, IL-8, fractalkine, IP-10), anti-inflammatory IL-10 and T-cell homeostatic cytokines (IL-2, IL-7) were increased during acute HIV-1 infection compared with matched preinfection samples. After adjusting for multiple comparisons, IL-1α, IL-1β, TNF-α, IP-10 and IL-10 remained significantly elevated (Fig. 1a). Most cytokines (24/30) tended to be elevated during acute infection (Fig. 1b). Acute infection plasma concentrations of each of the 30 cytokines were not associated with any of the demographic characteristics listed in Table 1 (data not shown). No associations between cytokine levels and STIs were found by logistic regression analysis; however, due to the small number of women without an STI ($n = 2$) and the prevalence of multiple infections in this group of participants, a more detailed analysis in a larger cohort of women would be required to confirm these findings.

It was found that IP-10, TNF-α, IL-1α, IL-1β, IFN-γ, and IL-10 correlated with the magnitude of viral load (Fig. 2; a heat map of the association between all 30 cytokines and viral load is shown in Supplementary Fig. 1). After adjustment for multiple comparisons, IP-10 (adjusted $P = 0.012$) and TNF-α (adjusted $P = 0.0165$) concentrations remained significantly associated with viral load.

Plasma cytokine concentrations during acute HIV-1 infection predict viral load set point

Univariate regression analysis was used to determine the relationship between plasma cytokine concentrations during acute HIV-1 infection and viral load set point (Supplementary Table 1). As IL-12p70 was most strongly associated with set point in the univariate analysis, this cytokine was used as a starting point to develop a multivariate model that included the cytokines that together most strongly predicted viral load set point. Five cytokines were incorporated into this model, each of which was significantly associated with viral load set point while controlling for the other cytokines included ($P < 0.005$; Fig. 3a). A positive IL-12p40 response and higher concentrations of IL-12p70 and IFN-γ were associated with lower viral load set point, whereas higher concentrations of IL-7 and IL-15 were associated with higher set point. The model was a good fit (F statistic $P < 0.0001$) and, together, the concentrations of these five cytokines in plasma during acute infection predicted 66% (adjusted $R^2 = 0.6577$) of the variation in viral set point at 12 months postinfection.

Table 2. Clinical characteristics of study participants.

Clinical characteristics	Median (IQR)	*N*
$CD4^+$ T-cell counts		
Acute infection $CD4^+$ T-cell count (cells/μl)	477 (385–676)	40
$CD4^+$ T-cell count set point (cells/μl; average of three visits overlying 12 months postinfection)	415 (314–607)	36
Plasma viral load		
Acute infection plasma viral load (copies/ml)	76 200 (117 775–339 250)	40
Plasma viral load set point (copies/ml; average of three visits overlying 12 months postinfection)	39 783 (6613–104 825)	36

Blood $CD4^+$ T-cell counts and plasma viral loads were determined for each woman ($n = 40$) during acute HIV-1 infection. $CD4^+$ T-cell count and viral load set points were defined as the average $CD4^+$ T-cell or viral load measurements of three consecutive visits overlying the 12 months postinfection time point for each of the 36 women who were followed for at least 12 months postinfection. IQR, interquartile range.

(a)

Function	Cytokine	Median cytokine concentration (IQR; pg/ml)		Median cytokine Concentration change (IQR; pg/ml)	*P*-value
		HIV negative	HIV positive		
Inflammatory	IL-1α	65.31 (0.32-211.9)	225.80 (130.1-668.3)	119.60 (55.12-515.5)	0.0002**
	IL-1β	0.27 (0.03-0.96)	1.42 (0.79-2.08)	0.98 (0.3-1.58)	0.0012**
	IL-6	2.44 (1.42-6.15)	4.52 (2.33-10.93)	1.30 (0.06-6.75)	0.0166*
	IL-12p40	8.23 (1.97-90.99)	1.97 (1.97-96.87)	0.00 (–6.26 to –13.63)	0.6406
	IL-12p70	0.05 (0.01-0.63)	0.03 (0.01-0.46)	0.00 (–0.17 to –0.18)	0.8311
	TNF-α	2.42 (1.66-3.41)	6.60 (4.86-8.30)	3.77 (2.58-5.77)	0.0001**
Chemokines	Eotaxin	42.77 (28.99-75.68)	58.85 (37.61-84.5)	10.58 (–3.6 to –20.59)	0.1909
	Fractalkine	34.63 (18.21-61.44)	60.52 (51.06-91.56)	32.26 (–6.69 to –62.63)	0.0295*
	IL-8	1.87 (1.07-3.73)	2.61 (1.36-5.21)	0.83 (0.11-1.62)	0.0295*
	IP-10	132.40 (81.38-223.5)	555.40 (188.2-1412)	220.30 (46.73-718)	0.0046**
	MCP-1	54.50 (24.6-130)	57.34 (31.72-144.7)	1.52 (–48.28 to –52.73)	0.7148
	MIP-1α	22.83 (10.26-47.7)	30.64 (23.54-41.01)	15.89 (–3.94 to –28.59)	0.0574
	MIP-1β	21.36 (13.02-42.87)	28.07 (18.63-40.66)	9.46 (–0.41 to –15.69)	0.1763
	RANTES	484.60 (436.8-1104)	467.10 (428.3-519.9)	0.00 (–222.7 to –28.74)	0.6221
Anti-inflammatory	IL-1ra	85.47 (45.84-335.5)	134.80 (72.96-309.4)	23.62 (–49.23 to –120.2)	0.391
	IL-10	3.21 (1.66-9.17)	18.16 (10.78-35.46)	12.17 (6.34-24.2)	0.0001**
Growth factors	TGF-α	4.47 (1.83-11.92)	3.99 (2.74-9.58)	0.09 (–1.81 to –4.97)	0.5879
	EGF	18.78 (10.97-54.13)	14.29 (11.4-51.85)	–6.80 (–14.36 to –17.54)	0.5016
	VEGF	18.88 (9.38-33.7)	14.49 (6.97-45.3)	–2.79 (–14.04 to –9.06)	0.6257
Hematopoietic	IL-7	0.11 (0.05-1.04)	1.07 (0.59-2.68)	0.95 (–0.003 to –1.78)	0.0398*
	G-CSF	48.42 (25.94-108.4)	77.04 (42.64-123.4)	8.77 (–10.34 to –72.04)	0.1531
	GM-CSF	0.05 (0.01-0.35)	0.38 (0.01-1.03)	0.22 (–0.03 to –0.95)	0.083
Adaptive	sCD40L	5050.00 (2067-12601)	6713.00 (4225-10386)	–199.9 (–2012 to –4694)	0.5879
	IFN-γ	0.63 (0.01-4.87)	3.76 (2.26-9.23)	2.87 (–0.55 to –6.63)	0.1272
	IL-2	2.21 (0.46-9.86)	10.87 (5.87-16.66)	7.74 (1.44-14.64)	0.0203*
	IL-4	33.68 (4.36-67.15)	30.42 (0.86-137.60)	2.11 (–9.42 to –83.79)	0.3575
	IL-5	0.17 (0.05-0.38)	0.28 (0.10-0.53)	0.09 (–0.01 to –0.2)	0.2166
	IL-13	8.31 (0.87-23.11)	6.65 (0.13-35.86)	0.13 (–2 to –7.42)	0.4697
	IL-15	0.04 (0.04-2.5)	2.01 (0.04-3.32)	0.29 (0-2.32)	0.1289
	IL-17	3.81 (0.34-5.64)	4.30 (2.49-5.9)	1.40 (–1.14 to –3.47)	0.5186

Fig. 1. Comparison of plasma cytokine concentrations in women ($n = 14$) before infection (median 25.5 weeks preinfection) and during acute HIV-1 infection (median 6 weeks postinfection). (a) Absolute IL-1α, IL-1β, IL-6, TNF-α, IL-8, fractalkine, IP-10, IL-10, IL-7 and IL-2 concentrations were elevated in women with acute HIV-1 infection relative to concentrations before infection. Wilcoxon signed ranks test was used for matched comparisons. *P* values less than 0.05 were considered significant and highlighted. *, Did not remain significant following false discovery rate adjustment for multiple comparisons. **, Remained significant following adjustment for multiple comparisons. (b) Fold upregulation in plasma cytokine concentrations following infection.

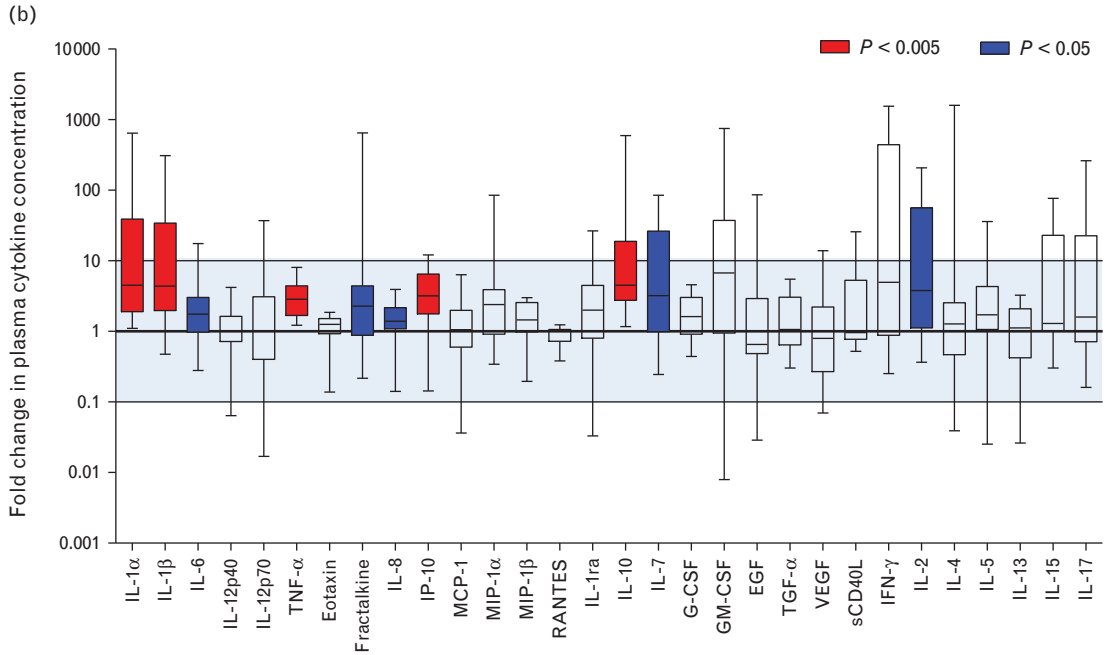

Fig. 1. (*Continued*).

The validity of the assumptions underlying the model was evaluated and outliers and influential data points were determined using an analysis of residuals. Exclusion of potential outliers from the dataset and reapplication of the model did not substantially influence the strength of the model. As the time from infection of sampling varied widely (1–12 weeks postinfection), this was included as a variable in the model. However, incorporation of time from infection did not significantly influence the strength of the model (adjusted $R^2 = 0.6435$), nor was it significantly associated with viral load set point ($P = 0.996$). Thus, the model presented does not include this variable (Fig. 3a). It was furthermore found that the concentrations of the cytokines included in the model did not demonstrate any association with timing in relation to the estimated date of infection. Upon evaluation of model performance by reapplication of the model to 10 randomly chosen three-quarter subsets of the study group, the influence of each variable on viral load set point remained statistically significant and the directionality of the relationships between the variables and set point remained constant, indicating that the model estimates are stable.

Predicted viral load set points were calculated for each study participant using the standardized β-coefficients of each of the cytokines included in the model (Fig. 3a) and the observed concentrations or response of each cytokine according to the following equation:

$$\begin{aligned}\log_{10}\ (\text{VL set point}) = {} & 10.07 + (-0.61 \\ & \times \log_{10} \text{IL-12p70}) + (0.63 \\ & \times \log10\, \text{IL-7}) + (-0.49 \\ & \times \log10\, \text{IFN-}\gamma) + (0.45 \\ & \times \log_{10} \text{IL-15}) + (-0.36 \\ & \times \text{IL-12p40 response})\end{aligned}$$

As expected, predicted viral load set points correlated well with observed set points (Fig. 3b). The model including IL-12p40, IL-12p70, IFN-γ, IL-7 and IL-15 concentrations during acute infection fitted the viral set point data of this cohort better ($R^2 = 0.6577$; $P < 0.0001$) than either acute infection viral load ($R^2 = 0.0941$; $P = 0.03$) or CD4 cell counts ($R^2 = 0.0734$; $P = 0.0577$) or the combination of both ($R^2 = 0.0800$; $P = 0.0917$). The substantially better R^2 value of the cytokine model is due in part to this model having been formulated with this cohort. Although the significance of the relationship between these cytokines and viral load set point was strongly upheld upon reapplication of the model to three-quarter subsets of the study group, assessment of the true

Fig. 1. *(Continued)* *P* values less than 0.005 remained significant following adjustment for multiple comparisons (red bars). Blue bars ($P < 0.05$) indicate cytokines that were significantly upregulated before adjustment for multiple comparisons. IQR, interquartile range.

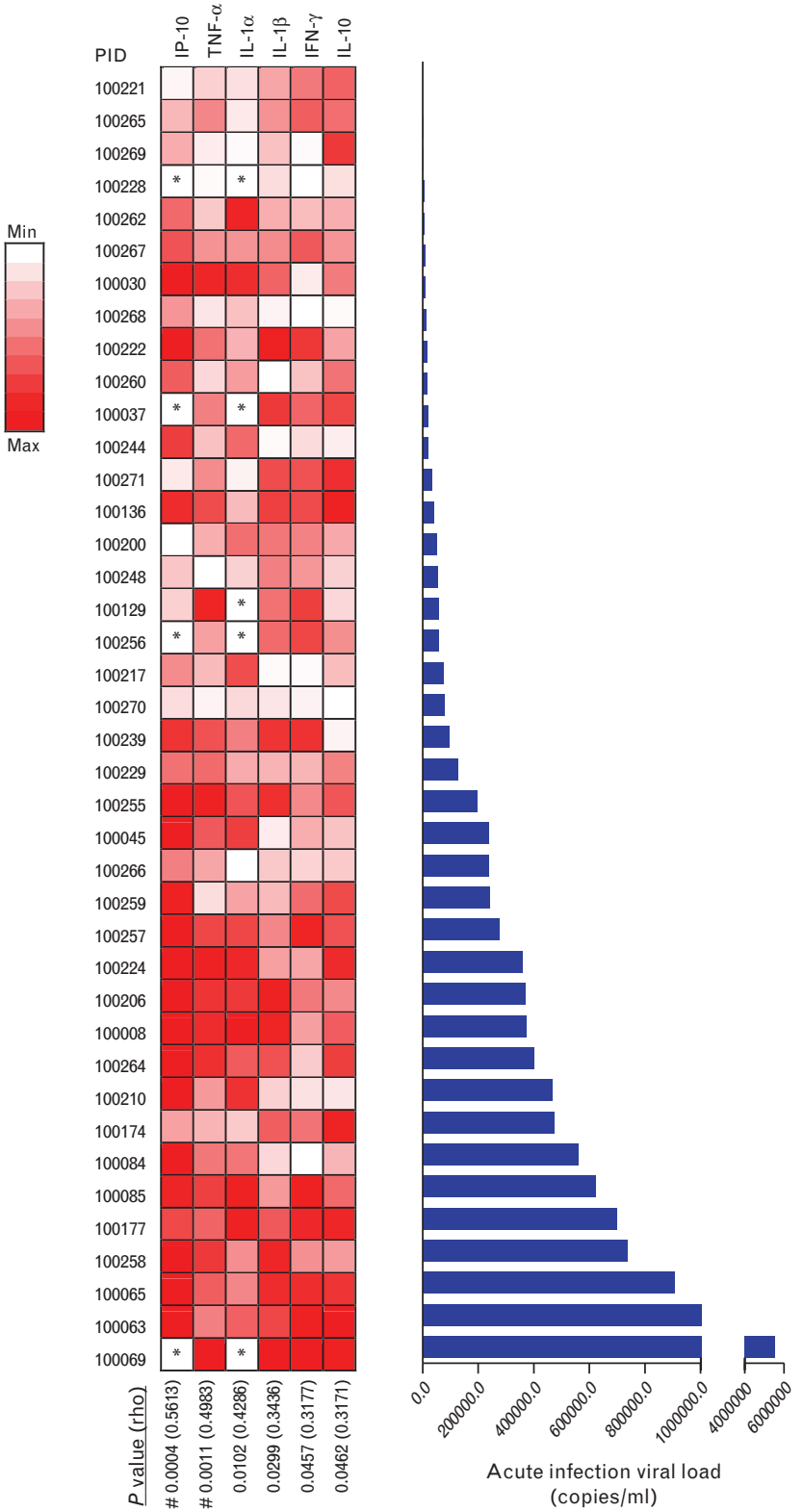

Fig. 2. Plasma inflammatory cytokine concentrations are associated with concurrent plasma viral loads in women with acute HIV-1 infection. Only cytokines that correlated significantly with viral load before adjustment for multiple comparisons are represented (*P* values and Spearman's rho values below heat map). Women are ranked according to acute infection viral load. Relative acute infection plasma cytokine concentrations of study participants are shown as a heat map, with each row representing the cytokine concentrations in an individual woman and falling alongside her viral load. For each particular cytokine, the concentrations found in this group of women were ranked and assigned an appropriate colour ranging from white

predictive power of this model would require application of the model to an entirely different, larger dataset.

Plasma cytokine concentrations during acute HIV-1 infection predict time taken for CD4 cell counts to fall below 350 cells/μl

We next determined a subset of cytokines that were most significantly associated with the time taken for participant CD4 cell counts to fall below 350 cells/μl using a Cox proportional hazards model. Using univariate survival analysis as a starting point (Supplementary Table 2), cytokines that were significantly associated with survival time were added to the model in a stepwise manner. Plasma concentrations of IL-1α, eotaxin and IL-7 were significantly associated with increased risk of CD4 loss, whereas GM-CSF and IL-12p40 were associated with reduced risk ($P < 0.05$; Fig. 4a). The model was a good fit (χ^2 test; $P < 0.0001$) and exclusion of potential outliers from the dataset and reapplication of the model did not substantially influence the strength of the model. Time (postinfection) of sampling was included in the model; however, this variable was not significantly associated with survival time ($P = 0.357$), whereas the relationships between each of the cytokines and survival time remained significant. Reapplication of the model to 10 randomly chosen three-quarter subsets of the study group revealed that model performance was good, with the directionality of the relationships between each of the variables and survival time remaining constant.

Risk scores were calculated for each participant using the β-coefficients of the Cox proportional hazards model (Fig. 4a) and observed acute infection plasma concentrations or response of each of the cytokines included in the model according to the following equation:

$$\begin{aligned}\text{risk score} = {} & 1.31(\log_{10}\text{eotaxin}) + 2.25(\log_{10}\text{IL-1}\alpha) \\ & + 0.72(\log_{10}\text{IL-7}) - 2.58 \\ & \times (\text{IL-12p40 response}) - 0.81 \\ & \times (\log_{10}\text{GM-CSF})\end{aligned}$$

HIV-1-infected participants were divided into low-risk, medium-risk or high-risk groups according to their risk scores. Women in the high-risk group ($n = 11$) experienced rapid $CD4^+$ T-cell loss to below 350 cells/μl during the study period (median time to event: 15 weeks postinfection; Fig. 4b), with the exception of a single woman who left the study at 52 weeks postinfection. Women in the low-risk group ($n = 7$) maintained CD4 cell counts above 350 cells/μl during the study (median follow-up: 76 weeks postinfection). The Cox proportional hazards model including acute infection IL-1α, eotaxin, IL-7, GM-CSF and IL-12p40 was a better model in terms of fit (AIC 85.09) when compared with models including only acute infection CD4 cell count (AIC 113.25) or viral load (AIC 124.81) or the combination of both (AIC 112.05).

Discussion

Immune activation during HIV infection has been identified as a major contributor to HIV disease progression and is the product of inflammatory responses to HIV-encoded Toll-like receptor ligands, microbial translocation and the homeostatic response to $CD4^+$ T-cell depletion [1,8,9,28,29]. Here, we propose two models, based on a restricted set of plasma cytokines measured during acute HIV-1 infection, which are useful for the prediction of viral load set point and CD4 decline. We show that concentrations of IL-7, IL-12p40, IL-12p70, IFN-γ and IL-15 during acute infection better predicted viral load set point than acute infection viral load, acute infection CD4 cell counts or the combination of both. Further, we show that plasma concentrations of IL-7, IL-12p40, IL-1α, eotaxin and GM-CSF during acute infection were strongly predictive of CD4 loss.

HIV viral loads in plasma and systemic CD4 cell counts are widely accepted predictors of HIV disease progression [16–19]. In addition, T-cell proliferative capacity and activation states during early and chronic HIV infection are predictive of disease progression [1,5,20,21]. Concentrations of soluble biomarkers such as TNF-RII, neopterin and β_2-microglobulin during chronic infection have also been shown to predict progression to AIDS and/or CD4 decline with a degree of accuracy comparable to that of CD4 cell counts and viral load measurements [17,22,23]. Although biomarkers of HIV disease progression identified during chronic infection are useful for determining rates of progression to AIDS, the ability of these markers to predict clinical course at earlier infection stages has not been tested.

We and others have shown that early HIV-1 infection is accompanied by a robust plasma pro-inflammatory cytokine response [4,11]. Here, we demonstrate that plasma immunoregulatory IL-10 and pro-inflammatory IL-1α, IL-1β, TNF-α and IP-10 were elevated in women with acute HIV-1 infection relative to preinfection. Upregulated pro-inflammatory cytokines, IP-10 and TNF-α, were significantly associated with higher HIV viral load, suggesting that the observed inflammatory cytokine 'storm' during acute infection is induced, at

Fig. 2. *(Continued)* (lowest concentration) to red (highest concentration). Repeated values were assigned the same rank and hence colour. IP-10, TNF-α, IL-1α, IL-1β, IFN-γ and IL-10 correlated with viral load. PID, patient identity number. #, IP-10 and TNF-α remained significantly correlated with viral load following adjustment for multiple comparisons. *, Not done.

(a)

Number of observations = 31

Adjusted R^2 = 0.6577

$P > F < 0.0001$

Cytokine	β-coefficient	SE	*P*	95% CI		Standard β-coefficient
Per positive response						
IL-12p40	–1.27	0.39	0.003	2.07	0.47	–0.36
Per 1 $\log_{10}$ pg/ml increase						
IL-12p70	–0.51	0.10	< 0.001	0.72	0.31	–0.61
IFN-γ	–0.38	0.09	< 0.001	0.57	0.19	–0.49
IL-7	0.73	0.15	< 0.001	0.42	1.06	0.63
IL-15	0.32	0.08	< 0.001	0.16	0.48	0.45

(b)

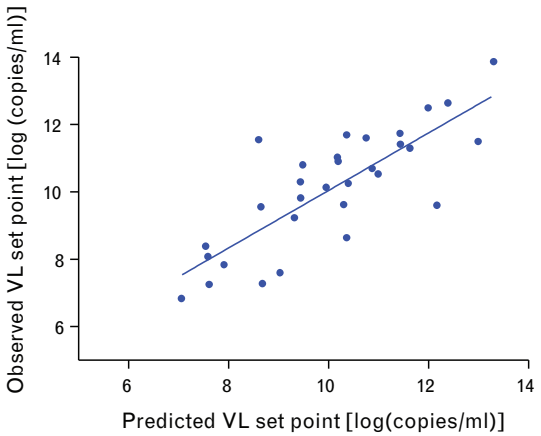

Fig. 3. Acute infection IL-12p40, IL-12p70, IFN-γ, IL-7 and IL-15 concentrations are predictive of viral load set point. (a) Each cytokine was significantly associated with viral load set point (*P* values <0.005). The model fitted the data significantly ($P > F < 0.0001$), and together the five cytokines predicted 65.77% (adjusted $R^2 = 0.6577$) of the variation in set point. (b) Set point viral loads as predicted by the model correlate with observed set point viral loads.

least in part, in response to the presence of HIV replication and products.

We found that higher concentrations of IL-12p70, IL-12p40 and IFN-γ were associated with lower viral set point, whereas IL-12p40 and GM-CSF were associated with prolonged maintenance of CD4 cell counts above 350 cells/μl. Production of these cytokines is partly regulated by a positive feedback loop, with IFN-γ and GM-CSF promoting IL-12p70 production and IL-12p70 in turn stimulating IFN-γ and GM-CSF secretion [30–33]. IL-12p70 and IFN-γ promote Th1 differentiation, favouring cell-mediated immunity and inhibiting Th2 responses [34–36]. IFN-γ has previously been identified as a correlate of better disease prognosis in HIV infection and was positively associated with $CD8^+$ T-cell and activated NK cell counts [37,38]. In simian immunodeficiency virus (SIV)-infected macaques, IL-12p70 treatment during acute infection was associated with decreased viral loads, increased $CD8^+$ NK and T cells, reduced naive $CD4^+$ T cells expressing homing markers, retention of HIV-specific cytotoxic T lymphocyte (CTL) and prolonged survival [39]. IFN-γ, GM-CSF and IL-12p40 are also principal macrophage-inducing cytokines, promoting their production, recruitment and/or activation [40–43].

In this study, elevated IL-7 and IL-15 concentrations were associated with higher viral load set point, whereas IL-7, IL-1α and eotaxin were associated with greater CD4 loss. Eotaxin and IL-1α are chemotactic for T cells, potentially recruiting targets for HIV infection [44,45]. IL-1α has additionally been found to strongly induce NF-κB activation, which binds to HIV-long terminal repeat sequences and in so doing may directly upregulate HIV replication [12,46]. IL-7 and IL-15 are the principal regulators of $CD4^+$ and $CD8^+$ T-cell homeostasis [47,48]. Picker *et al.* have proposed a model in which the balance between $CD4^+$ central memory (T_{CM}) and effector memory T cells (T_{EM}) dictates the rate of HIV disease progression [49]. T_{EM} home to effector sites and

(a)

Number of observations = 35

LR χ^2 = 32.79

$P > \chi^2 < 0.0001$

Cytokine	Hazard ratio	SE	*P*	95% CI		β-coefficient
Per positive response						
IL-12p40	0.08	0.07	0.005	0.01	0.46	–2.58
Per 1 $\log_{10}$ pg/ml increase						
GM-CSF	0.44	0.11	0.001	0.27	0.73	–0.81
IL-1α	9.49	6.03	< 0.001	2.73	32.97	2.25
Eotaxin	3.71	2.00	0.015	1.29	10.67	1.31
IL-7	2.06	0.61	0.016	1.15	3.69	0.72

(b)

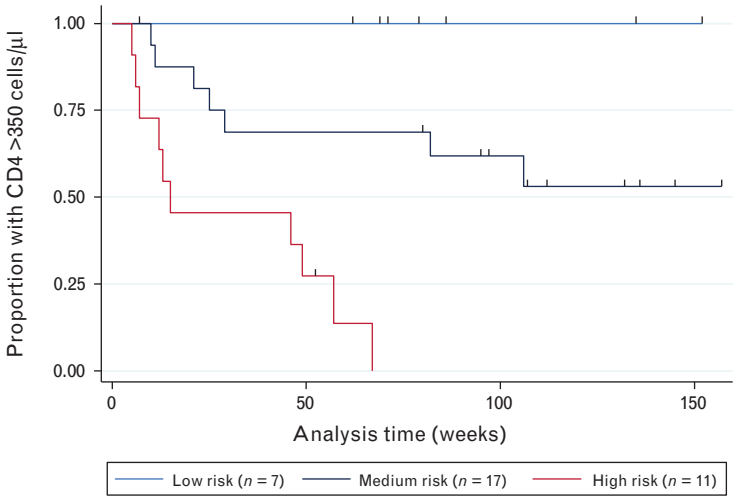

Fig. 4. Acute infection IL-12p40, GM-CSF, IL-1α, eotaxin and IL-7 concentrations were associated with the time taken for the study participant CD4 cell counts to fall below 350 cells/μl. (a) Each cytokine was significantly associated with survival time (*P* values <0.05) and the model fitted the data well ($P > \chi^2 < 0.0001$). (b) Kaplan–Meier survival estimates of women grouped according to risk score. Risk scores were calculated for each participant using the *β*-coefficients of each cytokine included in the Cox proportional-hazards model, and women were divided into low (0–15), medium (15–20) and high (20–25) risk groups based on risk scores. Women in the high-risk group experienced rapid CD4 cell count loss, whereas women in the low-risk group maintained CD4 cell counts above 350 cells/μl for the duration of follow-up. Each dash indicates a time point at which an individual woman left the study (censored event).

serve as the primary targets for HIV infection and destruction, but it appears to be their longer-lived T_{CM} precursors, which replenish these populations and decay more gradually, that determine the tempo of disease progression. Higher IL-7 levels are associated with lymphopenic states during HIV infection [9,50]. IL-7 selectively induces proliferation of naive T cells and T_{CM} cells and it has been proposed that, at high levels, IL-7 may disrupt the normal naive/memory differentiation pathway by inducing memory-like characteristics on naive cells. Exhaustion or excessive differentiation could reduce the longevity of this population, its ability to self-renew, expand and differentiate upon antigen stimulation [48]. IL-15 can induce antigen-independent proliferation and differentiation of T_{EM} from T_{CM} [48,51]. Thus, elevated IL-15 levels during early infection may accelerate the loss of T_{EM}, thereby depleting T_{CM} more rapidly. Additionally, increased IL-15 levels during acute SIV infection led to an upregulation of CD4 expression on memory $CD4^+$ T cells which increased in their susceptibility to SIV infection [52]. We recently demonstrated that a greater destruction of the $CD8^+$ T_{CM} compartment and accumulation of $CD8^+$ T_{EM} correlated with a higher viral set point [53]. This may lead to exhaustion of $CD8^+$ resources required for the control of HIV and other infections.

IL-15 has also been implicated in polyclonal B-cell activation in HIV infection [54]. Polyclonal B-cell activation and differentiation, together with the destruction of germinal centres, has recently been described in acute HIV infection [55], likely resulting in the characteristically 'delayed' antibody response to HIV. Early dysregulation of the B-cell response due to elevated IL-15 levels may lead to reduced viral control, as reflected in higher set point viral loads. Thus, memory $CD4^+$ T-cell dysfunction and depletion, $CD8^+$ T-cell exhaustion and B-cell dysfunction may partly be driven by elevated levels of IL-7 and IL-15 from the earliest stages of infection, setting the course for accelerated disease progression.

We found that anti-inflammatory IL-10 was significantly elevated during acute HIV-1 infection, was correlated directly with acute infection viral loads before adjustment for multiple comparisons and was associated with greater risk of $CD4^+$ T-cell loss in a univariate Cox survival analysis. Although IL-10 reduces HIV replication in macrophages [56], this cytokine may contribute to HIV persistence by suppressing effector T-cell responses [57–59]. In support, it has been demonstrated that serum IL-10 levels increase with disease progression in HIV-infected individuals [60]. Additionally, regulatory T cells, an important source of IL-10 [61], were shown to correlate inversely with the magnitude of SIV-specific CTL responses during acute SIV infection and may contribute to viral persistence [62].

In conclusion, we demonstrate the potential to use plasma cytokine concentrations during acute HIV-1 infection to predict subsequent disease progression. Two clusters of cytokines were more strongly predictive of viral load set point and $CD4^+$ T-cell loss than either acute infection CD4 cell counts, viral loads or both combined. The identification of cytokine biomarkers, which are indicative of early immune activation, predictive of subsequent HIV disease prognosis and can be measured directly in plasma samples from individuals with acute/early HIV infection, may inform approaches for evaluating the ability of therapeutic HIV vaccines and microbicides to control HIV infection.

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