

IMMUNE ACTIVATION AND CIGARETTE SMOKE EXPOSURE AS POTENTIAL DETERMINANTS OF FAILURE OF HAART IN THE SETTING OF MOTHER-TO-CHILD TRANSMISSION.

by

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[BSc (Hons) UL]

A DISSERTATION SUBMITTED TO THE FACULTY OF MEDICINE, UNIVERSITY OF PRETORIA, IN FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTERS OF SCIENCE.

OCTOBER 2014

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***I DEDICATE THIS DISSERTATION TO MY PARENTS, RICHARD AND
ANNAH, AND TO ALL MY FAMILY.***

SUMMARY

Persistent immune activation, even in the setting of virologically-suppressive HAART, is a hallmark of chronic immunodeficiency virus type (HIV-1) infection and a major force driving HIV-1 replication and progression to AIDS. Little is known about immune activation profiles and the effect of therapy in children infected with HIV-1 subtype C.

The objectives of this study were to i) investigate and compare levels of circulating biomarkers of immune activation in a cohort of mothers (n=46) infected with HIV-1 subtype C relative to those of 20 healthy controls; ii) compare the biomarkers of immune activation between mothers and their HIV-infected children (n=46); iii) monitor the effects of virologically suppressive and non-suppressive HAART immune activation profiles in a subgroup of children (n=28) and iv) determine the effects of active smoking as well as maternal smoking on the biomarkers of immune activation in the mothers and their children, respectively.

Multiplex bead array, ELISA and immunonephelometric procedures were used to measure plasma levels of the following biomarkers of immune activation: soluble CD14 (sCD14), beta 2 microglobulin (β 2M), C-reactive protein (CRP), interferon gamma ($\text{IFN}\gamma$), monokine induced $\text{IFN}\gamma$, $\text{IFN}\gamma$ -inducible protein 10 (IP10), tumour necrosis factor α ($\text{TNF}\alpha$), macrophage inflammatory protein α and β (MIP-1 α and β), transforming growth factor β ($\text{TGF}\beta$), interleukin-1 receptor antagonist (IL-2 Ra), granulocyte- and granulocyte macrophage colony stimulating factors (G-CSF and GM-CSF), and several interleukins including IL-2, IL-4, IL-6, IL-7, IL-8, IL-9, IL-10, IL-12, IL-13, and IL-17.

Relative to the healthy control subjects, almost all of the circulating biomarkers of immune activation, including sCD14, β 2M, CRP, MIG, IP10, $\text{IFN}\gamma$, $\text{TNF}\alpha$, $\text{TGF}\beta$ and several of the interleukins and colony stimulating factors, were elevated in the HIV-infected mothers ($P=0.0346$ - $P<0.0001$). The biomarker levels of the children were generally lower than those of the mothers with the exception of β 2M which was significantly higher ($P=0.001$). Virologically suppressive HAART caused decreases in sCD14, β 2M and MIG in a subgroup of the children ($P=0.0286$ - $P<0.0001$) while sCD14 and MIG were increased in the treatment failure groups relative to the

suppressed groups ($P=0.0407-0.0002$). An unexpectedly high number of mothers were smokers (21.7%); however no significant differences were observed between the non-smokers and smokers. In children exposed to maternal smoking, TGF β levels were higher ($P=0.0288$).

In conclusion, although somewhat lower than those of their mothers, HIV-infected children were found to have high levels of a range of circulating biomarkers of immune activation in the setting of higher viral loads. Successful HAART with virological suppression and increased levels of CD4+ T lymphocytes, was associated with significant decreases in some of the biomarkers, notably sCD14, beta 2 microglobulin and MIG, in children. Maternal smoking was associated with a significant increase in the concentration of immunosuppressive TGF β in children, however further studies in larger groups are necessary.

ACKNOWLEDGEMENTS

The writing of this dissertation has been one of the most significant academic challenges I have ever had to face. Without the support, patience and guidance of the following people, this study would not have been completed. It is to them that I owe my deepest gratitude.

- Prof AJ Theron who undertook to act as my supervisor despite her many other academic and professional commitments. Her wisdom, knowledge, commitment and patience has inspired and motivated me a lot throughout the study.
- Dr HC Steel and HM Mmakgomo for their assistance in conducting the experiments of this study, despite the work load that they were having and other commitments.
- Prof R Anderson for his constructive criticism and contributions towards the execution of the study.
- Dr TM Rossouw who generously accommodated me on the MSc project and was the main creator of the great ideas put together in this dissertation. Her great support, huge work experience and patience were necessary for finishing this thesis.
- Richard and Annah, my parents, and all my family who have always supported, encouraged and believed in me.
- Vukosi Angel, my girlfriend, without whom this effort would have been worth nothing. Your love, support and constant patience have taught me so much about sacrifice, discipline and compromise.
- Department of Medical Immunology for making it possible for me to pursue my studies.

Lastly, I owe a special thanks to Medical Research Council for financial support during the course of the study.

ABBREVIATIONS

AIDS	- Acquired immune deficiency syndrome
AZT	- Azidothymidine
CCR5	- C-C chemokine receptor type 5
cART	- Combination antiretroviral therapy
CD	- Cluster of differentiation
CMV	- Cytomegalovirus
CRF	- Circulating recombinant form
CRIs	- Co-receptors inhibitors
CTLs	- Cytotoxic T lymphocyte
CXCR4	- C-X-C chemokine receptor type 4
DNA	- Deoxyribonucleic acid
FIs	- Fusion inhibitors
HAART	- Highly active antiretroviral therapy
HCV	- Hepatitis C virus
HIV	- Human immunodeficiency virus
HLA-DR	- Human leukocyte antigen D-related
HSRC	- Human science research council
IFN	- Interferon
IL	- Interleukin
INIs	- Integrase inhibitors
LPS	- Lipopolysaccharides
LTNPs	- Long-term nonprogressor

MDM	- Monocyte-derived macrophage
MHC	- Major histocompatibility complex
MIP	- Macrophage inflammatory protein
NNRTIs	- Non-nucleoside reverse transcriptase inhibitors
NK cells	- Natural killer cells
NKT cells	- Natural killer T cells
NRTIs	- Nucleoside reverse transcriptase inhibitors
pDS	- Plasmacytoid dendritic cells
PD-1	- Programmed cell death-1
PIC	- Preintegration complex
PIs	- Protease inhibitors
RANTES	- Regulated on activation, normal T cell expressed and secreted
RNA	- Ribonucleic acid
RT	- Reverse transcriptase
SIV	- Simian immunodeficiency viruses
TGF	- Transforming growth factors
TNF	- Tumor necrosis factors
TLR	- Toll-like receptors
UNAIDS	- United Nations Programme on acquired immune deficiency syndrome
UNICEF	- United Nations International children's emergency fund
WHO	- World Health Organization

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CHAPTER 1

LITERATURE REVIEW

1.1. Literature review

1.1.1. HIV/AIDS Statistics.

Human Immunodeficiency virus (HIV) infection continues to be a major global public health issue with an estimated 35.3 million people worldwide living with the virus in 2012.^[1] An estimated 2.3 million people were newly infected with HIV, representing a 33% decline in the number of new infections worldwide, while the numbers of AIDS deaths also declined from 2001 to 2012 with 1.6 (1.4-1.9) million reported in 2012; down from 2.3 (2.1-2.6) million in 2005.^[2] These trends are depicted in Figure 1.

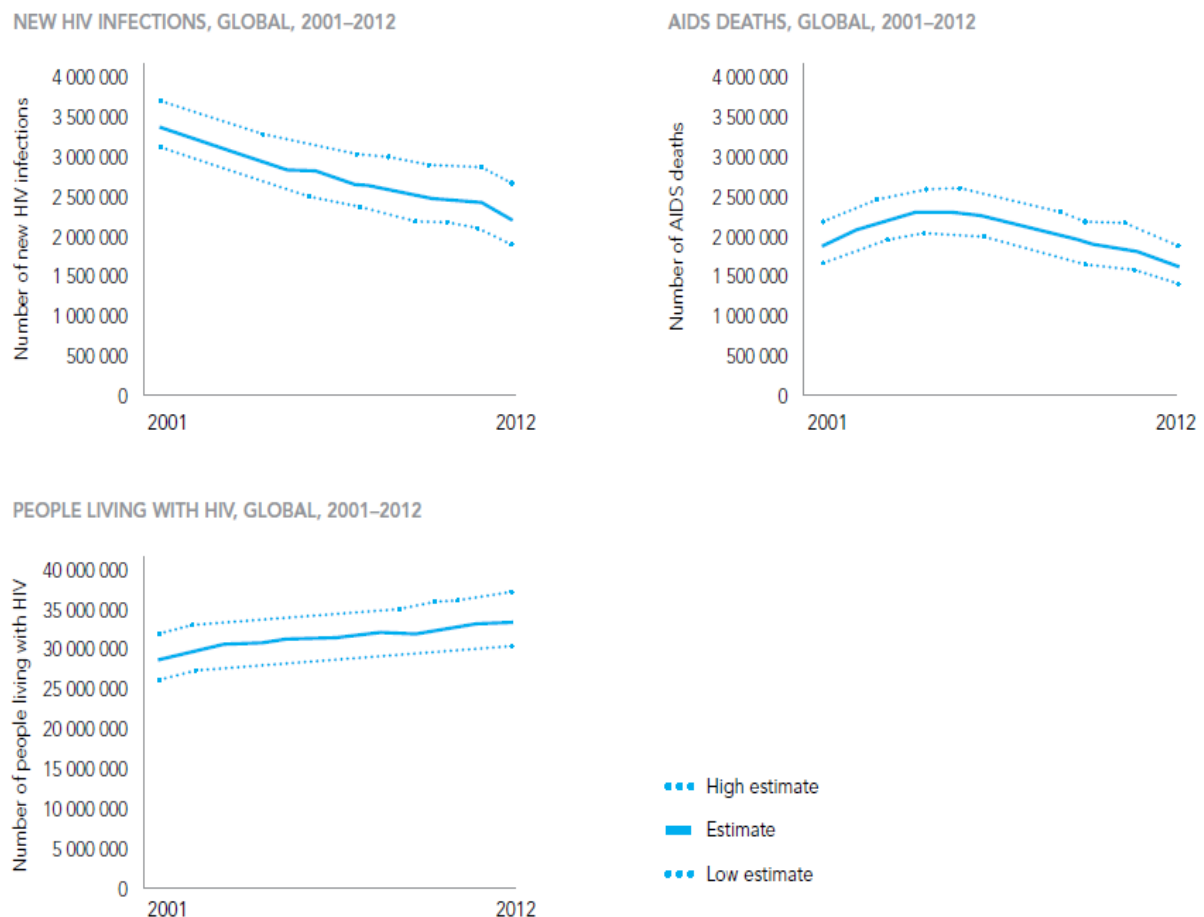
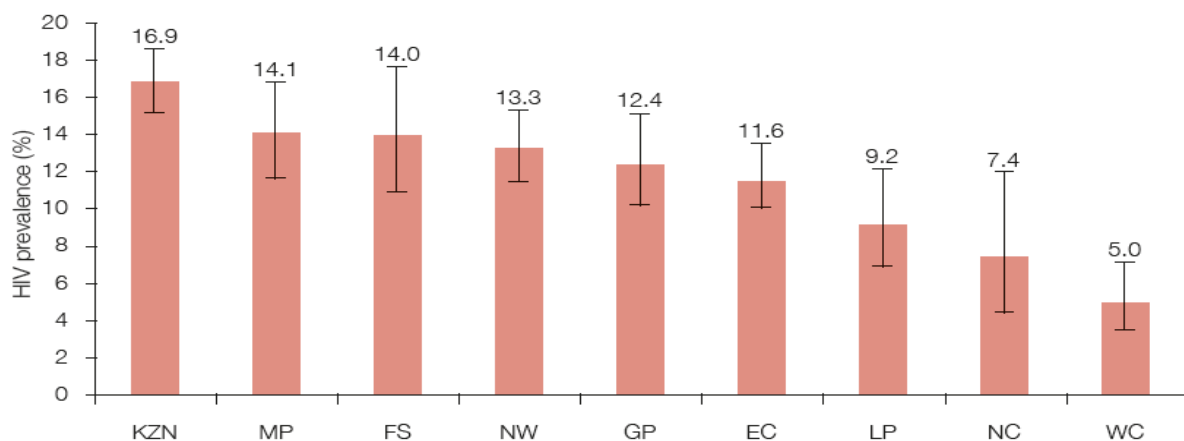


Fig 1. Numbers living with HIV, newly HIV infected, and AIDS death, 2001-2012, globally. Permission for use of figures was provided by UNAIDS (UNAIDS Report, 2013).^[2]

Sub-Saharan Africa is the most affected region with nearly 1 in every 20 adults living with HIV. Sixty nine percent of all people living with HIV, live in this region.^[1] More women than men are living with HIV in this area, and young women aged 15-24 years are as much as eight times more likely than their male counterparts to be HIV-

positive.^[3] In addition, each year around 1.5 million women living with HIV become pregnant^[4] and without antiretroviral drugs, there is a 15 to 45% chance that their child will also become HIV-infected.^[5] Mother-to-child transmission (MTCT) is when a HIV-positive mother passes the virus to her child during pregnancy, delivery or breastfeeding.^[5] In 2011, approximately 330,000 children under the age of 15 became infected with HIV and an estimated 230,000 died from HIV/AIDS.^[6] Almost all of these infections were as a result of mother-to-child transmission of children living in Sub-Saharan Africa.^[6]

The total number of people living with HIV in South Africa increased from an estimated 4 million in 2006 to 6.4 million by 2013. In a survey on HIV done in South Africa in 2012, HIV-prevalence was highest in Kwazulu-Natal, followed by Mpumalanga, Free State and then North West Province; while Western Cape, Northern Cape and Limpopo have the lowest HIV-prevalence.^[7] The overall prevalence (%) by province is shown in Fig 2.



Key: KZN – KwaZulu-Natal, MP – Mpumalanga, FS – Free State, NW – North West, GP – Gauteng, EC – Eastern Cape, LP – Limpopo, NC – Northern Cape, WC – Western Cape

Fig 2. Overall HIV prevalence by province, South Africa, 2012. Permission to use the figure was provided by HSRC.^[7]

These statistics demonstrate that the burden of HIV/AIDS is primarily in sub-Saharan Africa and even though worldwide trends of the disease seem to be decreasing, South Africa still shows increasing numbers. Although quite alarming, increased prevalence may just be an indicator that fewer people are dying from HIV-infection because of effective treatment strategies. However, the high incidence reported in the recent national HIV HSRC (Human Science Research Council) survey, may

indicate that South Africans are complacent about HIV. Worryingly, this latest survey showed plummeting condom use, increases in multiple concurrent partnerships and more boys having sex at a younger age.^[7]

1.1.2. Origin of HIV & AIDS.

HIV is a lentivirus, which mainly attacks certain cells of the immune system. Lentiviruses are in turn part of a larger group of viruses known as retroviruses. They possess a ribonucleic acid (RNA) core, encoded in the viral envelope.^[8] The first recognised cases of AIDS were officially reportedly in the 1980s. It is now generally accepted that HIV is a descendant of a simian immunodeficiency virus (SIV) because certain strains of SIV bear a very close resemblance to HIV-1 and HIV-2, the two types of HIV.^[9]

HIV-1 and HIV-2 infections cause immune suppression and progression to acquired immunodeficiency syndrome (AIDS), a condition that is accompanied by a profound decrease in the number of CD4 + T cells and characterised by the susceptibility to infection with opportunistic pathogen.^[10,11] HIV-2 infection is generally characterised by a longer asymptomatic stage, lower plasma HIV-2 viral loads, and a lower mortality rate compared with HIV-1.^[12] HIV-2 infection is endemic in West Africa and although HIV-2 has only limited spread outside this area, some sporadic cases have been reported elsewhere in Africa. The HIV-2 appears to be significantly less virulent than HIV-1.^[13]

1.1.3. Subtypes of HIV-1.

HIV-1 is characterised by extensive and dynamic genetic diversity, wherein distinct subtypes are expanding in different geographical regions.^[14] There are four major phylogenetic groups of HIV-1 variants: group M (Main), group O (Outlier), group N (non-M/non-O), and group P.^[15,16] The main group of HIV-1 variants, group M, accounts for the majority of infections in the worldwide HIV-1 epidemic and can be further subdivided into phylogenetic subtypes or clades (A to K) and circulating recombinant forms (CRFs). CRFs emerge from two different viral strains that fuse

together to form a new genetic variant or viral strain in the same individual.^[17] The average intersubtype genetic variability of the HIV-1 variant group M is 15% for the *gag* gene and 25% for the *env* gene.^[18]

The most prevalent HIV-1 genetic forms are subtypes A, B and C, where subtype C accounts for almost >80% of all HIV-1 infections worldwide.^[14] Subtype A recombinant variants are predominant in areas of central and eastern Africa (Kenya, Tanzania, Uganda and Rwanda) and in eastern European countries.^[13] Subtype B is the main genetic form in western and central Europe and North America. However, with increasing immigration and globalisation, >40% of new infections in Europe are presently non-B Africa and Asian variants.^[14] Subtype C viruses are predominant, accounting for >80% of all global HIV-1 infections. Indeed, clade C has become the epicentre of the HIV pandemic through its uncontrolled spread throughout Botswana, Zimbabwe, Malawi, Zambia, Namibia, Lesotho, South Africa, India, Nepal and China.^[19] Although the reason for the high prevalence of HIV subtype C is not known, Gordon *et al*, speculated that it may be related to host, viral, or socioeconomic factors. At the viral level it has been suggested that C viruses may be more stable, while their protease gene may have increased catalytic activity relative to the other subtypes.^[20]

1.1.4. Structure and molecular features of HIV.

HIV virions contain a virus capsid, which is composed of the following layers; *a*) the major capsid protein p24, *b*) the nucleocapsid protein p7/p9, *c*) diploid single-stranded RNA genome, *d*) the three viral enzymes, protease, reverse transcriptase (RT) and integrase. The matrix protein p17, which is located underneath the virion envelope, is the one surrounding the viral capsid.^[21]

The major viral structural proteins and enzymes are encoded by 3 different major HIV genes arranged in the orders 5'-*gag-pol-env*-3', and a series of genes, *vif*, *vpr*, *vpu*, *tat*, *rev* and *nef* encode for accessory and regulatory proteins. The first open reading frame of the *gag* gene encodes the matrix protein, p17, the major capsid, p24, and the nucleocapsid protein, p7/p9. The second open reading frame *pol* gene encodes the viral enzymes protease, reverse transcriptase and integrase.^[22,23] A

diagram of the HIV-1 genome organisation and reverse transcriptase (RT) structure is shown in Fig 3.

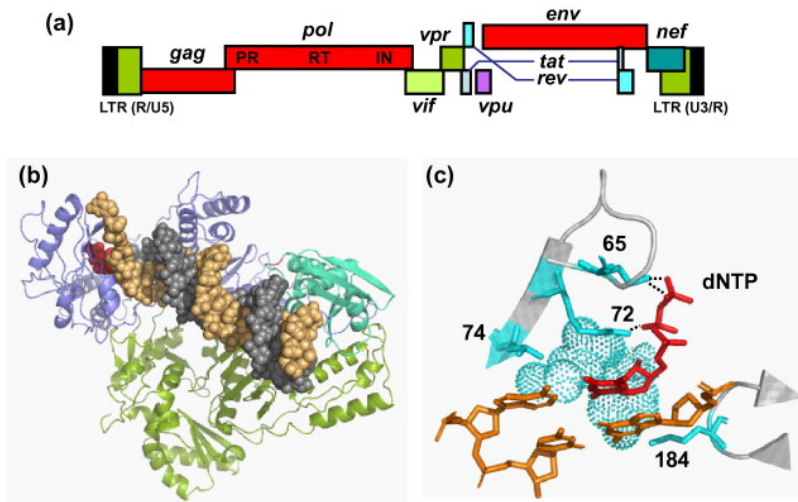


Fig.3 HIV-1 genome organisation and RT structure. (a) Major genes (*gag,pol,env*) and regulatory genes (*vif,vpr,vpu,tat,rev,nef*) in the HIV-1 genome. In the *pol* gene, antiretroviral drug targets such as protease (PR), reverse transcriptase (RT) and integrase (IN) are encoded. (b) Crystal structure of the ternary complex of HIV-1 RT, double-stranded DNA and incoming nucleotide. (c) The nucleotide binding site with the side chain of Lys⁶⁵ and Arg⁷² form a hydrogen bond with the phosphate group of the incoming nucleotide. Stick representation used to show the location of Lys⁶⁵, Arg⁷², Leu⁷⁴ and Met¹⁸⁴ (blue) and primer nucleotides (orange). Permission to use the figures was provided by Hang et al., 1998.^[24]

1.1.5.HIV entry and replication in the host cell.

The first stage of HIV-1 infection is viral attachment. On the surface of the virion, viral glycoprotein (Env) gp120 binds to the primary receptor, CD4 and co-receptor, typically either the CCR5 or CXCR4 chemokine receptors, which are present on susceptible cells such as T lymphocytes and macrophages. Subsequently, the binding of gp120 to the CD4 and co-receptor cause env gp41 to undergo a conformational change that induces fusion of the viral membrane with the target cell membrane.^[25,26]

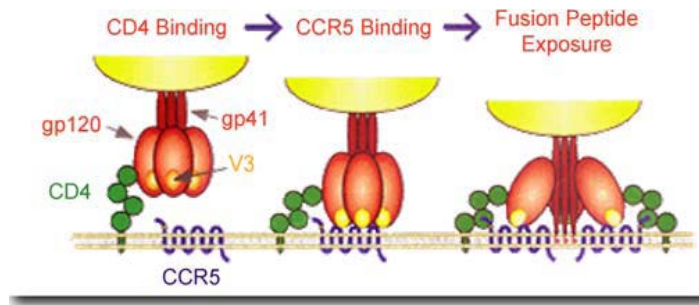


Fig 4. A representation of HIV-1 entry into target cells. Viral gp 120 binds to primary receptor CD4 and with the co-receptors CCR5 or CXCR4 in the target cell. The signal induced by the complex promotes fusion of the viral membrane to fuse with the target cell membrane. Permission to use the figure was provided by Chan *et al.*, 1998.^[25]

After attachment and fusion of the viral envelope with the target cell membrane, the viral capsid enters the cytoplasm, where it uncoats, releasing the viral genome and accessory proteins.^[27] HIV-1 envelope proteins and regulatory/accessory proteins are encoded by single and multiple spliced mRNAs.^[27] The viral enzyme reverse transcriptase transcribes the single-stranded, positive sense RNA genome of HIV-1 into a proviral DNA precursor consisting of both viral and host cellular proteins, that results in the formation of the preintegration complex (PIC). The preintegration complex (PIC) then traffics to the nucleus where the HIV-1 integrase promotes insertion of viral cDNA into the host cell genome.^[28]

In the late stage of viral life cycle, Gag and Gag-pol polyprotein precursors are synthesised and transported by an unknown mechanism to the plasma membrane. The gag protein of the retroviruses directs the assembly of the virion particles that are subsequently released from the infected cells.^[29] The assembled Gag protein complex induces membrane curvature, leading to direct formation and budding of virus-like particles.^[30] Immediately after budding, the viral protease cleaves the Gag and Gag-pol polyprotein precursors to its mature Gag and Pol proteins, resulting in the generation of mature, infectious virions which are now capable of initiating a new round of infection.^[31]

1.1.6. HIV transmission and the risk factors.

The primary method of spread of HIV infection worldwide is through sexual exposure. Globally, in the areas of highest HIV prevalence, approximately 70% of the overall sexual transmission occurs through heterosexual intercourse as the primary mode of transmission.^[32] Anal intercourse when compared with vaginal intercourse and oral intercourse, carries the highest risk of HIV transmission for both receptive and insertive partners; this may be due to the high density of lymphoid follicle target cells for HIV in rectal mucosa and it is more susceptible to abrasions than the vaginal mucosa.^[33] In addition, the risk factor is estimated to be between 5 and 18 times higher than the risk factor from receptive vaginal intercourse.^[36,37] Intravenous drug users have high rates of infection with HIV and other blood-borne viruses, such as hepatitis C virus.^[36] Risk factors of transmission include unsafe injecting practices, such as injection with a contaminated needle and sharing needles and syringes.^[37-39]

More than 3.2 million of HIV-infected positive children worldwide are infected via mother-to-child transmission, which can occur during pregnancy, delivery or breastfeeding.^[40] It has been estimated that the probability of vertical transmission during gestation and delivery in the absence of any preventive intervention ranges from 30%-45%.^[41] In South Africa, the implementation of an effective national prevention of mother-to-child transmission (PMTCT) programme has, however, decreased the transmission rates from 9.6% in 2008 to 2.8% in 2011.^[42]

A number of co-factors affect the risk of vertical transmission through breastfeeding, including duration, and pattern of breastfeeding, maternal breast health, and high HIV viral load. According to the results of two meta-analyses and a randomised control trial, the probability of mother-to-child transmission of HIV through breastfeeding ranges between 9% to 14%.^[43] This may be explained by regional differences in breastfeeding practices. Coovadia et al (2007) found that in Kwazulu Natal, South Africa 14.1% of exclusively breastfed infants were infected with HIV-1 by age 6 weeks and 19.1% by 6 months; the risk was significantly associated with maternal CD4 cell counts below 200 cells/ μ l and birth weight less than 2500g.^[44]

1.1.7. Pathogenesis of HIV-1 infection.

Once HIV infection is established, the virus replicates rapidly until viremia – the amount of circulating virus in the host’s blood – reaches a peak. This acute phase of HIV-infection persists for several weeks and is characterised by a dramatic change in peripheral CD4 counts and HIV viral load. This is followed by a stage of relative equilibrium between viral replication and the host immune response.^[45] At this stage, the immune response against HIV-1 is evident and viremia stabilizes to its set-point.^[45] This is followed by a chronic asymptomatic phase that can last for an average of a decade or more, even in the absence of treatment. CD4 cell turnover and viral replication remain active despite the relative clinical latency of HIV-infection.^[46] Unless treatment is initiated, most of the HIV-infected individuals will have progressive loss of CD4 lymphocytes and perturbation of immune functions [Figure 4]. At a level below 350 CD4+ T cells/ μ l of blood, HIV-1 infected patients can experience opportunistic infections.^[47,48] During HIV-infection, the rate of CD4 decline correlates with the level of HIV RNA in plasma, genetic and immune functions, co-infections as well as viral genetic variability, while a high viral load in plasma causes the high rapid progression to AIDS.^[49]

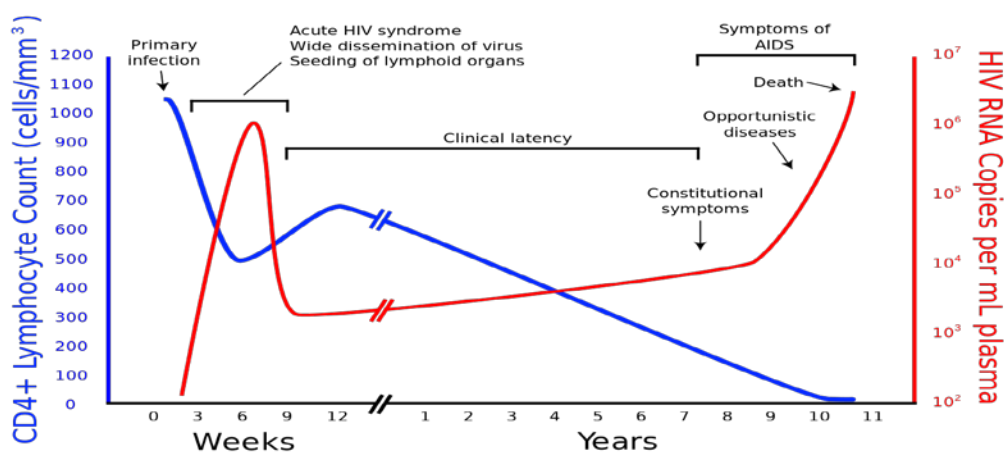


Fig 5: Typical course of HIV infection. During the early period after primary infection there is widespread dissemination of virus and a sharp decrease in the number of CD4 T cells in peripheral blood. An immune response to HIV ensues, with a decrease in viremia followed by a prolonged period of clinical latency. The CD4 T cell count continues to decrease during the following years, until it reaches a critical level below which there is a substantial risk of opportunistic infections and malignancy. Permission to use the figure was provided by Murillo, 2012.^[50]

1.1.8. Mechanism of T-cell depletion.

As compared to T-cells from HIV-uninfected individuals, several studies showed that T-cells from HIV-1 infected patients are more prone to cell death.^[51] The mechanisms leading to CD4+ T cell depletion are various and involve direct cytopathic effects of HIV-1 replication, killing by cytotoxic T lymphocytes (CTLs), effects of viral proteins and bystander apoptosis^[52,54] which will all be discussed in turn.

1.1.8.1 Direct and indirect effect of HIV-1.

Cell death is caused by the disruption of the cell membrane through the process of viral budding and/or by the cellular toxicity induced by the accumulation of RNA/DNA and protein from virus after direct infection of CD4+ T cells by HIV-1.^[55] Syncytia are giant multinucleated cells. They rapidly undergo apoptosis through the mitochondrial pathway and are hardly detectable in HIV-1 infected patients. Syncytia are formed by expression of env protein on the surface of infected cells allowing binding to cells expressing CD4 molecules through a virological synapse that leads to cell-to-cell fusion.^[56,57] The env protein can induce cell death via different mechanisms which activate the mitochondrial pathway.^[58] The Fas/Fas ligand (FasL) system is a key cellular apoptotic pathway that plays a major role in HIV-mediated cell death,^[59] and is important in regulation of lymphocyte survival and antigen-induced cell death.^[60] Infected cells, through the effect of nef, also up-regulate the expression of FasL, whereas the sensitivity of the cell to Fas-mediated apoptosis is mediated by vpu molecules. The expression of Bcl-2 in primary monocyte-derived macrophage is clearly upregulated by Tat protein. Consequently, an anti-apoptotic response by Bcl-2 may play a significant role in allowing HIV to establish a reservoir of actively replicating virus in the cells of the monocyte/macrophage lineage.^[57]

1.1.8.2. Killing by cytotoxic T lymphocytes.

Cytotoxic T lymphocyte (CTLs)-mediated killing of infected cells provide potent defences against virus infection and intracellular pathogens. However, CTLs have a

dark side — their lytic machinery can be directed against self tissues in autoimmune disorders, transplanted cells during graft rejection and host tissues to cause graft-versus-host disease, which is one of the most serious diseases related to CTL function.^[61-63] Studies have shown that as soon as 2 to 6 hours after infection, HIV-infected cells become targets for CTLs.^[64,65] The transition rate at which HIV-infected cells become recognised as target cells for CTLs is very fast and much higher than the typical decline rate of viral load after drug treatment (HAART).^[66] Interestingly, down-regulation of MHC-1 molecules on HIV-infected cells is one of the mechanisms initiated by HIV to partially evade killing by CTLs.^[67,68] The nef protein mediates the down-regulation of MHC-1 molecule which starts as early as 12 hours post-infection.^[64]

1.1.8.3. Bystander apoptosis.

Apoptosis of uninfected bystander cells is a key element of HIV pathogenesis and believed to be the driving force behind the selective depletion of CD4+ T cells leading to immunodeficiency.^[69,70] It is evident from studies over the years that direct infection is not sufficient to account for the entire loss of CD4 cells in HIV infections.^[71] Some of the key factors that regulate indirect mechanisms of bystander T cell death include the following: syncytium formation between infected and uninfected cells, triggering of apoptotic pathways in uninfected cells by soluble HIV-1 gene products or by infected macrophages expressing Fas-ligand, and cytokine dysregulation, such as overproduction of TNF- α , leading to T cell death.^[72,73]

1.1.9. Treatment of HIV/AIDS.

At this time, there is no cure for HIV/AIDS, but medications are effective in suppressing HIV replication and preventing the complications caused by immunodeficiency.^[74] In 1986, Yarchoan and his colleagues, discovered the first anti-HIV drug zidovudine (AZT), a nucleoside inhibitor of the reverse transcriptase enzyme. This drug was evaluated in a placebo-controlled clinical trial in patients with late-stage disease ^[75] in 1987 and revealed 1 death in the AZT treatment group compared to 19 deaths in the placebo group.^[76] This trial led to the implementation of

HIV treatment with a single drug, but it soon became evident that the treatment response was short-lived.

The discovery of several classes of antiretroviral drugs resulted in the successful development of combination antiretroviral therapy (cART), also known as highly active antiretroviral therapy (HAART). This therapy has resulted in a dramatic increase in the survival of HIV-infected patients, reductions in opportunistic infections, and morbidity and mortality associated with HIV infection.^[77] HAART involves the combination of three or more drugs, most commonly reverse transcriptase inhibitors with or without additional agents. The treatment is highly effective, decreasing viral replication and halting the progression of infection to AIDS and is also associated with partial restoration of the immune system.^[78]

There are currently several groups of antiretroviral drugs, targeting viral proliferation and multiplication; these are nucleoside and nucleotide reverse transcriptase inhibitors (NRTIs/NtRTIs), non-nucleoside reverse transcriptase inhibitors (NNRTIs), protease inhibitors (PIs), fusion inhibitors (FIs), co-receptors inhibitors (CRIs) and integrase inhibitors (INIs). Although these antiretroviral drugs effectively reduce HIV replication, they do not completely cure the disease.^[79-81]

The objective of developing drugs that will completely eliminate HIV has faded with the recognition of latently infected T lymphocytes with an extremely long half-life.^[82] The existence of these cellular reservoirs prevents the eradication of HIV with currently available antiretroviral therapy. As a result, HAART must be continued indefinitely to maintain virological suppression in HIV-1 infected patients.^[83]

1.1.10. HIV treatment failure.

Treatment failure occurs when HAART cannot control the HIV-infection, occurring due to poor adherence to HAART, drug resistance, poor absorption of drugs, inadequate dosing, and drug-drug interactions.^[84] It can be categorized as virological failure, immunologic failure, or clinical failure, the latter due to the occurrence of new opportunistic infections.^[84] Virologic failure is defined by persistently detectable viral loads exceeding 1000 copies/ml plasma after at least 6 months of using HAART while immunological failure occurs where there is a persistent CD4 level below 100

cell/mm³ in adults and 200 cell/mm³ or <10% in children.^[85] Limited data exist to confirm the specific threshold to define virological treatment success, (i.e., <50 copies/ml) but the benefits of viremic control are clear.^[86]

1.1.11. Drug Resistance.

Unfortunately, the effectiveness of ART can be markedly reduced by the emergence of drug resistance. Drug resistance refers to the ability of HIV to adapt (by mutation) so that the virus can survive and multiply in the presence of drugs that would normally be therapeutically effective.^[87] HIV-1 drug resistance is a major factor in the failure of ART.^[88] There are two main forms of HIV resistance. Primary or transmitted resistance occurs when an individual is infected with a strain of HIV-1 already resistant to one or more antiretroviral drugs by either a partner or a baby by its mother.^[89] Secondary or acquired resistance^[90] occurs when resistance develops while on antiretroviral therapy.^[90]

Some of the factors that play a role in the rapid and widespread emergence of resistance that is seen during HIV infection are related to the life-cycle and replication of the virus.^[87] The HIV reverse transcriptase (RT) enzyme is prone to errors when copying viral RNA into DNA. According to some estimates, HIV RT results in one error in each HIV genome per round of replication.^[87,91] translating into roughly 1 mutation for every 2000 nucleosides.^[87]

HIV also has an exceptionally high rate of replication. This high rate of replication coupled with the high rate of errors for RT means that numerous HIV “variants” are rapidly formed and propagated.^[87] Other factors that may contribute to the development of HIV drug resistance in patients taking antiretroviral treatment include lack of adherence to HIV treatment by patients and insufficient drug levels due to inferior potency, wrong dose, poor absorption, rapid clearance and/or drug interactions.^[92]

1.1.12. Immune activation.

In HIV infection the immune response is correlated with the presence of circulating chemokines and anti-inflammatory and pro-inflammatory cytokines, as well as other biochemical markers of immune activation, which differ quantitatively and qualitatively with disease progression.^[93-95] Persistent immune activation is hallmarked by activation of various cell types of the innate and adaptive immune system. This occurs, during persistent infection, when the immune system continues to respond to the virus by producing antibodies and activating killer T-cells.^[96,97] Persistent immune activation and inflammation, despite sustained HAART-mediated viral suppression, have emerged as a major challenge of the modern HIV treatment era.^[98] While immune activation, inflammatory, and coagulation markers typically decline during suppressive HAART, they remain abnormally elevated in many HIV-infected individuals and predict subsequent mortality and non-AIDS morbidities, such as cardiovascular disease.^[98]

This persistent activation is likely to be initiated predominantly at the level of innate immunity, particularly involving plasmacytoid dendritic cells (pDC) through Toll-like receptor (TLR) stimulation, involved in the activation of adaptive HIV-specific immune responses (humoral and cellular).^[99] Plasmacytoid DC act as effector cells and secrete high levels of mediators of immune activation, enhancing activation of peripheral T cells, B cells, NK cells, NKT cells and myeloid cells, as well as increasing the levels of the proinflammatory cytokines TNF, IL-6, IL-1 β and the chemokines MIP-1 α , MIP-1 β and RANTES, as well as immunosuppressive indoleamine-2,3-dioxygenase and transforming growth factor beta-1 (TGF- β 1).^[100,101]

These cytokines regulate the function of T cells by directing T cell polarization and up-regulating of expression of MHC class II and other T cell-stimulating molecules. The resultant production of pro-inflammatory cytokines, especially TNF, drives T-cell activation and activation-induced cell death.^[102-104] Replication and progression of HIV-1 to AIDS is therefore driven by excessive immune activation.^[105]

HIV-associated immune activation was first described in HIV-infected individuals with lymphadenopathy in whom there were increases in the levels of expression of markers of immune activation (HLA-DR, CD38) and proliferation (Ki-67) in both CD4⁺ and CD8⁺ T cells. A decline in circulating CD4⁺ T cell counts and development of

AIDS were associated with the increases in the numbers of HLA-DR⁺ and CD38⁺ CD8⁺ T lymphocytes.^[106]

Chronic immune activation with high production of proinflammatory cytokines characterizes the chronic phase of HIV infection,^[107,109] and is also responsible for clonal deletion^[109] and the loss of peripheral CD4 + T cells over time.^[110,111]

Several studies investigated biomarkers of immune activation in HIV infected patients. Malherbe *et al* (2014) who investigated these markers in patients with HIV-1 subtype C, found that there was increased levels of soluble CD14 (sCD14), beta-2 microglobulin (β 2M), transforming growth factor beta (TGF β), CXCL9 and CXCL10 in the HAART naïve study cohort relative to HIV uninfected controls. Soluble CD14 and β 2M are markers of cellular activation, while TGF β is an immunosuppressive cytokine.^[112] These findings were consistent with those of others who also found that β 2M was positively correlated with viral loads and inversely with CD4%.^[10,113] These biomarkers as well as others were also investigated in the study that formed part of this dissertation.

1.1.13. Possible causes of immune activation.

Microbial translocation during HIV infection was first described in 2006, when it was demonstrated that bioactive microbial products were significantly elevated in plasma from HIV-infected individuals.^[114] Microbial lipopolysaccharides (LPS) and nucleic acid directly stimulate the activation of both the innate and adaptive immune systems.^[114] During the acute phase of HIV-infection, the dysfunction of the intestinal barrier with resultant leakage of microbial products contributes to systemic immune activation^[115] and persistently high levels of plasma LPS and bacterial DNA throughout the course of the infection.^[116]

As mentioned above, HIV-1 infection induces a barrier defect of the intestinal mucosa, which is closely linked to immune activation and CD4+ T cell depletion.^[117-119] Epithelial damage may result from decreased expression of the epithelial repair tight junction gene, thereby increasing epithelial permeability.^[115] The gut mucosa is a protective barrier to harmful luminal pathogens, and also plays a major role in the absorption of nutrients. Disruption of this important barrier will therefore lead to

malabsorption and enteropathy^[120] The loss of Th17 CD4+ T cells that are normally present in the gut appears to be particularly relevant to the pathogenesis of HIV infection. Microbial translocation and impairment of Th17 function are likely to contribute to chronic immune activation.^[121]

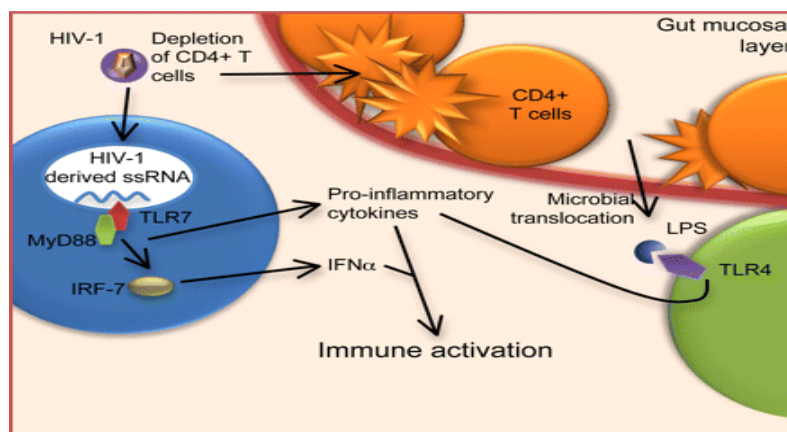


Fig 6. A representation of microbial products (LPS) leaking out of the gut due to a breach in the mucosal barrier that occurs as a result of depletion of CD4+ cells during HIV infection. Permission to use the figure was provided by Chang et al., 2008.^[122]

During HIV disease, the development of opportunistic infections may also have an impact on the disease progression to AIDS.^[123] Co-infection such as CMV (cytomegalovirus) and HCV (hepatitis C virus) is common in HIV-infected individuals. CMV-specific T cell responses are 3-5 fold higher in HIV-infected individuals than in uninfected individuals.^[124-126] Immune activation in HIV-infected patients can be reduced by using valganciclovir treatment, an antiviral medication with action against CMV and other herpes viruses.^[127]

A study recently reported by Shaun and colleagues demonstrated that even in virally suppressed individuals, HIV-specific cytotoxic T lymphocytes (CTLs) are inefficient at eliminating the infected CD4+ T cells in which HIV replication occurs.^[128] Increases in the production of proinflammatory cytokines (e.g. TNF- α , IL-1, and others) caused by non-antigen specific bystander activation of B- and T-lymphocytes, render them prone to activation-induced cell death by up-regulation of apoptosis related molecules (CD95, TRAIL, DR4/5) on the surface of T-cells.^[129,130] Dysfunctionality of the T regulatory cell subset, in comparison with other T-cell subsets, may also favour activation of Th 17 cells.^[131,133]

Apart from loss of CD4⁺ T cells, immune exhaustion also results in impairment of function of effector T cells, which become progressively less responsive, losing both their effector functions and proliferative capability due to the persistence of antigenic stimulation and inflammatory status,^[133] resulting in a progressive decrease in several T cell functions such as cytokine secretion, proliferation, and cytotoxic potential, loss of control over viral replication e.g. CMV and EBV (Epstein–Barr virus).^[134] The expression of PD-1 (Programmed cell death 1), a marker of immune exhaustion in both CD4⁺ T and CD8⁺ T cells, is associated with HIV viral load and loss of CD4⁺ T cells.^[135] A study conducted by Zhang *et al.* ^[136] has reported that in long-term nonprogressors (LTNPs), who maintain CD4⁺ T cell counts despite active viral replication, the expression of PD-1 is lower on HIV-specific CD8⁺ T cells, compared to individuals with progressive HIV-infection.

1.1.14. Consequences of cytokines on HIV-infection.

As mentioned earlier, cytokines are a family of proteins that play a role in inflammation and immune activation and in viral infection.^[137] In HIV pathogenesis, cytokines play a major role by regulating viral replication as well as orchestrating innate and adaptive immune responses.^[137] *In vitro* studies, as well as *in vivo* observations, have identified cytokines as important factors regulating the immunological and virological mechanisms involved in HIV persistence of subjects receiving suppressive HAART, resulting in a failure to completely eradicate HIV.^[138] There are two well-described barriers to HIV-eradication: (i) viral replication may occur in an anatomical reservoir inaccessible to antiretroviral drugs such as the gastrointestinal tract, lymph nodes and central nervous system; and (ii) HIV can also persist as proviral DNA in long-lived cellular reservoirs integrated into the host genome.^[139,140]

During the course of HIV-1 infection secretion of T-helper type 1 (Th1) cytokines, such as interleukin-2 (IL-2) and antiviral interferon (IFN)-gamma, is generally decreased,^[141] whereas production of T helper type 2 (Th2) cytokines, IL-4, IL-10, proinflammatory cytokines (IL-1, IL-6, IL-8) and TNF- α , is increased.^[142] Such abnormal cytokine production contributes to the pathogenesis of the disease by impairing cell-mediated immunity. A number of cytokines have been shown to

modulate HIV-1 replication in both CD4 T lymphocytes and cells of macrophage lineage *in vitro*.^[143,144] HIV-induced cytokines include: TNF-alpha, TNF-beta, IL-1 and IL-6, which stimulate HIV-1 replication in T cells and monocyte-derived macrophages (MDM); IL-2, IL-7 and IL-15, which upregulate HIV-1 in T cells; and macrophage-colony stimulating factor, which stimulates HIV-1 replication in MDM. HIV-suppressive cytokines include: IFN-alpha, IFN-beta and IL-16, which inhibit HIV-1 replication in T cells and MDM, and IL-10 and IL-13, which inhibit HIV-1 in MDM.^[145,146] Bifunctional cytokines such as IFN- γ , IL-4 and granulocyte-macrophage colony-stimulating factor have been shown to have both inhibitory and stimulatory effects on HIV-1 replication. The beta-chemokines, macrophage-inflammatory protein (MIP)-1 α , MIP-1 β and RANTES are important inhibitors of macrophage-tropic strains of HIV-1,^[147,148] whereas the alpha-chemokine, stromal-derived factor-1, suppresses infection of T-tropic strains of HIV-1.^[149]

Immunosuppressive cytokines such as IL-10 and transforming growth factor-beta (TGF- β) secreted by regulatory T cells, NKT cells and myeloid cells, might also contribute to the establishment of viral latency by dampening T cell activation and HIV production, thereby creating the necessary immune-virological conditions for the establishment of latent infection.^[150,151]

High levels of the cytokine IL-7, a cytokine that plays a role in homeostasis and survival of CD4+ T cells, may also promote the survival of these cells during HAART.^[152] Conversely, proinflammatory cytokines IL-2, TNF-alpha and IL-6 may favour HIV persistence by exacerbating low levels of ongoing viral replication in lymphoid tissues even after prolonged therapy.^[153]

1.1.15. Immune activation in HIV-infected children

Both pro-inflammatory and regulatory cytokines and other circulating biomarkers are produced during persistent immune activation in chronic HIV infection. Some of these have been investigated in children, but the data are sparse. Persaud *et al* demonstrated that plasma concentrations of tumour necrosis factor, granulocyte-macrophage colony-stimulating factor, interleukin 1 β , IL-2, and IL-8 were substantially higher in perinatally infected children despite being on HAART.

Concentrations of sCD14, a predictor of HIV disease progression and mortality in adults, were also higher in the HIV infected group relative to the perinatally exposed, but uninfected control group.^[154] It has also been reported that IL-2 is associated with recovery of CD4 + T cells while HIV viral loads correlated with levels of IFN γ , IL-4 and IL-10 in perinatally infected Asian children receiving HAART.^[155] Little is known, however, about the immune activation profiles of children infected with HIV-1 subtype C. Children with this type of HIV-infection were therefore incorporated in the study cohort that was investigated in the current study.

1.1.16. Clinical consequences of immune activation

Effective antiretroviral regimens for the treatment of HIV infection have increased life expectancy, and prolonged survival is accompanied by an increased frequency of non-AIDS related co-morbidities in these individuals.^[156] For children that have been perinatally infected, exposure to the virus starts in the uterus and continues through growth, puberty and development.^[156] Atherosclerotic cardiovascular disease (CVD) is a leading comorbidity and cause of mortality among HIV-infected adults (2).^[156] CVD risk factors such as dyslipidaemia, insulin resistance and central fat redistribution are also observed in HIV-infected children.^[156-159] The aetiology of the increased risk for CVD is probably multifactorial, however, there is mounting evidence to support that inflammation and immune activation are likely to be major drivers of atherosclerosis in HIV-infected patients.^[160] Chronic immune activation may also play a role in HIV-related complications such as malignancies and neurological diseases.^[161-163]

1.1.17. Effect of cigarette smoking on HIV-infection.

Cigarette smoke has been reported to contain >7300 different chemicals including stable and unstable reactive oxygen and reactive nitrogen species, mutagenic hydrocarbons such as benzo[a]pyrene, and other toxicants, including heavy metals.^[163] Chronic inhalation of cigarette smoke and consequent unrelenting exposure to these various toxicants result in suppression of critical innate and adaptive host defences in the upper and lower airways due not only to direct

cytotoxicity, but also to oxidative inactivation of intracellular signalling mechanisms. This, in turn, results in increased susceptibility to various respiratory pathogens, especially *Streptococcus pneumoniae* (the pneumococcus) and *Mycobacterium tuberculosis*.^[163] Pulmonary host defences which are compromised by exposure to cigarette smoke include: i) the highly orchestrated ciliary beating of ciliated respiratory epithelium; ii) the phagocytic activity of alveolar macrophages; iii) the antigen-presenting functions and anti-viral activities of myeloid and plasmacytoid dendritic cells respectively; iv) the anti-viral and anti-tumour activities of NK and iNKT cells; and v) the protective activities of T and B lymphocytes.^[163]

Somewhat paradoxically, however, both HIV infection and cigarette smoking cause systemic activation of circulatory neutrophils, which, in both cases, exacerbates immunosuppression via the increased generation of anti-proliferative reactive oxygen species and release of the granule enzyme, arginase, as well as via upregulation of expression of the programmed cell-death ligand 1 (PD-L1) which induces apoptosis of T cells following interaction with its receptor, PD-1.^[163-165] To date it appears that the issue of possible interactive, suppressive effects of smoking and HIV infection on pulmonary host defences have not been addressed.^[166] Nonetheless, even in the absence of supporting evidence, it seems reasonable to assume that the combination of HIV and smoking is likely to be particularly ominous with respect to interactive suppression of pulmonary host defences.

With respect to antiretroviral chemotherapy, it is conceivable, though not proven, that smoke-derived mutagens may cause genetic modifications in pro-viral HIV-1 DNA integrated into the genome of the infected host, favouring the emergence of drug-resistant mutants. In the case of antimicrobial chemotherapy, exposure of *Pseudomonas aeruginosa* to cigarette smoke and other environmental mutagens has been reported to promote antibiotic resistance [63,64], while smoking has been reported to promote treatment failure and recurrence of disease in patients with tuberculosis.^[167,168] Chronic systemic activation of neutrophils associated with both HIV infection and smoking may also predispose to antiretroviral drug/antibiotic resistance via exaggerated generation of mutagenic reactive oxygen species by neutrophils.^[163]

Worldwide, it is well recognised that HIV-infected individuals have higher rates of cigarette smoking than their non-infected counterparts.^[163,166] However, in South Africa, the overall prevalence of current smoking in HIV-infected patients has been reported to be 15%, which is similar to the frequency of smoking in the general population in this country.^[169] In addition to predisposing to respiratory infections, HIV-infected individuals who smoke are at particularly high risk for the development of non-AIDS defining illnesses, including cardiovascular and pulmonary disorders such as chronic obstructive pulmonary disease, as well as various non-AIDS-related malignancies such as lung cancer.^[166] The associated increased morbidity and mortality, even in the face of successful HAART, underscores the magnitude of the threat posed by smoking in the setting of HIV infection. Although the mechanisms which underpin the increased susceptibility of HIV-infected individuals who smoke for development of degenerative diseases and cancer remain uncertain, sustained inflammatory/oxidative stress due to chronic systemic activation of neutrophils may be implicated.

1.2. PURPOSE OF THE STUDY

1.2.1. Objectives

The primary objectives of this study were to investigate and compare:

- i. the levels of circulating biomarkers of immune activation in a cohort of mothers (n=46) infected with HIV-1 subtype C relative to those of 20 healthy controls.
- ii. the biomarkers between mothers and their HIV-infected children (n=46).
- iii. the effects of virologically suppressive and non-suppressive HAART on immune activation profiles in a subgroup of children (n=28).
- iv. the effects of active smoking and passive maternal smoking on the biomarkers of immune activation in the mothers and their children, respectively.

CHAPTER 2

MATERIALS AND METHODS

2.1. METHODOLOGY.

2.1.1. Study design.

It was a retrospective study because the immune activation and cigarette smoke determinants were measured on samples that had already been collected.

2.1.2. Study population.

HIV-infected mothers and their infants presenting for care at the Paediatric Immunology Clinic at Kalafong Academic Hospital in Pretoria, South Africa, after failed prevention of mother-to-child transmission (PMTCT) were included in this study. Ethics approval was granted by the Research Ethics Committee of the Faculty of Health Sciences at the University of Pretoria (Ethics Committee Approval No. 159/2009 and 175/2013). All mothers gave informed consent on behalf of themselves and their infants.

Eighty-six mother-infant pairs were recruited at the time infants presented to the clinic for initiation of highly-active antiretroviral treatment (HAART) and followed prospectively for up to 24 months as part of a HIV drug resistance study. Of these, 46 mother-infant pairs had adequate pre-initiation plasma samples for inclusion in this study (named the mother-infant group). Twenty-eight infants had adequate follow-up samples at month 6 (\pm 2 months) and at month 12 (\pm 2 months) post-initiation (named the longitudinal group). Children were evaluated at 6 and 12 months for the presence of virological treatment failure, defined as the presence of HIV viral load >1000 copies/ml at two separate occasions at least 4 weeks apart despite adherence counselling. Twenty healthy, HIV-uninfected, age-matched, females were included to serve as controls for the mothers. Due to the difficulty in obtaining blood samples from healthy, HIV-uninfected, age-matched infants, each participant infant served as his or her own control.

The median age of the mothers was 27.3 years (IQR 24.8 – 30.3) and of the controls 26 years (IQR 23.7-32.5). A median of 14 months (IQR 5 – 21) had elapsed between the birth of their infants and enrolment in the study. Thirty-eight mothers had received single-dose nevirapine and 11 had also received AZT (for between 7 and 192 days) as part of PMTCT. Only one mother had been started on HAART

(tenofovir, lamivudine, efavirenz) at the time of study entry. None of the mothers had any signs of active opportunistic infections at the time of study enrolment.

The median age of the infants in the mother-infant group was 12.7 months (IQR 6.8 – 20.7). The male to female ratio was 1:1,47. Thirty-four (74%) infants had received nevirapine after birth (for between 7 and 270 days) and only seven infants had been on formula milk. The infants in the longitudinal group were slightly younger with a median age of 9.8 months (IQR 4.9 – 20.5) and a male to female ratio of 1:1. Twenty-six (93%) infants had received nevirapine after delivery and only 1 had been on formula milk. All infants in the longitudinal group were started on HAART in the form of abacavir, lamivudine and either ritonavir-boosted lopinavir (n=25) or efavirenz (n=3). Fifteen infants started HAART at the time of the first study visit, 12 started with one month of the first study visit, and one only started HAART after 3.8 months. One infant defaulted treatment in the first month and was re-initiated a month later. All infants were on co-trimoxazole prophylaxis and four had a diagnosis of tuberculosis around the time of HAART initiation (between 14 days before and 40 days after HAART).

Whole blood samples were collected in EDTA vacutainers, processed within 24 hours to separate the plasma component by centrifugation, and stored at -70°C for up to 24 months. CD4+ T-lymphocyte counts (CD4+) (Beckman Coulter SA (Pty) Ltd) and HIV-1 RNA (VL) (Nuclisens HIV-1 Viral Load Assay v1.2 or v2.0) were measured by standard flow cytometric and PCR-based procedures respectively, according to manufacturer's instructions. These assays were performed by Ms Gisela van Dyk, Dept Immunology, University of Pretoria.

2.2. METHODS.

2.2.1. Preparation of plasma samples.

Whole blood samples were collected in EDTA vacutainers, processed within 24 hours to separate the plasma component by centrifugation, and stored at -70°C for up to 24 months.

2.2.2. Measurement of biomarkers of inflammation (cytokines/chemokines) in the plasma.

The following cytokines (IL-1 β , IL-1 receptor antagonist, IL-2, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-12, IL-13, IL-17, eotaxin, G-CSF, GM-CSF, IFN γ , IP10, MCP-1, MIP-1 α , MIP-1 β , TNF, MIG and TGF- β) were tested in the plasma of patients and controls using the multiplex bead suspension array assays (Bio-RAD Laboratories Inc, Hercules, California). The Bio-Plex suspension array system employs multiplex technology that used up to 100 colour-coded bead sets, each of which was conjugated with a specific reactant. Each reactant was specific for a different target molecule.

Bio-Plex cytokine assays were designed in a capture sandwich immuno-assay format. Antibody specifically directed against the cytokine of interest was covalently coupled to colour-coded 5.6 μ m polystyrene beads. The antibody-coupled beads were allowed to react with a sample containing an unknown amount of cytokine, or with a standard solution containing a known amount of cytokine. After performing a series of washes to remove unbound protein, a biotinylated detection antibody specific for a different epitope on the cytokine was added to the beads. The reaction mixture was detected by the addition of streptavidin-phycoerythrin (streptavidin-PE) (50 μ l), which binds to the biotinylated detection antibodies. The contents of each well were drawn up into the flow-based Bio-Plex suspension array system, which identifies and quantitates each specific reaction based on bead colour and fluorescence. The magnitude of the reaction was measured using fluorescently labeled reporter molecules associated with each target protein. Unknown cytokine concentrations were automatically calculated by Bio-Plex Manager™ software using a standard curve derived from a recombinant cytokine standard.

The sample for TGF- β measurement was prepared according to manufacture specifications. Briefly, 10 μ l of 1N hydrochloric acid (HCl) was added to an aliquot of plasma followed by neutralization with 1.2N sodium hydroxide (NaOH)/0.5 HEPES. Seventy five μ l of sample diluent was added to make a dilution of 1/16 of the sample.

2.2.3. Measurement of soluble CD14 in plasma.

Human sCD14 was measured utilizing the Abcam ELISA kits (Abcam Cambridge, MA, USA), following the manufacturer's specifications. The sandwich ELISAs employ specific capture antibodies coated on a 96-well plate. Standards and samples were pipetted into the wells; the target protein in the standards and samples binds to the immobilized antibody. The wells were washed and the biotin-labeled detection antibody was then added. After washing away the unbound biotinylated antibodies, HRP-conjugated streptavidin was pipetted into the wells, followed by a colourimetric substrate solution. The intensity of colour development in the wells was proportional to the amount of target protein bound. The concentration of the analytes was calculated using a standard curve that was generated via serial dilutions of the standard (220-6.8ng/mL) concentrations.

2.2.4. Measurement of β 2-microglobulin and CRP in plasma.

β 2-microglobulin and CRP were analysed using a Dade Behring BNII nephelometer (Siemens Healthcare Diagnostics). Polystyrene particles coated with monoclonal antibodies to CRP or β 2-microglobulin, were agglutinated when mixed with sample containing the analytes. The amount of light scatter detected by the nephelometer was proportional to the concentration of β 2-microglobulin or CRP. The concentration of the analytes was calculated using a standard curve that was generated via the serial dilutions of the standard (1.09-2.53 mg/L) concentrations.

2.2.5. Measurement of cotinine in plasma of HIV-infected mothers.

Cotinine levels in the stored plasma samples were measured by using a Calbiotech ELISA (Spring Valley, California). This kit was a solid phase competitive ELISA. The samples and cotinine enzyme conjugate were added to the wells coated with anti-cotinine antibody. Cotinine in the samples competes with a cotinine enzyme (HRP) conjugate for binding sites. Upon addition of the substrate, the intensity of colour was inversely proportional to the concentration of cotinine in the samples. The

concentration of cotinine was calculated using a standard curve that was generated via the serial dilutions of standard (0-100ng/mL) concentrations.

2.3. DATA ANALYSIS AND STATISTICS.

All data followed a non-normal distribution and are presented as the median, minimum, and maximum concentrations (range) for each of the measured cytokines/chemokines, as well as for cotinine. Median concentrations of each parameter were compared between cohorts using the Mann-Whitney test for independent groups. Statistical significance was set at $P \leq 0.05$.

CHAPTER 3

RESULTS AND DISCUSSION

3.1 RESULTS

3.1.1 Demographic data of paired mothers and children at baseline

These data are shown in Table 1 (page 37) for the entire cohort (n=46), as well as for the subgroup (n=33) for which flow cytometric analysis of CD4⁺ and CD8⁺ T cells was available. The children had significantly higher CD4⁺ and CD8⁺ T cell counts than the mothers, as well as significantly higher HIV viral loads. The CD4% was, however, not significantly different between the two groups.

3.1.2 Comparison of immune activation profiles of mothers and adult controls

These results are shown in Table 2 (page 38). Relative to the control group, the mothers showed significant increases ($P=0.0233$ - $P<0.0001$) in the concentrations of almost all of the tested circulating biomarkers of immune activation with the exception of MIP-1 α . Other cytokines that were also found to be increased in mothers relative to the controls are shown in Table 3 (page 39). These are G-CSF, GM-CSF, IL-2, IL-4, IL-6, IL-7, IL-8, IL-9, IL-10, IL-12, IL-13, IL-17 and eotaxin.

3.1.3 Comparison of immune activation profiles of mothers and their children

These are shown in Table 4 (page 40). Beta 2 microglobulin was found to be significantly increased, while the other markers (IFN γ , TNF α , TGF β , ILRa) were found to be significantly decreased in the children relative to the mothers. Other cytokines that were also found to be decreased in children relative to the mothers are shown in Table 5 (page 41). These are GM-CSF, IL-2, IL-4, IL-6, IL-9, and IL-17.

Four children with tuberculosis (TB) were identified in the group of children. When their values were omitted from the data analysis, no significant changes were observed.

3.1.4 Longitudinal follow-up of a subgroup of the children.

Twenty eight children were followed longitudinally from baseline to 12 months and stratified thereafter according to treatment response with viral loads below and above 1000 copies/ml, representing virological suppression and non-suppression, respectively. These results are shown in Table 6 (page 42).

Relative to the baseline group, sCD14, beta 2 microglobulin and MIG were decreased in the children on virologically-suppressive antiretroviral therapy at 6 months and 12 months. Soluble CD14 and MIG were significantly increased in the treatment failure group relative to the virologically suppressed group at 6 months and 12 months. Beta 2 microglobulin was significantly decreased in the treatment failure group at 12 months, yet it still reached higher levels than the suppressed group. IP10 was unexpectedly low in the treatment failure group at 6 months. The data for the remaining biomarkers are shown in Table 7 (page 43). No significant differences were observed in these.

Significant increases in the circulating CD4 counts and significant decreases in the HIV viral load were observed in the suppressed groups at 6 and 12 months (Table 6). Omitting the values of the children with TB from the data analysis had no significant effects on the data showed.

3.1.5 The effects of active and maternal smoking on the immune activation profiles of the mothers and their children.

Of the 46 mothers of the study cohort, 10 were smokers (21.7% of study population). The effects of active smoking in this study group are shown in Table 8 (page 44). No significant differences were observed between smokers and non-smokers, except for the CD8 count which was increased in the group of smokers. The effects of maternal smoking on the immune activation profiles of children are shown in Table 10 (page 46). TGF β was significantly increased in the smoke-exposed children while increased trends, albeit not attaining statistical significance, were observed for sCD14, CRP, MIG, HIV viral loads and the CD8 T cell count. The data for the remaining cytokines are shown in Tables 9 and 11 (page 45 and 47). No significant differences were observed in these.

3.2. Discussion

According to the data, the mothers had relatively low CD4⁺ T cell counts (median, 330 cells/ μ l) and a high HIV viral load (median, 61000 copies/ml). With the exception of one, these individuals were not on HAART. The children at baseline had higher CD4⁺ T cell counts than the mothers (median, 774 cells/ μ l) - it is however difficult to attribute any significance to these differences as lymphocyte counts in infants are higher than those of adults.^[170] The CD4% was, however, not significantly different

between the two groups. The HIV viral load in the children was markedly increased, a finding which is in agreement with previous reports which found that HAART naïve children tend to have higher viral loads relative to those of adults.^[171,172] The reason for this may be that their immune system is still relatively immature and less effective in suppressing HIV replication.

Relative to the healthy controls, the HIV-infected, adult women (mothers of the children) showed increases in almost all of the circulating biomarkers of immune activation. The biomarkers that were raised included inflammatory cytokines (IFN γ , TNF α) chemokines (MIG, IP10, MIP-1 β), plasma markers of cellular activation (sCD14 and β 2-microglobulin), CRP, the anti-inflammatory cytokine, TGF β , and ILRa. As indicated, several interleukins and colony-stimulating factors were also found to be increased in this cohort. These findings are consistent with those of others, who also found increases in soluble IL2R, soluble TNFR1, neopterin and soluble UPAR (soluble urokinase type plasminogen activator receptor) in HAART naïve, HIV-infected subjects.^[10,112,113]

These trends of immune activation were also observed in HIV-infected children. Persaud et al (2014) reported that perinatally HIV-infected children, showed increases in circulating TNF, GM-CSF, IL1- β , IL-2 and IL-8, despite being on HAART. They further stated that sCD14, a predictor of HIV disease progression and mortality in adults, was also increased in this cohort relative to exposed, but HIV-uninfected controls.^[154] Another study on children indicated that IL-2 was associated with recovery of CD4 T cells, while HIV viral load correlated with IFN γ , IL-4 and IL-1.^[155]

Relative to their mothers, the children at baseline showed significantly higher levels of beta 2 microglobulin. This observation is consistent with a report that this marker is higher in neonates and infants up to one year than in adults.^[173] Levels of IFN γ , TNF α , TGF β , ILRa and several other interleukins were however lower in the children than those of their mothers, which again point to the relative immaturity of the children's immune system. These findings are consistent with those of Lilic et al (1997) who found that in healthy children, cytokine production is decreased or altered when compared to those of adults, and that this may result in suboptimal immune responses and an increased susceptibility to infection.^[174]

CD4 counts were significantly increased and viral loads markedly decreased in children who received virologically-suppressive HAART (suppressed groups) at 6 months and 12 months. Children in these groups also showed significantly lower levels of sCD14, beta 2 microglobulin and MIG following HAART. This is consistent with the study of Malherbe et al (2014) who showed that successful HAART was associated with significant decreases in the concentrations of several markers of immune activation including beta2 microglobulin, MIG and IP10.^[112] Soluble CD14 and MIG were significantly higher in the treatment failure groups compared to the suppressed groups at the 6 and 12 month time points. Unexpectedly IP10 was very low in the children with treatment failure at 6 months which may be explained by variability in our relatively small study group. According to Malherbe et al (2014) persistently elevated levels of the biomarkers of immune activation in patients failing therapy in the setting of a marked reduction in these markers in patients on successful HAART may not only be useful to monitor immune activation during HAART, but may also distinguish between good and poor responders.^[112]

A high percentage of mothers were active smokers (21.7%). This was unexpected as it is well known that Africans, particularly females, are less likely to smoke than their American and European counterparts. A recent South African based-study of Waweru et al, for example, observed that only 7.5% of the African, HIV-infected women were current smokers.^[175]

With the exception of an increase in the circulating CD8+ T cell count in smokers as shown by others,^[176] no significant differences were observed between the immune activation profiles of active smokers and non-smokers. Associations may have been obscured by the effects of high HIV viral load or by low levels of tobacco exposure. However further studies in a larger patient cohort are necessary. Children exposed to maternal smoking, however, showed significantly increased levels of TGF β as well as trends, albeit not reaching statistical significance, for increased levels of sCD14, CRP and MIG, as well as higher CD8+ T cell counts and HIV viral loads. TGF β is an anti-inflammatory cytokine with protective functions; however overexpression of it, may lead to pathogenic manifestations.^[181] TGF β , through its profound and broad inhibitory effects on antiviral defense mechanisms, including a key role in progressive lymphoid tissue fibrosis during HIV-infection, may facilitate more rapid

progression of virus infection resulting in increased in susceptibility to opportunistic infections and malignancies.^[177,178]

3.3. Conclusions

Although somewhat lower than those of their mothers, HIV-infected children were found to have high levels of a range of circulating biomarkers of immune activation in the setting of higher viral loads. The concentrations of these biomarkers were differentially affected following administration of HAART to the children, decreasing in some cases, specifically sCD14 and MIG, and associated with viral suppression. With the exception of CD8⁺ T cell counts, cigarette smoking did not significantly alter the circulating biomarker profiles of the HIV-infected mothers. Maternal smoking was, however, associated with a significant increase in the concentration of immunosuppressive TGF- β 1 in the children, while a trend towards increases in the concentrations of sCD14, CRP, MIG, as well as the HIV viral load and circulating CD8⁺ T cell count, albeit statistically insignificant in all cases, was evident. While seemingly consistent with an adverse effect of maternal smoking on immune activation, interpretation is tempered by the small number of smoke-exposed infants in the study.

Table 1. Demographic data of paired mothers and their children.

	Mothers [Median (Range)] n=46	Children [Median (Range)] n=46	P-value
Age	27.3 years (24.8-30.3)	12.7 months (6.8-20.7)	<0.0001
CD4 count (Cells/ μ l)	330 ⁺ (115-744)	774 ⁺⁺ (66-2,856)	<0.0001
CD4 T cells (%)	22 ⁺ (7-37)	21 ⁺⁺ (7-45)	0.8852
CD8 count (Cells/ μ l)	740 ⁺ (265-2,942)	1,675 ⁺⁺ (181-6,301)	<0.0001
CD4/CD8 ratio	0.4 ⁺ (0.1-1)	0.5 ⁺⁺ (0.1-2)	0.2879
HIV-Viral Load (Copies/ml)	70,000 ⁺ (240-3,400,000) 61,000 [⊕] (240-3,400,000)	1180,000 ⁺⁺ (500-26,000,000) 980,000 [⊕] (440-50,000,000)	<0.0034 <0.0001

⁺Available data of 33 patients

⁺⁺Available data of 32 patients

[⊕] Data for the whole group

Table 2. Comparison of the circulating biomarkers of immune activation of mothers at baseline and adult controls.

	Mothers Baseline n=46 [Median(Range)]	Adult Controls n=20 [Median(Range)]	P-value
sCD14 (ng/ml)	8,068 (0.00-19,431)	5,971 (853-8,220)	<0.0011
β 2 M (μ g/ml)	2.84 (0.847-6.86)	1.360 (1.02-3.77)	<0.0001
CRP (μ g/ml)	1.8 (0.173-10.3)	0.8 (0.173-7.5)	0.0242
MIG (pg/ml)	2,143 (595-19,734)	190.4 (84.9-2,932)	<0.0001
IP10 (pg/ml)	6,866 (2267-64,710)	1,075 (690-12,005)	<0.0001
IFN γ (pg/ml)	1924 (510-5,109)	854 (310-2,010)	<0.0001
TNF α (pg/ml)	654 (168-1,412)	373 (212-756)	<0.0001
MIP-1 α (pg/ml)	38 (14-352)	34.96 (26-382)	0.5802
MIP-1 β (pg/ml)	166 (75-325)	91.5 (70.23-185)	<0.0001
TGF- β (pg/ml)	22,480 (52.8-33,685)	10,960.7 (3,157.6-31,806)	0.0093
IL-1Ra (pg/ml)	1,495 (3.6-3,437)	628 (263-1,526)	<0.0001

Abbreviations: sCD14 (soluble CD14), β 2M (β 2-microglobulin), IFN γ (interferon gamma), MIG (monokine induced IFN γ), IP10 (IFN- γ -inducible protein 10), TNF α (tumour necrosis factor α), MIP-1 α and β (macrophage inflammatory protein α and β), TGF- β (transforming growth factor β), IL-1 Ra (IL-1 receptor antagonist).

Table 3. Comparison of the circulating biomarkers of immune activation of mothers at baseline and adult controls.

	Mothers Baseline n=46 [Median(Range)]	Adult Controls n=20 [Median(Range)]	P-value
G-CSF (pg/ml)	765 (375-1,392)	586 (480-1,054)	<0.0001
GM-CSF (pg/ml))	148.2 (4.94-397)	8.615 (3.4-168)	<0.0001
IL-1 β (pg/ml)	26.2 (2-8,291)	20.2 (13-8,291)	0.1404
IL-2 (pg/ml)	59 (13.65-135)	41 (2.45-2,342)	<0.0001
IL-4 (pg/ml)	27 (9-68)	16.7 (9.5-32.6)	<0.0001
IL-6 (pg/ml)	85 (19-1,044)	47 (23-88)	0.0346
IL-7 (pg/ml)	82.19 (17-180)	73.77 (47-112)	0.0051
IL-8 (pg/ml)	95.23 (27-1,056)	55.31 (38-85)	<0.0290
IL-9 (pg/ml)	82 (26-252)	38.3 (18-87)	<0.0001
IL-10 (pg/ml)	44.68 (2-155)	28.3 (11.4-56)	<0.0001
IL-12 (pg/ml)	132 (4-427)	93.66 (20-161)	0.0005
IL-13 (pg/ml)	44.23 (24-200)	28 (19-49)	0.0022
IL-17 (pg/ml)	332 (88-576)	222 (62-420)	<0.0001
Eotaxin (pg/ml)	595 (393-1,116)	371 (139-790)	<0.0001

Abbreviations: G-CSF (granulocyte colony stimulating factor); GM-CSF (granulocyte macrophage colony stimulating factor).

Table 4. Comparison of the circulating biomarkers of immune activation of mothers and children at baseline.

	Mothers Baseline n=46 [Median(Range)]	Children Baseline n=46 [Median(Range)]	P-value
sCD14 (ng/ml)	8,128 (0-19,431)	9,741 (481-20,448)	0.0820
β 2 M (μ g/ml)	2.84 (0.847--6.86)	4 (1.8-7.4)	<0.001
CRP (μ g/ml)	2 (0.2-79)	5 (0.2-144)	0.0950
MIG (pg/ml)	2,491 (595-19,734)	3,808 (1,058-13,818)	0.7830
IP10 (pg/ml)	6,867 (2,267-64,710)	7,171 (1,054-636,325)	0.8607
IFN γ (pg/ml)	1,924 (510-5,109)	1,207 (211-3,770)	<0.0001
TNF α (pg/ml)	654 (168-1,412)	421 (93-1,224)	<0.0001
MIP-1 α (pg/ml)	38 (14-352)	46 (16-569)	0.0132
MIP-1 β (pg/ml)	166 (75-325)	163 (46-872)	0.8667
TGF- β (pg/ml)	22,480 (52.8-33,685)	12,627 (67-30,336)	<0.0001
IL-1Ra (pg/ml)	1,604 (606-86,729)	904 (201-2,913)	<0.0001

Table 5. Comparison of the circulating biomarkers of immune activation of mothers and children at baseline.

	Mothers Baseline n=46 [Median(Range)]	Children Baseline n=46 [Median(Range)]	P-value
G-CSF (pg/ml)	766 (375-1,392)	682 (236-1,751)	0.0873
GM-CSF (pg/ml)	172 (35—24,876)	85 (7-24,236)	0.0124
IL-1 β (pg/ml)	24 (4-55)	24 (6-89)	0.1780
IL-2 (pg/ml)	61 (14-135)	39 (5-116)	<0.0001
IL-4 (pg/ml)	27 (9-68)	22 (5-43)	<0.0001
IL-5 (pg/ml)	36 (6-80)	37 (11-83)	0.3027
IL-6 (pg/ml)	84 (19-259)	64 (28-1,012)	0.0202
IL-7 (pg/ml)	85 (17-180)	86 (27-240)	0.3045
IL-8 (pg/ml)	95 (27-246)	101 (38-1,231)	0.5348
IL-9 (pg/ml)	82 (25-197)	61 (20-200)	0.0007
IL-10 (pg/ml)	48 (7-4,750)	51 (10-148)	0.5713
IL-12 (pg/ml)	139 (8-895)	136 (23-367)	0.6200
IL-13 (pg/ml)	45 (24-200)	47 (20-196)	0.7756
IL-17 (pg/ml)	334 (88-576)	209 (17-462)	<0.0001
Eotaxin (pg/ml)	597 (392-1,116)	528 (120-1,011)	0.0796

Table 6. A subgroup of the children at baseline (ART naïve) and children at second visit (6 months) and third visit (12 months) (both on ART) stratified according to treatment failure.

	Baseline children (n=28) [Median (Range)]	Children at 6 months: <u>Virologically suppressive ART</u> (Suppressed) n=20 [Median (Range)]	Children at 6 months: <u>Virologically non-suppressive ART</u> (Failing) n=8 [Median (Range)]	Children at 12 months: <u>Virologically suppressive ART</u> (Suppressed) n=22 [Median (Range)]	Children at 12 months: <u>Virologically non-suppressive ART</u> (Failing) n=6 [Median (Range)]
sCD14 (ng/ml)	9,838 (481-18,591)	7,270 (889-15,466)	11,114 ** (6,062-18,591)	6,669 * (734-13,241)	5,887 (817-12,511)
β2 M (µg/ml)	4 (1.8-8.8)	2 * (1.7-5)	3 (1.9-5)	2.5 * (1.3-4.5)	2.9 * (1.9-4)
CRP (µg/ml)	4 (0.2-144)	1.3 (0.2-42)	1.7 (0.6-49)	1.6 (0.2-43)	9 (0.2-27)
MIG (pg/ml)	4,665 (847-14,037)	1,441 * (611-11,355)	3,289 (269-12,258)	813 * (385-6,081)	2,142 ** (384-11,926)
IP10 (pg/ml)	9,014 (1,054-64,710)	6,023 (1,335-18,749)	2,531 * ** (1,446-7,282)	4,614 (997-16,679)	4,789 (1,567-8,942)
IFN _γ (pg/ml)	1,671 (148-3,770)	1,822 * (811-5,108)	1,738 (558-3,668)	1,415 (764-2,491)	1,506 (965-2,336)
TNF _α (pg/ml)	527 (81-1,224)	636 (337-1,421)	634 (2,367-1,167)	547 (285-894)	798 (381-1,167)
MIP1 _α (pg/ml)	39 (9-569)	41 (22-676)	52 (36-256)	40 (22-352)	35 (24-75)
MIP1 _β (pg/ml)	176 (47-872)	164 (66-872)	173 (100-300)	165 (55-300)	138 (81-226)
TGF _β (pg/ml)	12,489 (67-30,336)	13,419 (39-23,940)	9,198 (149-22,691)	14,117 (1,021-18,364)	14,017 (134-19,422)
IL1 Ra (pg/ml)	1,132 (201-2,913)	1,345 (555-3,375)	1,306 (370-2,404)	1,162 (548-1,874)	1,121 (720-1,888)
CD4 count (cells/µl)	778 (66-2,856)	1,724* (31-6,401)	1,576 (343-2,860)	1,731* (635-3,828)	1,329 (662-3,753)
CD8 count (cells/µl)	1,649 (181-9,764)	1,819 (25-5,984)	2,709 (1,278-6,191)	1,785 (44-2,792)	2,216 (808-6,787)
Viral Load (copies/ml)	2600,000 (500-220,000,000)	25* (25-200)	4,100* ** (1,620-3,000,000)	25* (25-320)	195,700 (3,200-8,000,000)

Abbreviations: ART: antiretroviral treatment; Failing: treatment failure

* For comparison with baseline values; p<0.05

** For comparison with the same time-point, virologically suppressed group; p<0.05

Table 7. A subgroup of the children at baseline (ART naïve) and children at second visit (6 months) and third visit (12 months) (both on ART) stratified according to treatment failure.

	Baseline children (n=28) [Median (Range)]	Children at 6 months: <u>Virologically suppressive ART</u> (Suppressed) n=20 [Median (Range)]	Children at 6 months: <u>Virologically non- suppressive ART</u> (Failing) n=8 [Median (Range)]	Children at 12 months: <u>Virologically suppressive ART</u> (Suppressed) n=22 [Median (Range)]	Children at 12 months: <u>Virologically non- suppressive ART</u> (Failing) n=6 [Median (Range)]
G-CSF (pg/ml)	607 (212-1,751)	659 (268-1,268)	765 (428-1,140)	567 (59-773)	681 (333-1,233)
IL-1 β (pg/ml)	23 (4-89)	26 (13-793)	28 (13-36)	23 (9-35)	21 (17-41)
IL-2 (pg/ml)	53 (15-9,935)	58 (16-132)	59 (14-108)	45 (16-90)	51 (39-96)
IL-4 (pg/ml)	23 (5-42)	27 (13-65)	30 (12-42)	21 (11-40)	27 (15-37)
IL-5 (pg/ml)	34 (6-80)	38 (11-80)	48 (22-78)	34 (11-58)	36 (18-88)
IL-6 (pg/ml)	62 (18-1,012)	62 (21-1,044)	63 (37-139)	60 (27-96)	64 (28-143)
IL-7 (pg/ml)	73 (17-218)	87 (42-254)	119 (43-204)	74 (30-143)	89 (40-221)
IL-8 (pg/ml)	107 (34-1,231)	129 (35-1,000)	122 (48-216)	97 (41-197)	115 (63-193)
IL-9 (pg/ml)	75 (18-200)	97 (21-304)	105 (39-153)	73 (28-132)	81 (36-135)
IL-10 (pg/ml)	31 (5-138)	36 (15-134)	50 (19-147)	35 (13-100)	28 (16-148)
IL-12 (pg/ml)	79 (3-467)	74 (41-256)	128 (35-285)	93 (26-174)	106 (42-252)
IL-13 (pg/ml)	39 (21-200)	40 (23-78)	59 (22-156)	39 (22-97)	45 (23-84)
IL-17 (pg/ml)	240 (48-30,153)	297 (136-554)	305 (85-470)	237 (93-406)	266 (87-377)
Eotaxin (pg/ml)	570 (224-1,116)	521 (318-890)	581 (373-833)	519 (341-930)	539 (418-740)

Table 8. Effects of active smoking on immune activation profiles of mothers.

	Mothers		P-value
	Non-smokers n=36 [Median (Range)]	Smokers n=10 [Median (Range)]	
sCD14 (ng/ml)	7,893 (1233-19,431)	8,554 (5265-19,431)	0.9575
β 2 M (μ g/ml)	3 (0.9-7)	3 (0.9-5)	0.5491
CRP (μ g/ml)	2 (0.2-10)	3 (0.2-9)	0.6329
MIG (pg/ml)	2,143 (595-19,734)	1,943 (465-5,603)	0.8417
IP10 (pg/ml)	6,342 (2,776-64,710)	7,439 (1,824-24,421)	0.8003
IFN γ (pg/ml)	2,013 (509-9,992)	1,779 (992-2,491)	0.3053
TNF α (pg/ml)	658 (169-1,412)	556 (368-888)	0.1043
MIP1 α (pg/ml)	40 (14-199)	32 (25-352)	0.1395
MIP1 β (pg/ml)	168 (75-325)	137 (98-235)	0.1096
TGF β (pg/ml)	20,995 (52.8-33,686)	23,485 (13,153-27,170)	0.2961
IL1 Ra (pg/ml)	1646 (739-3,437)	1,287 (606-1,962)	0.1767
CD4 count (cells/ μ l)	323 (115-744) ⁺	349 (225-573) ⁺⁺	0.2523
CD8 count (cells/ μ l)	696 (267-2,600) ⁺	1,383 (316-2,942) ⁺⁺	0.0386
Viral load (copies/ml)	51,000 (820-3,400,000)	(116,000 (240-520,000)	0.8836

⁺Available data of 26 patients

⁺⁺Available data of 7 patients

Table 9. Effects of active smoking on immune activation profiles of mothers.

	Mothers		P-value
	Non-smokers n=36 [Median (Range)]	Smokers n=10 [Median (Range)]	
G-CSF (pg/ml)	796 (375-1,392)	715 (595-1,387)	0.9999
GM-CSF (pg/ml)	190 (35-24,876)	110 (58-24,876)	0.1101
IL-1 β (pg/ml)	27 (4-54)	23 (15-35)	0.2534
IL-2 (pg/ml)	60 (14-134)	57 (39-92)	0.3582
IL-4 (pg/ml)	30 (9-68)	25 (18-41)	0.2929
IL-5 (pg/ml)	36 (6-81)	31 (19-48)	0.3795
IL-6 (pg/ml)	85 (19-1,043)	78 (50-108)	0.3053
IL-7 (pg/ml)	85 (17-180)	67 (45-142)	0.5315
IL-8 (pg/ml)	93 (27-247)	95 (52-149)	0.7900
IL-9 (pg/ml)	85 (26-198)	69 (41-132)	0.2206
IL-10 (pg/ml)	48 (7-155)	33 (20-63)	0.2972
IL-12 (pg/ml)	133 (8-8,954)	139 (70-191)	0.8734
IL-13 (pg/ml)	49 (25-116)	38 (24-200)	0.2749
IL-17 (pg/ml)	333 (87-576)	317 (215-447)	0.7192
Eotaxin (pg/ml)	581 (393-932)	671 (454-1,116)	0.3445

Table 10. Effects of maternal smoking on immune activation profiles of children.

	Children of non-smoking and smoking mothers		P-value
	Non-smokers n=36 [Median (Range)]	Smokers n=10 [Median (Range)]	
sCD14 (ng/ml)	9,615 (481-14,620)	11,924 (5427-20,448)	0.1172
β 2 M (μ g/ml)	4 (1.8-7.3)	4 (2.5-7)	0.4477
CRP (μ g/ml)	4 (0.173-144)	9 (1.9-37)	0.1232
MIG (pg/ml)	3,836 (1,057-13,818)	5,182 (1,639-8,768)	0.4716
IP10 (pg/ml)	7,014 (2,092-636,325)	8,448 (1,054-10,918)	0.8899
TNF α (pg/ml)	400 (92-1,224)	514 (207-762)	0.3465
MIP1 α (pg/ml)	46 (16-569)	46 (28-77)	0.8681
MIP1 β (pg/ml)	155 (46-872)	183 (155-616)	0.8463
TGF β (pg/ml)	11,916 (67-22,879)	17,972 (4,932-30,336)	0.0288
IL1 Ra (pg/ml)	853 (201-2,913)	963 (501-1,579)	0.4802
CD4 count (cells/ μ l)	645 (66-2,856)	1,181 (233-2,600)	0.5879
CD8 count (cells/ μ l)	1,559 (297-5,731)	2,968 (181-6,301)	0.0695
Viral load (copies/ml)	780,000 (440-26,000,000)	1,960,000 (5,200-50,000,000)	0.1580

Table 11. Effects of maternal smoking on immune activation profiles of children.

	Children of non-smoking and smoking mothers		P-value
	Non-smokers n=36 [Median (Range)]	Smokers n=10 [Median (Range)]	
G-CSF (pg/ml)	699 (236-1,751)	665 (382-1,189)	0.3395
GM-CSF (pg/ml)	86 (7-24,876)	84 (23-14,036)	0.9448
IL-1 β (pg/ml)	25 (6-89)	20 (17-38)	0.9999
IL-2 (pg/ml)	36 (5-116)	51 (14-60)	0.1178
IL-4 (pg/ml)	22 (5-43)	25 (12-32)	0.4464
IL-5 (pg/ml)	37 (12-83)	36 (19-72)	0.9338
IL-6 (pg/ml)	65 (28-164)	60 (29-1,012)	0.6182
IL-7 (pg/ml)	87 (27-240)	82 (52-221)	0.9558
IL-8 (pg/ml)	100 (37-1,231)	134 (51-261)	0.3756
IL-9 (pg/ml)	59 (20-200)	77 (43-87)	0.2991
IL-10 (pg/ml)	57 (10-147)	43 (19-133)	0.9890
IL-12 (pg/ml)	137 (23-3,670)	128 (49-315)	0.8463
IL-13 (pg/ml)	51 (20-196)	45 (24-130)	0.6378
IL-17 (pg/ml)	207 (17-462)	214 (108-303)	0.5242
Eotaxin (pg/ml)	524 (120-1,011)	545 (418-1,006)	0.5795

LIMITATION AND STRENGTHS OF THE STUDY

Limitations and strengths of the study

Limitations of the study

Relatively small numbers of HIV-infected mothers who smoke, as well as smoke-exposed infants;

The relative short duration of administration of HAART to the study infants.

Insurmountable difficulty in recruiting a control group of healthy age-matched infants;

In keeping with the previous limitation, an inability to establish reference ranges for the various test biomarkers for infants.

Strengths of study

Given the success of the South African prevention of mother to child transmission program (PMTCT) with MTCT rates now very low, the prevalence of perinatally infected children is very low. In this context this study has relatively large numbers.

Children are difficult to keep in care. Seen in this context, relatively large numbers (n=28) returned for the longitudinal study.

Confirmation of the apparent utility of several biomarkers in monitoring the response to HAART in infants;

The apparent adverse effects of maternal smoking on biomarkers of immune activation in smoke-exposed HIV-infected infants. Although these must be considered as preliminary findings, the current study should serve as a template for future, more definitive studies.

CHAPTER 4

REFERENCES

4.1. REFERENCES.

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