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UMI

Mutants of IκBα interfere with NF-κB regulated gene expression and HIV-1 replication

by

Hakju Kwon

Division of Experimental Medicine McGill University, Montreal March 2000

A thesis submitted to the Faculty of Graduate Studies and Research in partial fulfillment of the requirements of the degree of Doctor of Philosophy.

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Canadä

To my wife Monica for your love and understanding

To my mother and my brother Hyungju for all your support

Abstract

Human immunodeficiency virus type 1 (HIV-1) utilizes the NF- κ B/Rel pathway to mediate, in part, its transcriptional regulation through NF- κ B binding sites present in the HIV-1 LTR. In unstimulated cells, DNA binding NF- κ B subunits are retained in the cytoplasm by inhibitory I κ B proteins. Upon stimulation by cytokines, viruses or dsRNA, I κ B α is rapidly phosphorylated and degraded, resulting in the release of NF- κ B and the subsequent increase in NF- κ B-regulated gene expression.

The effect of transdominant mutants of $I\kappa B\alpha$ (TD-I $\kappa B\alpha$) on the synergistic activation of the HIV-1 LTR by TNF α and the HIV-1 transactivator Tat, was examined in Jurkat T cells. Co-expression of WT I $\kappa B\alpha$ and TD-I $\kappa B\alpha$ inhibited Tat-TNF activation of HIV-1 LTR in a dose dependent manner. TD-I $\kappa B\alpha$ also effectively inhibited HIV-1 multiplication in a single cycle infection model in COS-1 cells. To examine the effect of inducible expression of TD-I $\kappa B\alpha$ on *de novo* HIV-1 multiplication, we generated Jurkat T cells inducibly expressing TD-I $\kappa B\alpha$ by doxycycline (Dox). Dox induction of TD-I $\kappa B\alpha$ dramatically reduced both NF- κB DNA binding activity and LTR directed gene activity. The time course of *de novo* HIV-1 infection was altered by Dox induction of TD-I $\kappa B\alpha$ in Jurkat cells, resulting in a dramatic inhibition of HIV-1 multiplication.

Interestingly, induced expression of TD-I κ B α also progressively decreased the expression of endogenous I κ B α to undetectable levels by 24h after induction, indicating that TD-I κ B α was able to repress endogenous NF- κ B dependent gene expression. We also demonstrated that production of TD-I κ B α reduced endogenous I κ B α gene transcription, due to the continued cytoplasmic sequestration of ReIA(p65) by TD-I κ B α . *In vivo* genomic footprinting revealed stimuli-responsive protein-DNA binding not only to the -63 to -53 κ B1 site but also to the adjacent -44 to -36 Sp1 site of the I κ B α promoter. *In vivo* protection of both sites was inhibited by Dox-inducible TD-I κ B α expression. Prolonged NF- κ B binding and a temporal switch in the composition of NF- κ B complexes bound to the -63 to -53 κ B1 site of the I κ B α promoter were also observed; with time after induction, decreased levels of transcriptionally active p65-p50 and increased c-rel-p50 heterodimers were detected at the κ B1 site. Mutation of either the κ B1 site or the Sp1 site abolished transcription factor binding to the respective sites, as well as the inducibility of the I κ B α promoter in transient transfection studies. Based on these results, specific activation of TD-I κ B α can block NF- κ B-regulated gene expression and HIV-1 infection.

Resumé

La régulation du niveau transcriptionnel du Virus de l'Immunodéficience Humaine de type 1 (HIV-1) se fait en partie, par la voie de signalisation NF- κ B/Rel due à la présence de sites de fixation à NF- κ B au niveau du LTR (Long Terminal Repeat) de HIV-1. En absence de stimulation, les sous-unités de NF- κ B capables de lier l'ADN sont séquestrées au niveau du cytoplasme par les proteines inhibitrices I κ B. Suite à une stimulation induite soit par des cytokines, soit par une infection virale ou par la présence d'ARN double brin, il y a phosphorylation de la sous-unité α de I κ B et dégradation de la protéine I κ B. Ainsi, ce processus conduit à une libération de NF- κ B et à une augmentation de l'expression des genes régulés par ce facteur.

La caractérisation de mutants transdominants de I κ B α (TD-I κ B α) a été effectuée dans des cellules Jurkat (lymphocyte T) en évaluant leurs effets sur le degré d'activation du LTR de HIV-1 suite à l'action simultanée du TNF- α (Tumor Necrosis Factor) et de la protéine transactivatrice Tat du HIV. Nos études démontrent que la co-expression de la protéine IkBa de type sauvage avec la protéine mutée transdominante, TD-IkBa, inhibe l'effet svnergique de Tat-TNF α sur l'activation du LTR de HIV. Ce degré d'inhibition est proportionnel au niveau d'expression de la protéine mutée. De plus, le mutant TD-IkBa est capable d'inhiber la multiplication virale lors d'un premier cycle d'infection dans les cellules COS-1. Afin d'observer l'effet de l'expression de TD-IxBa sur la mutilplication de novo de HIV, nous avons choisi d'établir des lignées de cellules Jurkat pouvant exprimer TD-IkBa de façon régulée. Ainsi, le contrôle de l'expression génique dans ces cellules est modulé par la presence ou l'absence de doxycycline (Dox) dans le milieu de culture. En présence de Dox, l'expression induite de TD-IκBα diminue la capacité de NF-κB à lier l'ADN de même que niveau d'activation de gènes régulés par le LTR. Un suivi de l'infection dans le temps de ces cellules démontre une inhibition de la multiplication du HIV suite à l'expression de TD-1kBa de manière induite. 24 heures suivant l'expression de TD-1kBa, nous observons une diminution du niveau d'expression de la protéine endogène IkBa. TD-IkBa serait donc capable de réprimer l'expression de gènes régulés par NF-kB. La production de protéine TD-IkBa provoque également une réduction du niveau transcriptionnel du gène IkBa, due à une sequestration au niveau du cytoplasme de la protéine Rel A (p65) par TD-I κ B α . Une empreinte génomique effectuée in vivo, révèle la présence d'éléments régulateurs de la transcription non seulement au site $\kappa B1$ en position -63 à -53 mais également à un site adjacent au site Sp1 (-44 à -36) du promoteur IkBa. Des essais de protection in vivo démontrent que ces sites ne sont plus protégés suite à une induction de l'expression du mutant transdominant. L'attachement de NF-kB à son inhibiteur est prolongé et on observe un changement dans la composition des complexes NF- κ B capables de lier le site κ B1 du promoteur I κ B α . En effet, on note une réduction au site κ B1 de la forme transcriptionnellement active (p65-p50) et une augmentation de la forme hétérodimérique crel-p50. Des mutations affectant soit le site κ B1 ou Sp1 empêchent l'attachement du facteur de transcription à ces sites de même que l'activation transcriptionnelle du promoteur I κ B α . L'ensemble de ces résultats démontre que l'activation d'un répresseur transdominant de I κ B α peut bloquer non seulement l'expression des gènes régulés par NF- κ B mais également une infection virale à HIV.

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Preface

In accordance with the guidelines for thesis preparation, I have chosen to present the results of my research in classical form. A General Introduction is presented in Chapter I, followed by detailed Materials and Methods in Chapter II. The results are described in Chapters III, IV and V and appear in the following articles:

 Beauparlant P*, Kwon H*, Clarke M, Lin R, Wainberg M, Sonenberg N, Hiscott J.
 1996 Transdominant mutants of IκBα block the Tat-TNF synergistic activation of HIV-1 gene expression and virus multiplication. J. Virol. 70: 5777-5785.
 (*both authors contributed equally to this paper)

2. Hiscott J. Beauparlant P. Crepieux P, DeLuca C, Kwon H, Lin R, Petropoulos L. 1997 Cellular and viral protein interactions regulating $I\kappa B\alpha$ activity during human retrovirus infection. J. Leukocyte Biol. 62: 82-91.

3. **Kwon H.** Pelletier N, DeLuca C, Genin P, Cisternas S, Lin R, Wainberg M, Hiscott J. 1998 Inducible expression of $I\kappa B\alpha$ repressor mutants interferes with NF- κB activity and HIV-1 replication in Jurkat T cells. J. Biol. Chem. **273**: 7431-7440.

4. Algarte M*, **Kwon H***. Genin P*, Hiscott J. 1999 Identification by In Vivo genomic footprinting of a transcriptional switch containing NF- κ B and Sp1 that regulates the I κ B α promoter. *Mol. Cell. Biol.* **19**:6140-6153.

(*These authers contributed equally to this paper)

5. DeLuca C, Kwon H, Lin R, Wainberg M, Hiscott J. 1999 NF-κB activation and HIV-1 induced apoptosis. *Cytokine and Growth Factor Reviews* 10:235-253.

A General Discussion and summary of the results appear in Chapter VI. References cited in this thesis are found Chapter VII.

The candidate was responsible for all the research described in this thesis and would like to acknowledge the contribution of several experiments carried out by colleagues. Results obtained by Dr. Pierre Beauparlant and Michelle Clarke are shown in Figure 8, 9, 11 and 12. Dr. Rongtuan Lin generated inducible expression vectors used in Chapter IV. Nadine Pelletier is responsible for the results presented in Figure 18. In vivo genomic footprinting presented in Figure 22 to 25 were performed by Drs. Pierre Genin and Michelle Algarte. The candidate also wishes to acknowledge Sonia Cisternas and Dana Zmeureanu for technical assistance.

The candidate was also involved in studies with other reseachers in the laboratory which resulted in the following publications:

6. Crepieux P, Kwon H, Leclerc N, Spencer W, Richard S, Lin R, Hiscott J. 1997 I κ B α physically interacts with a cytoskeleton-associated protein through its signal response domain. *Mol. Cell. Biol.* 17: 7375-7385.

7. DeLuca C, Kwon H, Pelletier N, Wainberg M, Hiscott J. 1998 NF-κB protects HIV-1-infected myeloid cells from apoptosis. *Virology* 244: 27-38.

8. Spencer W, **Kwon H**, Crepieux P, Lin R, Hiscott J. 1999 Taxol selectively blocks microtubule dependent NF- κ B activation by phorbal ester via inhibition of I κ B α phosphorylation and degradation. *Oncogene* 18:495-506.

9. Genin P, Mamane Y, **Kwon H**, Hiscott J. 1999 Differential regulation of CC chemokine gene expression in human immunodeficiency virus-infected myeloid cells. *Virology* **261**:205-215.

Mamane Y, Heylbroeck C, Genin P, Algarte M, Servant M, LePage C, DeLuca C,
 Kwon H, Lin R, Hiscott J. 1999 Interferon Regulatory Factors: The Next Generation.
 Gene 237:1-14.

11. Ishii T, **Kwon H**, Hiscott J, Mosialos G, Koromilas A. Enhanced $I\kappa B\alpha$ phosphorylation and NF- κB activation in NIH-3T3 cells expressing mutants of the IFN-inducible protein kinase PKR (Submitted to JBC).

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Abbreviations

AIDS	Acquired immunodeficiency syndrome
ARM	Arginine rich RNA binding motif

CAK	cyclin-dependent kinase-activating kinase
СВР	CREB-binding protein
CD4	Cluster determination antigen 4
CDK	Cyclin-dependent kinase
CKII	Casein kinase II
CMV	Cytomegalovirus
CREB	cAMP response element binding protein
CTD	C-terminal domain (Pol II)
ddC	2'.3'-Dideoxycytidine, Zalcitabine
ddI	2',3'-Dideoxyinosine, Didanosine
d4T	2',3'-Didehydro-3'-deoxythymidine, Stavudine
DNA	Deoxyribonucleic acid
Dox	Doxycycline
dsRNA	Double stranded RNA
EBV	Epstein-Barr virus
FADD	Fas associated death domain protein
G-CSF	Granulocyte colony stimulating factor

GM-CSF	Granulocyte/macrophage colony stimulating factor
HIV-1	Human immunodeficiency virus-1
HLH	helix-loop-helix
HTLV-1	Human T cell leukemia virus-l
IAP	Inhibitor of apoptosis protein
ICAM-1	Intercellular adhesion molecule-1
IFN-β	β-interferon
ΙκΒ	Inhibitory kappa B protein
IKK	IkB kinase
IL	Interleukin
IL-1RAcP	IL-1 receptor accessory protein
IL-1RI	cell surface type-I receptor
IRAK	IL-1 receptor associated kinase
IRF	Interferon regulatory factor
LBP	Leader binding protein
LEF-1	lymphoid enhancer binding factor-1
LMB	leptomycin B
LPS	Lipopolysaccharide
LTR	Long terminal repeat
LT-β	Lymphotoxin β
LZ	leucine zipper

MAP3K Mitogen-activated protein kinase kinase kinase

MEKKI	Mitogen-activated protein kinase/extracellular signal-
	regulated kinase kinase 1
MHC	Major histocompatibility complex
mRNA	Messenger RNA
NES	Nuclear export sequence
NFAT	Nuclear factor of activated T cells
NF-ĸB	Nuclear factor kappa B transcription factor
NIK	NF-kB Inducing kinase
NLS	Nuclear localization sequence
NRE	Negative regulatory element

PBMC	Peripheral blood mononuclear cells
p/CAF	p300/CBP-associated factor
PDGF	Platelet-derived growth factor
PEST	Proline, glutamic acid, serine, threonine rich domain
РНА	phytohemagglutinin
PICOT	PKC-interacting cousin of thiredoxin
РІЗК	phosphatidylinositol 3-kinase
PKA .	cAMP-dependent protein kinase A
РКС	protein kinase C
PKR	dsRNA dependent protein kinase
РМА	phorbol myristate acetate
PP2A	protein phosphatase 2A
P-TEFb	positive transcriptional elongation factor b

Rev	
RHD	Rel homology domain
RIP	receptor interacting proteins
RNA	Ribonucleic acid
RNAPII	RNA polymerase II
RRE	Rev response element
SV40	Simian virus 40
TAL	transactivation domain 1
TABI	TAK1 binding protein 1
TAHs	Tat-associated histone acetyltransferases
TAKs	Tat-associated kinases and
ΤΑΚΙ	TGF-β Activated Kinase 1
TAR	Tat responsive element
Tat	trans-activator of transcription
TBP	TATA-binding protein
TFIIH	transcription factor II H
TGF-β	Transforming growth factor-β
ΤΝFα	Tumor necrosis factor-a
TNFR	TNF receptor
TRADD	TNFR associated death domain
TRAF	TNFR associated factor
UBP	Upstream binding protein

VCAM-1 Vascular cell adhesion molecule-1

wild type

WT

CHAPTER I

GENERAL INTRODUCTION

1.0 The NF-kB family of transcription factors and the IkB family of inhibitory proteins

The NF- κ B/Rel family of transcription factors plays a pivotal role in immunomodulation through the activation of cellular genes that encode cytokines, cell surface receptors, and acute phase proteins as well as viral genes such as the human immunodeficiency virus type 1 (HIV-1) long terminal repeat (LTR) (16, 20, 365, 429). In unstimulated cells, NF- κ B/Rel proteins are sequestered in the cytoplasm by the I κ B inhibitory proteins. Upon stimulation with cytokines, viruses or dsRNA (double stranded RNA), I κ B α is rapidly phosphorylated and degraded, resulting in the release of NF- κ B and a subsequent increase in NF- κ B-regulated gene expression. The I κ B α gene contains NF- κ B binding sites in its promoter, so NF- κ B is able to regulate the transcription of its own inhibitor (55, 74, 185, 228, 407). This autoregulatory control of I κ B α expression by NF- κ B is in part responsible for the transient nature of NF- κ B activation. The first section will discuss each member of the NF- κ B/Rel and I κ B families and some recent findings in this field of research.

1.1 The NF-xB family of transcription factors

The NF- κ B/Rel (here on referred to as NF- κ B) family can be subdivided into two subgroups based on structure and function (Figure 1): the DNA binding and non-DNA binding proteins. The DNA binding proteins include NF- κ B1 (p50) (52, 140, 208), NF- κ B2 (p52) (50, 302, 381), RelA (p65) (309, 368), c-Rel (56) and RelB (369, 370). The non-DNA binding proteins include NF- κ B precursor proteins NF- κ B1 (p105) and NF- κ B2 (p100) which are proteolytically cleaved to generate the DNA binding proteins p50 and p52, respectively (50, 52, 140, 208, 302, 381). Each member of the family shares an N-terminal 300 amino acid domain known as the Rel homology domain (RHD), which is involved in the formation of a DNA binding dimer complex that associates with a

Figure 1. The NF-KB family of transcription factors and IkB family of inhibitory proteins. NF-kB family members contain well-conserved N-terminal rel homology domains (RHD): , which are composed of the DNA binding domain: , dimerization domain, and nuclear localization sequence (NLS): (N). p50 and p52 are produced by a unique cotranslational process involoving 26S proteasome or by proteolysis of the precursor proteins, p105 and p100, respectively. Both p105 and p100 contain a glycine rich region (GRR): [G], which is important for proteolysis of these precursors, and the Cteminal ankyrin repeats: which are present in IkB proteins. There is also a wellconserved protein kinase A (PKA) site: D in the RHD of p65, p50, c-rel, -105, p65, crel and rel B contain transactivation domain: **E** in their C-termini. Rel B also contains a leucine zipper () in the N-terminus. IkB proteins contain ankyrin repeats: , through which, they interact with NF-kB proteins. NLSs are also present in IkBa, IkBβ, and Bcl-3. N-terminal signal response and C-terminal PEST domains are designated by and respectively. N- and C-terminal proline- and serine-rich domains in bcl-3 are shown as P and S/P. IKK complex and CKII phosphorylation sites are shown by (P) and (P). respectively, as well as other sites (🕑) phosphorylated by unidentified kinases.



decameric consensus sequence 5'-GGGPuNNPyPyCC-3' in the promoters of target genes. The RHD is also responsible for nuclear localization and dimerization between different NF- κ B members. Nuclear import of NF- κ B proteins is accomplished by virtue of a nuclear localization sequence (NLS) that is located at the C-terminal region of the RHD and is characterized by a short stretch of basic amino acids which resembles the classical NLS (RKKKRKV), as typified by the NLS of simian virus 40 (SV40) large T protein (29, 128, 143, 467). Although a direct involvement of the importin- α -importin- β (importin- α - β) receptor in the nuclear import of rel proteins has not been demonstrated, the presence of a classical NLS within NF- κ B proteins strongly suggests that nuclear import may be mediated by this pathway. Among NF- κ B family members, p65, c-rel and relB contain C-terminal transactivation domains. The dimer composition of different NF- κ B subunits and the sequence context of NF- κ B sites in different promoters contributes to the differential specificity of gene activation (66, 125, 223, 229, 251, 331).

1.1.1 RelA (p65)

The most abundant complex of NF- κ B in cells is the p50/p65 heterodimer, in which the p65 subunit contains the transcriptional activation domain. Along with phosphorylation of I κ B proteins, p65 is also phosphorylated during the activation of NF- κ B by inducers such as tumor necrosis factor- α (TNF α), lipopolysaccharide (LPS) and hydrogen peroxide (101, 298, 475). An inactive form of the cAMP-dependent protein kinase A catalytic subunit of PKA, PKAc, has been shown to be associated with the NF- κ B/I κ B complex (475). During induction of NF- κ B by LPS, the associated PKAc becomes active and the concomitant phosphorylation of the p65 subunit on serine 276 in the RHD occurs. This phosphorylation is required for efficient transcriptional activation by NF- κ B and occurs after the degradation of NF- κ B with CBP (CREB-binding protein) and p300, which plays an essential role in NF- κ B transcriptional activity (138, 330, 476). NF- κ B-dependent

transcription has been shown to be inhibited by adenovirus E1a protein, which blocks the ability of CBP to associate with the histone acetylase p/CAF (p300/CBP-associated factor), which suggests that histone acetylation plays an important role in transcription through NF- κ B (323, 462).

Recently, p65 has been shown to be phosphorylated in vitro by the immunoprecipitated IkB kinase (IKK) complex (composed of IKK $\alpha/\beta/\gamma$, see below) and by a recombinant wild type IKK α or a constitutively active mutant of IKK β with a specificity constant similar to that of $I\kappa B\alpha$ (281, 282). Two other phosphorylation sites in p65 have been identified: TNF α -induced phosphorylation of p65 at serine 536 has been shown to be mediated by IKKs prior to the nuclear translocation, although the functional importance of this phosphorylation site has not been investigated (373). An additional TNF α -induced phosphorylation site was mapped at serine 529 within the C-terminal transactivation domain 1 (TA1) of p65 (435). This phosphorylation was shown to increase NF-kB transcriptional activity without affecting its nuclear translocation or DNA binding affinity. The kinase responsible for phosphorylation at serine 529 and the mechanism by which this phosphorylation potentiates transcriptional activity is currently unknown. The transactivational potential of p65 was also shown to be mediated by p38 and mitogenactivated protein kinases (MAPKs) (427). In addition, phosphorylation and transcriptional activity of a defined region within the TA2 domain were shown to be stimulated upon phorbol myristate acetate (PMA) (383). On the other hand, activation of NF- κ B by Interleukin (IL)-1 α has been shown to be accompanied by casein kinase II (CKII)-mediated phosphorylation of p65 in which two potential CKII phosphorylation sites located at serine 276 and 539 (41). Finally, phosphatidylcholine-specific phospholipase C, protein kinase C (PKC) and phosphatidylinositol 3-kinase (PI3K) have also been shown to be implicated in the phosphorylation and activation of p65 upon IL-18 or TNF α treatment (36, 403). Therefore, these studies strongly suggest that a second signaling pathway, which is activated in parallel to the cascade leading to $I\kappa B\alpha$ phosphorylation and degradation by NF- κB inducers mentioned above, is required for p65-mediated transcriptional competency.

1.1.2 *c-rel*

p50/p65 complexes have been the most extensively studied NF-kB dimers, therefore much less is known about the regulation and function of the transactivating subunit c-rel. As c-rel is the cellular homolog of the viral oncogene v-rel, it is not surprising that there is a correlation between the amplification/overexpression of the c-rel gene and oncogenesis (142). c-rel is present in both nuclear and cytoplasmic NF- κ B complexes (21, 289). While p65 is found in the nucleus during early phase of NF-kB activation, the induced expression of nuclear c-rel is largely delayed for several hours, which may be due to the fact that c-rel gene expression is also regulated by NF- κ B (151, 154, 289). Like p65, c-rel also contains a C-terminal transactivation domain which was shown to have a weaker transactivation potential and which lacks homology with the corresponding domain in p65 (57, 184, 196, 350). Therefore, in promoters such as the HIV-LTR and the IL-2R α promoters, c-rel acts as a specific inhibitor of nuclear p65 function through interference with p65 binding to the κB enhancer (105). Both proteins have been shown to interact with TATA-binding protein (TBP) although, unlike p65, crel has not yet been shown to directly interact with p300/CBP (60, 138, 206, 330, 384). In addition, the cytoplasmic and nuclear regulation of c-rel has recently been shown to be controlled by the discrete functional domains of $I\kappa B\alpha$ (263).

1.1.3 Rel B

Rel B is a strong transcriptional activator that exhibits many of the classical features of the NF- κ B family (49, 50, 103, 370). However, unlike other NF- κ B members, RelB

cannot form homodimers and only heterodimerizes efficiently with p50 and p52 (104). Rel B heterodimers have a much lower affinity for IkBa than other NF-kB complexes, which makes them less susceptible to inhibition by IxBa. As a result, RelB heterodimers are predominantly localized to the nucleus, where they represent constitutive NF-kB activity (104, 236). In lymphoid tissues, high levels of RelB heterodimers are expressed, which suggests that they play an important role in the constitutive expression of κB regulated genes in lymphoid tissues (65, 236, 237, 334, 439). Unlike p65 and c-rel, Rel B lacks a PKA phosphorylation site in the RHD which has been shown to be important for the transactivational potential of p65 (475, 476) and is also quite divergent in sequence in that region of the Rel domain. Recently, RelB was shown to be an important transcriptional suppressor in fibroblasts by limiting the expression of proinflammatory mediators such as IL-1 α , IL-1 β and TNF α upon LPS stimulation and by modulating the stability of $I\kappa B\alpha$ protein (457). It is also possible that RelB can inhibit p65/RelA or c-rel activities by driving the expression of $I\kappa B\alpha$ since it can strongly induce the expression of I κ B α and is inefficiently inhibited by I κ B α (104, 114). Finally, RelB has been shown to be an important player for kB-dependent gene demethylation in B cells, which represents the first demonstration of a trans-acting factor involved in cell-type-specific demethylation (211, 212, 457).

1.1.4 p105/50 and p100/52

Unique among the NF- κ B family members, the NFKB1 and NFKB2 genes encode two proteins each: p105/p50 and p100/p52 (50, 140, 208, 302, 381). The N-terminal portion of p105 and p100 correspond to the p50 and p52 subunits of NF- κ B, respectively, which appear to be produced by proteolytic processing. The C-terminal portions of p105 and p100 contain ankyrin repeats, which allow them to function as an I κ B (15, 20, 273, 349). Proteolytic processing of p105 to p50 appears to be a constitutive event because p105 and
p50 are produced in nearly stoichiometric amounts in most cells (248, 249, 299). Ubiquitination and the 26S proteasome have been shown to be involved in the generation of p50, which requires a glycine-rich region in the C-terminal region of p105 (112, 249, 320). Some research publications have indicated that like $I\kappa B\alpha$, induced processing of the precursor p105 is followed by phosphorylation of the proteins upon stimulation with TNFa, dsRNA or phorbol ester, therefore, signal-induced enhanced processing to p50 has been proposed (265, 278, 280, 298, 303). However, recent information suggests that p105 can be completely degraded without giving rise to the processing product p50 when the MAP3K, Cot/Tpl-2, is overexpressed (32). In addition, only modest changes were observed in the p50/p105 ratios upon stimulation. Likewise, in LPS-stimulated monocytes, p105 was shown to undergo degradation without enhanced generation of p50 by processing (157). Therefore, a classical product-precursor relationship between p105 and p50 is not probable. Instead, processing of p105 and p100 has recently been shown to occur co-translationally by a proteasome-mediated process which also does not follow a classical product-precursor relationship (169, 248). In addition, like p65 and IxBa, p50 can also be phosphorylated upon induction such as PMA/Phytohemagglutinin (PHA) induction and this phosphorylated form of p50 binds to kB site with a much greater affinity (239).

1.2 IkB family of inhibitory proteins

NF- κ B activity is regulated in part at the level of subcellular localization. In unstimulated cells, the NF- κ B complex is retained in the cytoplasm through the interaction with the inhibitory I κ B proteins. The members of the I κ B family (Figure 1) include I κ B α (162), I κ B β (415), I κ B γ (137), I κ B ϵ (448) and Bcl-3 (164), as well as the precursor proteins p105 (256) and p100 (280). These proteins contain multiple ankyrin repeats that bind to NF- κ B and mask the NLS within the RHD, thus preventing the translocation of the DNA-

binding proteins (27, 29). Each I κ B family member has a different specificity for different NF- κ B proteins: p100 and p105 can bind efficiently to all mammalian NF- κ B factors (163, 164, 183, 256, 280, 299, 349, 379); I κ B α , I κ B β and I κ B ϵ strongly prefer dimers containing p65 or c-rel (162, 255, 415, 421, 448); Bcl-3 has a strong preference towards p50 or p52 homodimers (51, 308, 456).

1.2.1 *ΓκΒα*

The structure and degradation mechanism of $I\kappa B\alpha$ has been the most extensively studied among the IkB family members. IkB α , which was the first IkB protein to be identified, is encoded by the human cDNA clone MAD3, which is highly homologous to cDNA clones isolated from chicken, rat and pig, called pp40, RL-IF1, and ECI-6, respectively (14, 89, 90, 162, 414). The $I \kappa B \alpha$ proteins can be divided into three domains: the N-terminal signal response domain, the ankyrin repeat domain and the PEST (proline, glutamine, serine, threonine) domain (Figure 2). The C-terminal 35 amino acid PEST region is composed of negatively charged residues which contain multiple CKII phosphorylation sites. While this portion of the protein is not required for inducible degradation or interaction with NF-kB, phosphorylation in this domain regulates the constitutive degradation of the protein (7, 22, 250, 276, 386, 406, 424). Mutations of Ser-283, Thr-291 and Thr-299 of the CKII phosphorylation residues to alanine increased the intrinsic stability of $I\kappa B\alpha$ without affecting inducer-mediated degradation (250). In contrast, Cterminal truncation of $I\kappa B\alpha$ has been shown to prevent inducer-mediated degradation and the PEST regions have been involved in protein breakdown catalyzed by the proteasome (26, 53, 54, 320, 351, 449). Therefore, the function of the IxBa C-terminus still remains unclear. Furthermore, the PEST domain of IkBa has also been implicated in the inhibition of p65/RelA and c-rel DNA binding but not for cytoplasmic retention of c-rel or p65/relA homodimers (111, 163, 372).

Figure 2. Regulatory elements in human $I \times B \alpha$. IxB α can be divided into three domains; N-terminal signal response domain which is composed of Lys 21/22 for ubiquitination and Ser 32/36 for phosphorylation by IKK complex as well as Tyr 42 phosphorylation site; the six ankyrin repeats indicated by red boxes, which mediate the interaction with, and sequestration of, NF-xB family members; and PEST domain (rich in proline, glutamic acid, serine and threonine residues; indicated by green box) which contains three CKII phosphorylation sites, which are Ser 283, Thr 291 and Thr 299 and important in regulating constitutive IxB α protein turnover. Two nuclear export sequences (NESs, in purple letters) are found in the N- and C-terminal regions and permits nuclear IxB α to remove DNA bound NF-xB and translocate it to the cytoplasm. A nuclear localization signal (NLS, in green letters) is located in the second domain of the ankyrin repeats.



Ankyrin repeats, the common structural feature of all IkB proteins, are multiple, closely adjacent and homologous 33 amino acid sequences (46, 307). The ankyrin repeats are not only restricted to IkB proteins but are also present within a family of proteins that regulate interactions between a variety of membrane structures and the cytoskeleton (264). The repeats bind specifically to the dimerization domain of NF-kB proteins (164, 183, 256, 456). Structure-function analysis reveals that the entire repeat domain is required for interaction with NF-kB, and association with NF-kB results in the dissociation of preformed NF-kB-DNA complexes as well as the hindrance of nuclear translocation of NF-kB (45, 164, 167, 256, 467). Recently, the structure of IkB-NF-kB complexes was revealed by crystallography (13, 180, 186). Binding of IkB α to the dimerized RHDs of NF-kB (p65/p50) through ankyrin repeat domains may inhibit NF-kB from binding to DNA due to the rotation of the N-terminal Immunoglobulin (Ig)-like domain of the p65 RHD. As expected, this interaction also masks the nuclear localization sequence (NLS) of p65 by inducing the unstructured NLS into an α -helical conformation, thus preventing translocation of p65 to the nucleus.

Most attention was focused on the N-terminal signal-response domain, since phosphorylation at Ser-32 and Ser-36 caused inducer-mediated degradation of $I\kappa B\alpha$. Therefore, the main and first task for researchers was to identify the kinase responsible for the phosphorylation at Ser-32 and Ser-36. Long term efforts by many researchers recently resulted in the identification of the I κ B kinase (IKK) complex (discussed later in the thesis). Phosphorylation at serines 32 and 36 marks I $\kappa B\alpha$ for ubiquitination at lysines 21 and 22; which leads to subsequent degradation by the proteasome (4, 19, 53, 54, 72, 99, 353, 354, 380, 416, 449). When the N-terminal I $\kappa B\alpha$ sequences containing these serine and lysine residues were fused to a heterologous protein, they served as an inducible destruction box (455). Even in the absence of stimuli, the I $\kappa B\alpha$ protein is continuously degraded. This continuous basal turnover may be controlled by a different mechanism, since neither the IKK phosphorylation sites nor the ubiquitination attachment are required, but this process is also mediated by the proteasome (218).

Newly synthesized $I\kappa B\alpha$ accumulates in the cytoplasm but has also been shown to be able to enter the nucleus and dissociate NF- κ B from its DNA binding sites and export NF- κ B back to the cytoplasm, thus terminating NF- κ B-dependent transcription in the nucleus (8, 9, 466). Recently, the NLS and two NESs (Nuclear export sequences) of IkBa were identified, which strongly supported the idea that $I\kappa B\alpha$ is able to shuttle between the nucleus and the cytoplasm. These two leucine-rich NES elements in IkBa are homologous to the NES found in shuttle proteins such as the HIV-1 Rev protein and protein kinase A inhibitor. N- and C-terminal NES are located from amino acid 45 to 55 and from 265 to 277, respectively (9, 116, 124, 193, 442). The $I\kappa B\alpha$ -derived NES can functionally substitute for the NES in HIV Rev (9, 124). The nuclear protein CRM1 (also known as exportin 1) has also been recently identified as the NES receptor (119, 127, 315, 405). In addition, nuclear $I\kappa B\alpha$ appears to be resistant to signal-induced phosphorylation and degradation. This results in nuclear accumulation of transcriptionally inactive $I\kappa B\alpha/NF-\kappa B$ complexes when cells are treated with leptomycin B (LMB), an inhibitor of NES-mediated nuclear export (352). However, contradictory results were obtained by Hope and co-workers which indicated that nuclear NF- κ B/I κ B α complexes are also sensitive to signal-induced degradation of IkBa through a proteasome-mediated mechanism (193). Moreover, proteasomes were also found in the nucleus, suggesting that degradation can occur directly in the nucleus (347).

Nuclear localization of $I\kappa B\alpha$ has recently been shown to be mediated by a novel nuclear import sequence within the second ankyrin repeat of $I\kappa B\alpha$. This sequence does not resemble the classical NLS, which is characterized by a short stretch of basic amino acids (371). Although the second ankyrin repeat of $I\kappa B\alpha$ contains the predominant nuclear

import sequence, other ankyrin repeats may also contribute to the nuclear localization of the full length $I \kappa B \alpha$ protein (371). Recently, $I \kappa B \alpha$ has been shown to be imported into the nucleus by a piggy-back mechanism (371) that involves additional protein(s) which contain a basic NLS and are able to interact with the ankyrin repeats of IkBa. This process requires GTP hydrolysis by Ran (a small GTPase) as well as the basic NLS receptors importin α and β (419). However, an unidentified NLS sequence in the first ankyrin repeat has been shown to be sufficient for temperature-dependent nuclear import of $I\kappa B\alpha$ (193). Interestingly, when $I\kappa B\alpha$ is overexpressed as an NF- κ B-bound form, it localizes exclusively in the cytoplasm, which suggests that NF- κ B interaction with $I\kappa$ Ba in the cytoplasm could mask a region of $I\kappa B\alpha$ involved in its nuclear import (467). Therefore, a mutual masking of the sequences responsible for the nuclear import of both NF- κ B and $I\kappa$ B α causes cytoplasmic retention of both proteins (419). In contrast, Johnson et al. recently proposed a shuttling model in which individual proteins or a complex of NF- κ B and I κ B α can shuttle between the nucleus and the cytoplasm (193). Thus, further analysis is required to resolve the mechanism of the nuclear import and export of NF-kB and IkB proteins.

1.2.2 **ΓκΒ**β

I κ B β protein was first identified by Zabel and Baeuerle (466) and, subsequently, human cDNAs for I κ B β were isolated (232). Unlike I κ B α , basal phosphorylation of I κ B β is required for interaction with NF- κ B (255). I κ B β has been shown to associate with different NF- κ B members depending on its phosphorylation status. Recombinant, unphosphorylated I κ B β could bind to p65 but not to c-rel, however, I κ B β phosphorylated at the C-terminal PEST domain could efficiently bind to c-rel (77). Human T-cell leukemia virus type 1 (HTLV-1) Tax-induced degradation of I κ B β leads to the release of c-rel-containing complexes, which emphasizes the physiological importance of c-rel-I κ B β

complexes (145). In different studies, recombinant $I \times B\beta$ did not exhibit a preference Furthermore, the major sites of constitutive between p65 and c-rel (415). phosphorylation of IkBB have been mapped to Ser 313 and Ser 315. These residues have been shown to be phosphorylated by CKII, which also phosphorylates the C-terminal region of $I\kappa B\alpha$ (77). Carboxy-terminal phosphorylation by CKII of $I\kappa B\beta$ has also been shown to increase its affinity to NF- κ B (417). Similar to I κ B α , I κ B β is also proteolytically degraded after stimulation with LPS, IL-1, $TNF\alpha$, or HTLV-1 Tax and contains the conserved N-terminal serines and lysines, suggesting that these molecules are controlled by similar mechanisms (99, 277, 415). Inducible phosphorylation residues were identified as Ser 19 and Ser 23 (99, 277), which were shown to be phosphorylated by a recently identified IKK complex (100, 346). Therefore, mutations of serine 19 and 23 to alanines in IkBB creates a dominant-negative form that is no longer degraded upon induction (99, 156, 277). Inducible degradation of IkBß was also blocked by the proteasome inhibitor MG132, which suggests that ubiquitination is required (99, 277). Furthermore, T cells from transgenic mice expressing a dominant negative mutant of $I\kappa B\beta$ showed a complete inhibition of persistent NF- κB activation (see below) upon PMA/PHA stimulation (11).

In contrast to $I\kappa B\alpha$, $I\kappa B\beta$ is not resynthesized immediately after stimulation and is degraded with delayed kinetics, which allows for persistent activation of NF- κB (415). Newly synthesized $I\kappa B\beta$ first accumulates as an underphosphorylated species which interacts with p65 without masking the NLS, thus maintaining NF- κB activity by protection of p65 from $I\kappa B\alpha$ in both the nucleus and the cytoplasm (408). A nuclear localization sequence (NLS) has not been identified in $I\kappa B\beta$, but has been suggested to be within the second ankyrin repeat (371). Previously, it was proposed that, due to the failure of masking NF- κB 's NLS by newly synthesized underphosphorylated $I\kappa B\beta$, the NF- $\kappa B/I\kappa B\beta$ complex is able to enter the nucleus by a piggy-back mechanism and activate transcription (408, 417). Recently, nuclear I κ B β has been shown to maintain persistent NF- κ B activation in HIV-1-infected myeloid cells (95). In addition, two different forms of human I κ B β , termed I κ B β 1 (43kDa) and I κ B β 2 (41kDa) were identified. The former is the most similar to I κ B α in responsiveness to inducing agents while the latter, which contains a truncated PEST domain in the C-terminus, is either degraded incompletely or inert in response to certain inducers (170). This emphasizes the importance of the C-terminal PEST domain on efficient proteolysis of I κ B β (159, 441).

1.2.3 **ΙκΒ**γ

IkB γ is the C-terminal half of p105 containing multiple ankyrin repeats which was believed to be produced by an alternative transcription start site in the intron of NFKB1 gene, thus p105, p50 and IkB γ are produced from the same gene (183, 256, 287). Unlike p105 which is ubiquitously expressed, IkB γ mRNA is specifically present in murine lymphoid cell lines (183). It associates with p65/p50, p50/p50 and c-rel, and inhibits crel nuclear translocation and c-rel-mediated transactivation. It was suggested that the activity of IkB γ is also regulated by phosphorylation since it contains a consensus sequence for phosphorylation by CKII and others (183). Moreover, the amount of IkB γ mRNA was decreased during B-cell differentiation suggesting a cell-type specific role of IkB γ (256).

1.2.4 **ΓκΒ**ε

IkBe, the most recently identified IkB family member, was isolated by two hybrid screens using p52, p50 and p65 as baits (245, 402, 448). Human IkBe, a 45 kDa protein, exists as multiple phosphorylated isoforms in resting cells and contains conserved serine residues (at 18 and 22) which closely resemble the signal response domain of IkB α but has no PEST-like sequences in the C-terminus (448). I κ B ϵ binds predominantly to p65 and c-rel, weakly to p50 and p52, and is able to displace NF- κ B from its DNA binding sites as well as inhibit NF- κ B-mediated transcription (245, 402, 448). Like I κ B α and I κ B β , upon induction with PMA/ionomycin and LPS, I κ B ϵ is proteolytically degraded with slower kinetics compared to I κ B α . The two conserved serine residues are required for the induced degradation of I κ B ϵ (448). Interestingly, I κ B ϵ expression is also upregulated by similar stimulants that activated I κ B α expression, suggesting that I κ B ϵ gene is also NF- κ B regulated (245, 448). Furthermore, the C-terminal region of murine I κ B ϵ is required for efficient inhibition of NF- κ B DNA binding (402).

1.2.5 *bcl-3*

Bcl-3, which was identified as a putative oncoprotein , is a unique IkB member, since it is most abundant in the nucleus and is not degraded upon activation of NF-kB-stimulating pathways (51, 120, 206, 308, 311). Bcl-3 was shown to bind p50 or p52 homodimers and induce p50 homodimers from cytosolic p105/p50 complexes without enhancing the processing of p105 (436). Recently, cellular Bcl-3 was shown to bind p50 but not p52 homodimers (166). Lower expression of p52 and less efficient processing of p100 to p52 may explain this observation, along with the fact that Bcl-3-p50 complexes are more abundant in some cell types (40, 61, 436). As p50 and p52 do not contain transactivation domains, it has been proposed that Bcl-3 may antagonize p50-mediated inhibition by dissociating p50 or p52 homodimers from DNA (121, 182, 205, 456). Conversely, ectopic expression of Bcl-3 enhanced the DNA-binding activity of p50 homodimers in the murine thymus (61). Supporting the latter, Bcl-3 has been demonstrated to form ternary complexes with p50 or p52 homodimers bound to DNA and act as a transcription activator which requires N- and C-terminal proline- and serine-rich domains (51, 126, 171, 321). The activation potential of Bcl-3-p50 complexes can be further stimulated by interaction of Bcl-3 with the histone acetylase Tip60 (91). The presence of two basic NLS in the N-terminal domain of bcl-3 and the inability of bcl-3 to mask NF- κ B NLS results in the nuclear import of the Bcl-3/p50 homodimer complex, mediated either by p50 NLS or bcl-3 NLS (473).

1.3 Homozygous disruption of NF-kB and IkB proteins

The generation of single and double knockouts and transgenic mice has yielded invaluable information about the physiological functions of various NF- κ B and I κ B proteins. Recently, Gerondakis *et al.* reviewed these genetic approaches in order to understand the function of these proteins (136). The phenotypes of single knockout mice are briefly discussed here.

1.3.1 Mice lacking NF-kB proteins

One of the interesting phenotypes of mice lacking p65 was a massive liver degeneration due to apoptosis implicating p65 in the inhibition of apoptosis (31). This was shown to be due to an increased sensitivity to TNF α -induced apoptosis (28, 423, 433). In addition, TNF α /p65 double deficient mice were found to be viable and have normal liver (106). These data further suggest that p65 protects the cells from TNF α -induced apoptosis. Although homozygous *nfkb1*-deficient mice develop normally, these mice are defective in B-cell activation (153, 392). Knockout mice lacking p52/p100 also develop normally but exhibit multiple defects in the immune system, which is consistent with the knowledge that p52-containing dimers, p52-c-rel and p52-RelB appear to play a particularly important role in the terminal stages of B-cell differentiation (62, 122, 150, 257). Based on studies with homozygous *c-rel*-deficient mice, c-rel plays an essential role in lymphocyte proliferation, immune and inflammatory responses, and T-cell development (48, 216). A dramatic reduction in constitutive kB-binding activity and specific defects in lymphoid tissues were observed in mice lacking relB (59, 440).

1.3.2 Mice lacking IxB proteins

Knockout mice lacking IkB α develop normally but die post-natally due to severe widespread inflammatory dermitis and granulocytosis (30, 214). Fibroblasts from these mice exhibited a prolonged NF-kB activation upon stimulation, suggesting that IkB α is required for post-induction repression of NF-kB. At present, no information on *IkBg*^{-/-} and *IkBb*^{-/-} mice is available. However, one would expect a similar phenotype in *IkBb*^{-/-} mice as seen in IkB α knockout mice due the functional similarity between the two proteins. Homozygous *bcl-3*-deficient mice also develop normally, but show defects in antigen-specific B- and T-cell responses (123, 387). Surprisingly, unlike *IkBa*^{-/-} and *bcl-3*^{-/-}, mice lacking IkB ϵ are indistinguishable from wild type animals, although IkB ϵ has been shown to have common features with IkB α (245, 279, 402, 448)

2.0 Mechanism of NF-kB activation

In response to a variety of stimuli, including TNF α , IL-1 β , LPS or viral infection (319), the most studied I κ B protein, I κ B α is phosphorylated at serine 32 and 36 residues by the recently identified 500-900 kDa I κ B kinase (IKK) complex. Phosphorylation targets I κ B α for ubiquitination, which is ATP dependent and involves the covalent attachment of multiple ubiquitin molecules to I κ B α lysine residues 21 and 22 by the recently identified I κ B α -ubiquitin ligase-E3 (pI κ B α -E3, (463)), targeting I κ B α for degradation by the 26S proteasome. This results in the release of NF- κ B proteins (72) which can now translocate to the nucleus to activate gene transcription (Figure 3). The function of the IKK complex and the upstream kinase that activate the IKK complex will be discussed in this section.

Figure 3. The biochemistry of NF-kB activation. NF-kB is sequestered in the cytoplasm by inhibitory IkB proteins. Stimulation by a diverse collection of agents and pathogens including TNF α , PMA, LPS and viruses lead to the activation of signaling cascades that are believed to culminate with activation of the IKK complex. The IKK complex is preferentially composed of IKK α , IKK β and IKK γ (A). Cell stimulation enhances the phophorvlation of all three IKK subunits which activates IKK complex (92). Activated IKK in turn phosphorlyates $I\kappa B\alpha$, which marks it for ubiquitination by recently identified plkBa-E3 and subsequent proteosome mediated degradation (B). NF-kB is released and translocates to the nucleus where it transactivates κB responsive genes (C). Target genes are selectively regulated by the distinct transcriptional activation potential of different subunit combinations. The I κ B α gene is regulated by NF- κ B leading to its resynthesis (C). De novo synthesized IkB α can associate with free NF-kB sequestering it in the cytoplasm and can enter the nucleus removing DNA bound NF-kB, thereby establishing an autoregulatory mechanism by which NF- κ B activation is limited (D). In addition, activated IKKs become autophosphorylated at the C-terminal serine cluster, which decrease IKK activity (E).



2.1 NF-kB Activation by the IkB Kinase (IKK) Complex

Except for induction with UV radiation and anoxia, NF- κ B activation requires the phosphorylation of I κ B α at the two N-terminal serines and its subsequent degradation (33, 181, 242). Early I κ B α degradation induced by UV irradiation requires intact N-(positions 1-36) and C-terminal (positions 277-287) sequences of I κ B α , while later I κ B α degradation requires the phosphorylation of the N-terminal serines (32 and 36) that is caused by the autocrine and paracrine action of IL-1 α (33, 242). However, I κ B α degradation by a different type of photonic radiation, γ radiation, required the phosphorylation of two serine residues (242). On the other hand, phosphorylation at tyrosine 42 of I κ B α induced by reoxygenation of hypoxic cells, led to NF- κ B activation in the absence of I κ B α degradation. This represents a proteolysis-independent mechanism of NF- κ B activation which implicates the tyrosine kinase p56^{lck} (181). Recently, tyrosine 42 phosphorylated I κ B α was shown to be sequestered by the p85 subunit of PI3 kinase via its SH2 domain from NF- κ B (35).

Based on mutational analysis of $I\kappa B\alpha$, it was suggested that the physiological $I\kappa B$ kinase should be serine specific, as substitution of the serine residues with threonines prevented inducible phosphorylation of $I\kappa B\alpha$ (99). Two high-molecular-weight (500-900 kDa) kinase complexes that appeared to specifically phosphorylate Ser-32 and -36 of $I\kappa B\alpha$ were recently identified (73, 100, 230, 282, 346, 451, 471). The difference between these two kinase complexes was that the activity of one complex was regulated via ubiquitination by an unknown mechanism while the other was not. The latter kinase complex has been shown to contain at least two catalytic subunits IKK α and IKK β and the regulatory subunit IKK γ /NF- κ B essential modulator (NEMO)/IKK-associated protein 1 (IKKAP1) (100, 281, 282, 346, 362, 451, 459, 471). IKK γ is devoid of a catalytic domain but contains three large α -helical motifs and a LZ, and has been shown to be absolutely essential for NF-kB activation by HTLV-1 Tax, LPS, PMA and IL-1 (281, 362, 459). IKK α was previously known as CHUK (conserved helix-loop-helix (HLH)) ubiquitous kinase], whose function was unknown (85). By searching the expressed sequence tag (EST) database, a protein kinase exhibiting an overall homology to IKK α of 52% was identified and named IKKβ (282, 346, 451, 471). Both IKKα and IKKβ are ubiquitously expressed. The structures of IKK α and IKK β are similar to each other, however they are unlike other known Ser/Thr kinases. Each protein is composed of an Nterminal kinase domain followed by a leucine zipper (LZ) region and a C-terminal helixloop-helix (HLH) domain. They can form homo- or heterodimers, which is mediated through binding between the LZ domains (282, 451, 470, 471). However, the predominant form of IKK complex (Figure 3A) is an IKK α /IKK β heterodimer associated with a dimer of IKK γ (282, 362) which is mediated by an interaction between IKK β and IKK γ (281, 459). Furthermore, the HLH region is not required for dimerization between IKK α and IKK β but is indispensable for efficient kinase activity through interaction with the kinase domain or possibly with upstream activators (92, 471). The LZ domain present in the C-terminal region of IKKg was also suggested to be involved in the interaction with the upstream kinases and/or activators (362). Some differences in the activities between IKK α and IKK β were identified by overexpressing wild type (WT) or dominant negative (kinase inactive) forms of each subunit: 1) when transfected alone, the activity of IKK α is relatively low compared to IKK β , which is constitutively active and requires costimulation with TNF α to become fully activated (282, 451, 471), 2) A dominant negative form of IKKB efficiently inhibited NF- κ B activation upon TNF α or IL-1 while inhibition of NF-kB activation by a dominant negative form of IKKa was not consistent (100, 282, 346, 451, 471), 3) Both IKKa and IKKB phosphorylate Ser-32 and -36 of IkBa in vitro, with IKKB exhibiting much greater activity than IKKa (231, 470). Conversely, IKK β could phosphorylate both Ser-19 and -23 of IkB β equally, while IKK α phosphorylated poorly and preferentially Ser-23 alone (100, 282, 346, 451). Once

activated, IKK β became autophosphorylated at a carboxy terminal serine cluster, which decreased IKK activity and prevented prolonged activation of the inflammatory response which can be an additional regulatory step to inhibit prolonged NF- κ B activation (Figure 3E) (92). Furthermore, IKK activity was inhibited by the protein phosphatase 2A (PP2A) catalytic subunit, which was also found in the IKK complex (100). The *in vivo* function of PP2A on IKK activity is currently unknown. Recently, two different functions of IKK α in the IKK complex have been suggested: Inhibition of IKK β activity by IKK α in the absence of inducers and the induction of IKK β by IKK α in the presence of inducers (310). In the latter case, IKK α plays a role in relaying upstream signals to IKK β in a directional manner, therefore IKK α is a pre-requisite for induction of IKK β activity, which is contradictory to the previous suggestion (92).

2.2 Upstream kinases activating IKK

After the identification of the IKK complex, attention focused on the upstream kinases in many different signal transduction pathways that all converge to the IKK complex. Among the upstream kinases, four are MAP3Ks. This is not surprising because MAP kinase consensus sequences were identified in both IKK α and IKK β . Throughout the course of studies on these upstream kinases, many contradictory results have emerged. This section summarizes the recently identified upstream kinases of IKK complex.

2.2.1 NF-KB Inducing kinase (NIK)

NIK (MAP3K, serine/threonine kinase) was initially identified as a TNFR associated factor-2 (TRAF-2) interacting protein by two-hybrid screening of a human B-cell cDNA library (268). Subsequently, IKK α was also isolated through a yeast two hybrid screening as a protein that interacts with NIK (346). NIK was shown to be a part of IKK

complex isolated from IL-1-stimulated cells (83). Overexpression of NIK enhanced the ability of the IKKs to phosphorylate IkB and activate NF-kB (100, 282, 346, 451, 471) while dominant negative mutants of NIK suppressed NF-kB activation by TNFa, IL-1, TNFR associated death domain (TRADD), receptor interacting proteins (RIP), TRAF-2, TRAF-5 and TRAF-6, which suggests that the convergence of these signaling pathways leading to NF-kB activation might be at the level of this kinase (Figure 4) (268, 404). NIK physically associates with and activates both IKK α and IKK β , and the carboxyterminal domain of NIK, which is also responsible for interaction with TRAF-2, mediates its interaction with IKK α (253, 268, 346, 451). Selective deletion of each of the three structural domains did not affect the ability of NIK to bind to IKK^β, suggesting that this association occurs via multiple interactions between the two proteins through different domains of IKK β (451). However, IKK α has been shown to be a better substrate than IKKß for phosphorylation by NIK in vitro and the Ser-176 in the kinase activation loop of IKKa was identified as the phosphorylation target by NIK (254). Thr-559 within the activation loop of NIK kinase domain plays a critical role in regulating the activation and autophosphorylation of this kinase (253). Nevertheless, involvement of NIK in NF-kB activation has become controversial based on three publications: binding of NIK to TRAF2 and its catalytic activity was not stimulated by TNF α (23). NIK is implicated in lymphotoxin (LT) signaling rather than in TNF α signaling (397). NF- κ B release was intact upon TNF α treatment of cells expressing a catalytically inactive mutant of NIK (469). However, inhibition of TNF α -induced NF- κ B dependent gene expression was observed, suggesting that NIK may affect transactivation potential of NF-kB but not IKK activation and release of NF- κ B from inhibitory complexes (469). Further analysis is required to elucidate the involvement of NIK in NF-kB signaling under more physiological conditions, since many studies have been performed by overexpression, which almost certainly does not accurately reflect physiological signaling events. Knockout mice lacking NIK as well as transgenic mice expressing catalytically inactive Figure 4. Signal transduction pathways of different activators of NF- κ B and upstream kinases of IKK complex. Binding of TNF α to its receptor causes recruitement of TRADD to the receptor. TRADD interacts with TRAF2 which is connected to IKK through NIK. RIP is interacting with TRADD, TRAF2 and p62 which transduces TNF signal to IKK through aPKC. Signal transduction pathway leading to IKK activation by TNF α is outlined in red arrows. IL-1 induced IKK activation (outlined in blue arrows) requires the recruitement of IL-RACP, MyD88 and IRAK to IL-1RI upon the engagement of IL-1. IRAK then dissociates from the receptor complex and interacts with TRAF6 that transduces the IL-1 signal to NIK and then to the IKK complex through TAK1/TAB1. CD3/CD28 costimulatory signaling pathways converge on NIK, leading to activation of the IKK complex (in black arrows). PMA induces IKK activation through PKC α (in green arrows).



mutants of NIK would provide more reliable information on the role of NIK in NF-κB activation.

2.2.2 Mitogen-activated protein kinase/extracellular signal-regulated kinase kinase 1 (MEKK1)

NF-kB activation occurs under conditions that also stimulate the MAPK pathway and, vice versa, the MAP kinase pathway can be activated by other known inducers of NF-kB such as the small GTPases Cdc42 and Rac1, which have been shown to activate NF- κ B (172, 230, 268, 283, 332, 345). MEKK1, which is a mammalian serine/threonine kinase in the MAP3K group (226) was copurified during the purification of the IKK complex, and both IKK α and IKK β contained a canonical MAP kinase kinase (MAP2K) activation loop (Ser-X-X-Ser) within their catalytic domains (282). Mutational analysis revealed that these serine residues (Ser-177 and Ser-181) in IKKB were essential for kinase activity, suggesting activation of IKK β by MEKK1 (Figure 4) (282). Recombinant MEKK1 has been shown to stimulate IKK β -mediated phosphorylation of IkB α , and overexpression of MEKK1 induced IKK β activity and NF- κ B reporter activity in the presence or absence of TNFa or IL-1 (231, 295, 301, 465). Many publications showed that MEKK1 is a much weaker activator of the NF- κ B transcriptional reporter compared to NIK (231, 297, 404). Some data suggest that there is the existence of a differential specificity of MEKK1 and NIK to IKK complex subunits: IKK β is the substrate of MEKK1, whereas IKKa is the substrate of NIK (254, 295). HTLV-1 Tax-induced NF-xB activation has been shown to mediated through the action of MEKK1, which then directly activates IKK β but not IKK α (465). In addition, recent studies show that IKK activation by Tax occurs through IKKy, which acts as a bridge between two molecules (78, 158, 192) and also through NIK (420). Involvement of MEKK1 also became controversial since MEKK-1 did not play a role in NF-kB activation in some studies, inconsistent with

those described above (100, 259, 297, 404). Other MAP3Ks, including MEKK2 and MEKK3, have been shown to activate IKKs *in vivo*, but MAP3Ks such as MEKK4, ASK1 and MLK3 failed to activate NF- κ B (108, 474), suggesting a specificity of NF- κ B activation by only a subset of MAP3Ks.

2.2.3 TGF-β Activated Kinase 1(TAK1)

TAK1, a recently identified MAP3K, together with its activator protein, TAK1 binding protein 1 (TAB1) (396), has been shown to be a kinase that links TRAF6 to the NIK-IKK cascade in IL-1 signaling (306). Therefore, the signaling pathway of NF-kB activation by IL-1 may be as follows (Figure 4). IL-1 binds to the cell surface type-I receptor (IL-1RI), which forms a complex with the accessory protein IL-1RAcP (IL-1 receptor accessory protein) and the adapter protein MvD88 as well as a Ser/Thr kinase named IRAK (IL-1 receptor associated kinase) (147, 292, 444). IRAK then dissociates from the receptor complex and interacts with TRAF6, which transduces the IL-1 signal to NIK and then to the IKK complex through TAK1 (63, 64, 306, 443). Although TAK1 was first shown to be activated by TGF- β and bone morphological protein (458), no functional relationship between TGF- β signaling and the NF- κ B activation has been documented. In other words, TGF- β treatment could not induce the nuclear translocation of NF- κ B (375). Therefore, TAK1 may be involved in the NF-kB activation induced by stimuli other than TGF- β , such as IL-1 and TNF α (see below). TAK1 has also been shown to interact with both IKK α and IKK β and induce IkB α degradation (374). Furthermore, TAK1/TAB1 complex also plays a role in TNF α -induced NF- κ B activation (374). In contrast to the above study which suggests that TAK1-induced IKK activation is mediated through NIK, TAK-1 mediated NF- κ B activation has been shown to be independent of NIK and the further study revealed that dominant negative (DN) mutants of NIK partially inhibited TAK 1-induced NF- κ B activation (374). Therefore, understanding the precise relationship between TAK1 and NIK in TNF α -induced NF- κ B activation requires further investigation.

2.2.4 Cot/Tpl-2

The proto-oncogene Cot/Tpl-2, another MAP3K related serine-threonine kinase which stimulates both the ERK and JNK pathways (288, 324), has been shown to physically assemble and phosphorylate NIK in vivo (252). It was proposed to be an upstream kinase of NIK upon TCR/CD3 (Figure 4) and CD28 costimulation, but not TNF α in NF- κ B activation (Figure 4). In contrast, another study by Belich et al., showed that Cot/Tpl-2 was involved in TNF α -induced NF-xB activation through increased complete degradation of p105 (32). Both studies used almost identical systems, except for two different kinaseinactive mutants of NIK to analyze their effects on TNF α -induced NF- κ B activation. The latter observed an inhibitory effect of the Cot/Tpl-2 mutants on TNF α -induced NF- κ B activation. Therefore, at present, it is not clear whether Cot/Tpl-2 is involved in TNF α signaling. Belich et al. also demonstrated a direct interaction between p105 and Cot/Tpl-2, however, no direct phosphorylation by Cot/Tpl-2 could be demonstrated which suggests that it may regulate p105 phosphorylation through an unidentified downstream kinase, reminiscent of the regulation of $I\kappa B\alpha$ phosphorylation by NIK (32). To date, no evidence exists for the ability of IKK α or IKK β to phosphorylate other IkB isoforms such as IkBe and IkBy, which also contain N-terminal serine residues crucial for its regulation (448). However, Heissmeyer *et al.* recently demonstrated that NF- κ B p105 (434) but not p100 precursors are equivalent targets of the IKK complex like IkBa and IkBB, and phosphorylation occurs at the C-terminal serines (921, 923 and 932) of p105 (166). It would be interesting to see whether Cot/Tpl-2 interacts with IKKa because both kinases interacted with a similar region at the C-terminus of p105 as well as whether IKK complex can phosphorylate $I\kappa By$, which contains exactly identical C-terminal region of p105 including these IKK phosphorylation sites (32, 166, 183).

2.2.5 PKR ,PKC and Akt

Before the identification of the IKK complex, many kinases such as PKC_z, PKA, Raf-1, PKR and pp90-rsk were candidates for IkB kinases (98, 115, 139, 221, 385). However, these kinases did not fulfill the requirement for IkB kinase, which should phosphorylate In $B\alpha$ in vivo at both of the N-terminal serine residues (Ser-32 and -36). For example, the 90 kDa ribosomal S6 kinase (pp90-rsk), downstream of the Raf-MAPK/extracellular signal-regulated kinase pathway, is involved in phorbol ester-induced NF-kB activation by phosphorylating Ser 32 but not Ser 36. Interestingly, recent studies revealed the involvement of some of these kinases in IKK activation. As opposed to a direct kinase, PKR has been shown to be implicated in dsRNA-induced NF- κ B activation which is mediated by NIK and IKK activation (76, 469). Also, overexpression of PKC activated IKK β but not IKK α activity and dominant-negative mutants of PKC ζ inhibited IKK β activation in TNF α , but not in PMA-stimulated cells (224). This suggests the involvement of the atypical protein kinase C (aPKCs) in TNF α -mediated NF- κ B activation through the regulation of IKK^β activity. A more precise mechanism showing the link between the TNF α receptor and aPKC was revealed recently by Sanz *et al* (378). In this study, they proposed that the interaction of p62 (a novel aPKC-interacting protein) with RIP, which interacts with TRADD, serves to link aPKCs to NF- κ B activation by TNF α (Figure 4). Previous studies also demonstrated the existence of a trimolecular complex composed of TRADD, RIP and TRAF2 (177, 178). TRAF2 has been shown to interact with NIK in NF-kB activation pathway (268). Therefore, RIP is at the center of NF-kB activation through two independent and redundant pathways, connecting TRAF2 to NIK and p62 to aPKCs. This may explain why TNFa could induce NF-kB in TRAF-2deficient or TRAF-2 dominant transgenic mice (234, 464), while TNF α -induced NF- κ B activation was severely defective in RIP-deficient mice (203). PMA-mediated NF-kB

activation was also shown to involve PKC α , which binds to IKKs in vitro and in vivo, and PMA-induced IKK β activation was dependent on the activity of PKC α (Figure 4) (224). Interestingly, PKC θ -mediated NF- κ B activation has been shown to occur exclusively via IKK β homodimers (310), which together with other studies shown above strongly suggest that IKK α and IKK β are selective for different upstream kinases, which may be due to different structural determinants for this specificity in both IKKs and upstream kinases. Furthermore, a novel PKC θ -interacting protein named PICOT (PKCinteracting cousin of thioredoxin) has recently been shown to inhibit CD3/CD28 induced NF- κ B activation, therefore it would be interesting to see whether PICOT can inhibit PKC θ -mediated NF- κ B activation (450).

The serine-threonine kinase Akt (also known as protein kinase B, PKB) which is a downstream target of PI3K, has also been shown to be involved in TNF α -, plateletderived growth factor (PDGF)- and PMA-induced NF-kB activation (197, 207, 318, 356). In TNF α -treated and serum-starved IKK α -transfected cells, Akt was shown to mediate IKKa phosphorylation at threonine 23 (318). IKKB does not contain a putative Akt phosphorylation site, which is another example of differential regulation of IKK α and IKK^β by upstream kinases (318). Although no direct interaction was observed between Akt and IKKs in TNF α -stimulated cells, in PDGF-stimulated cells, NF- κ B activation was shown to be mediated by Akt which transiently interacted with IKK α and IKK β (356). Since PDGF has been shown to activate NF-kB and inhibit c-Myc-induced apoptosis by activating the Ras/PI3K/Akt (202, 204, 314), it was suggested that activation of NF-kB by PDGF contributes to inhibition of c-Myc-induced apoptosis by induction of NF-kB regulated anti-apoptotic genes (see below) (75, 152, 356, 432, 433, 478). Interestingly, Akt-mediated NF-kB DNA binding activity and NF-kB specific reporter activity was inhibited by DN mutants of NIK in Akt-transfected cells in the absence or presence of PMA treatment (197), suggesting the involvement of NIK in Akt-mediated NF-kB

activation. Recently, in contrast to the above reports, indicating Akt-mediated NF- κ B activation occurs through IKK dependent degradation of I κ B α , Madrid *et al.* observed that activated PI3K or Akt stimulated NF- κ B-dependent transcription; however, this acts through stimulating TA1 domain of the p65 subunit rather than inducing NF- κ B nuclear translocation via I κ B α degradation (266). Furthermore, mutation of Serine 529, previously shown to be important for the transcriptional activity of p65, inhibited the ability of Akt to activate p65 transcription (266, 435). Therefore, further investigation is required to analyze Akt-mediated NF- κ B activation.

2.3 Mice lacking IKKα and IKKβ

Initially, IKK α and IKK β were thought to be interchangeable IkB kinases in the complex. Based on a number of experiments, IKK β was later shown to be a stronger kinase with greater activity for phosphorylation of $I\kappa B$ proteins than IKK α . However, it is now clear that these two kinases play different roles in the IKK complex after observations of knockout mice lacking IKK α or IKK β . Homozygous *ikk* β -deficient mice died at about 14 days of gestation due to massive hepatic cell apoptosis, a phenotype remarkably similar to that seen in mice deficient in the RelA(p65) subunit of NF- κ B (31, 244, 246, 410). This may be due to the loss of the anti-apoptotic effects of NF-kB as shown by decreased NF- κ B activation upon TNF α or IL-1 in fibroblasts from these mice (244, 410). Although IKK α has IxB kinase activity and is involved in phosphorylation of the IxB proteins, this observation clearly provided that IKK α homodimers found to be still in the complex cannot perform IkB kinase activity (244, 410). In contrast, mice lacking IKKa showed functional NF-kB activation upon TNFa treatments but exhibit profound epidermal and morphogenic abnormalities and die in utero or soon after birth (179, 243, 409). These findings are clearly contradictory to earlier studies showing that catalytically inactive mutants of IKK α or addition of anti-sense IKK α RNA inhibits NF- κ B activation in response to many inducers. Moreover, a similar phenotype of skin abnormality was observed in mice lacking $I\kappa B\alpha$ compared to *ikk\alpha-/-* mice (214). Further studies are required to understand whether this phenotype is due to uncontrolled NF- κ B activation by IKK β homodimers in the absence of IKK α , which was shown to be a negative regulator of IKK β in uninduced condition (241, 310, 470) and to search for the real function of IKK α , which may be related to morphogenic and epidermal development.

3.0 NF-KB REGULATED GENES

Numerous genes regulated by NF-kB are listed in Table 1 (319). About one third of known NF-kB-regulated genes are involved in the host immune response, which include cytokines/chemokines, immunoreceptors, cell adhesion molecules and genes encoding for proteins that are involved in antigen presentation. In addition to its important role in the immune response, NF-kB also activates genes that are involved in the stress response, apoptosis and cell growth. Therefore, NF- κ B is a central mediator of the human stress response (319). A number of anti-apoptotic genes are positively regulated by NF- κ B, including cellular Inhibitor of apoptosis protein 1 (c-IAP1), c-IAP2, TRAF1, TRAF2 and the Bcl-2 homologue A1/Bfl-1 (75, 259, 432, 434, 454). Therefore, when NF-kB activity is inhibited, cells become sensitive to $TNF\alpha$ or DNA damaging drug-induced apoptosis (28, 222, 423, 433). Conversely, NF- κ B is also involved in promoting apoptosis (149, 247). It is possible that this discrepancy of the role of NF- κ B in promoting or inhibiting apoptosis is dependent on cell type and which apoptosis-inducing agent is used. Interestingly, NF-kB has also been implicated in the activation of Fas, FasL and TRAIL gene expression, which are $TNF\alpha$ superfamily members involved in apoptosis. Expression of these genes is upregulated when cells are treated with inducers that activate NF-kB (68, 191, 200). Therefore, the mechanisms of how many of these anti-apoptotic gene products protect cells from apoptosis still remain unclear. In addition, NF-kB

Table 1. Genes regulated by the NF- κ B family of transcription factors.

Class	Target Genes
Cytokines/chemokines	Interleukin $1\alpha,\beta$ (IL- $1\alpha,\beta$) Interleukin 2, 6, 8, 9, 11, 12, 15 (IL-2, 6, 8, 9, 11, 12, 15) γ -interferon (IFN- γ) β -interferon (IFN- β) Tumor necrosis factor α (TNF- α) Lymphotoxin α (LT- α)/Tumor necrosis factor β (TNF- β) Lymphotoxin β (LT- β) Cytokine-induced neutrophil chemoattractant (CINC) CXC chemokine ligand for CXCR3 (CXCL11) Macrophage chemotactic protein-1 (MCP-1) Macrophage inflammatory protein- $1\alpha,\beta$ (MIP- $1\alpha,\beta$) Macrophage inflammatory protein- 2 (MIP- 2) Regulated upon Activation Normal T lymphocyte Expressed and Secreted (RANTES)
Immunoreceptors	Immunoglobulin κ light chain Immunoglobulin ε heavy chain IL-2 receptor α -chain CC chemokine receptor-5 (CCR-5) TNF receptor, p75/p80 T cell receptor β chain T cell receptor α chain (human) Major histocompatability class II (E α^d) β 2-microglobulin
Cell adhesion molecules	Endothelial leukocyte adhesion molecule-1 (ELAM-1) Vascular cell adhesion molecule-1 (VCAM-1) Intercellular adhesion molecule-1 (ICAM1) P-selectin Mucosal addressin cell adhesion molecule -1 (MadCAM-1) Tenascin-C
Acute phase proteins	Angiotensinogen Serum amyloid A precursor Complement factor B Complement factor C4 Urokinase-type plasminogen activator Pentraxin PTX3 Lipopolysaccharide binding protein C-reactive protein Tissue-factor 1
Antigen presentation	Proteasome subunit LMP2 Peptide transporter TAP1

Table 1. Genes regulated by the NF-kB family of transcription factors.

Class	Target Genes
Stress response	Angiotensin II Cyclooxygenase (COX)-2 Ferritin H chain 5-Lypoxygenase 12-Lypoxygenase Inducible nitric oxide (NO) synthase NAPDH quinone oxidoreductase Mn superoxide dismutase (SOD) Phospholipase A2
Apoptotic regulators	Bcl-2 Pro-survival Bcl-2 homologue Bfl1/A1, Bcl-xL and Nrl3 c-IAP1 and 2 TRAF-1 and -2 Fas ligand and receptor (CD95) Fas like interleukin-1β converting enzyme (FLICE) TNF receptor 1 and 2
Growth factors	Granulocyte/macrophage colony stimulating factor (GM-CSF) Granulocyte colony-stimulating factor (G-CSF) Macrophage colony-stimulating factor (M-CSF) Platelet-derived growth factor (PDGF) B chain Proenkephalin Thrombospondin Vascular endothelial growth factor (VEGF) C Insulin-like growth factor binding protein-1,2 (IGFBP-1,2)
Transcription factors	c-Rel NFκB1 (p105) and NFκB2 (p100) IκBα c-myc Interferon regulatory factor 1 and 2 (IRF-1 and IRF-2) A20 p53
Cell cyle	p53 cyclin D1 and D3
Viruses	Human immunodefiency virus (HIV-1) Cytomegalovirus (CMV) Simian virus 40 (SV40) Adenovirus (E3 region) Avian Leukosis virus Bovine Leukimia virus Epstein-Barr virus (EBV) Simian immunodeficiency virus (SIV) Measles virus

induces expression of many transcription factors such as c-myc, A20, interferon regulatory factor-1 (IRF-1), IRF-2, *jun*B and p53 which would result in amplification of many other genes that are under the control for these transcription factors, as well as its own family members and inhibitors (see below).

3.1 Regulation of NF-kB/IkB gene expression: autoregulation of NF-kB activation

Since the $I\kappa B\alpha$ gene contains NF- κB binding sites in its promoter, NF- κB is able to autoregulate the transcription of its own inhibitor (55, 74, 90, 162, 185, 228, 407). Autoregulatory control of IkBa expression by NF-kB is in part responsible for the transient nature of NF- κ B activation of gene expression as mentioned earlier. The I κ B α gene has also been shown to be regulated by RelA(p65) both at the mRNA and protein levels: RelA(p65)-IkB α protein interactions increased the half-life of the inhibitory protein and $I\kappa B\alpha$ mRNA was induced by ReIA(p65) as a consequence of increased $I\kappa B\alpha$ gene transcription (44, 389). Stimulation of Jurkat T cells by TNF α or PMA induced degradation of the IkBa protein concomitant with NF-kB release and activation (238, 286). Activation is followed by de novo IkBα synthesis in an NF-kB-dependent manner, and cycloheximide treatment prior to induction resulted in the inhibition of IkBa resynthesis, as well as prolonged NF-kB DNA binding (407). Furthermore, NF-kB also upregulates expression of other NF-xB family members such as c-rel, NFKB1 and NFKB2, which all contain NF- κ B binding sites in their promoters (80, 81, 151, 154, 260, 412). Many studies suggest that p50 and p52 homodimers which do not contain transactivation domains, act as the transcriptional repressors by competing for NF-kB binding sites in the promoter, while p105 and p100 sequester NF-kB in the cytoplasm (51, 69, 105, 223, 335, 381, 382). This further controls the transient nature of NF- κ B activation.

3.2 Promoter elements regulating HIV-1 gene expression

Viral gene expression of Cytomegalovirus (CMV), Simian virus 40 (SV-40) and HIV-1 (Table 1) is induced by NF- κ B and vice versa, viral infection can lead to activation of NF- κ B (148, 198, 293, 363-365, 376). Therefore, chronic HIV-1 infection may be caused in part by constitutive NF- κ B activation due to constitutive activation of the IKK complex, leading to increased degradation of I κ B α (94, 96, 173, 275, 363-365). Many viral proteins also participate in their gene expression, for example, the HIV-1 Tat (transactivator of transcription) protein has been shown to be involved in induced expression of the HIV-1 LTR. Thus, a complex interaction between host and viral proteins is involved in viral gene expression. This section will discuss host transcription factors and viral proteins involved in HIV-1 gene expression.

3.2.1 host transcription factors

The HIV-1 promoter, located in the U3 region of the viral long terminal repeat (LTR), is composed of positive and negative transcriptional regulatory elements (Figure 5A) that are required for the expression of the integrated proviral genome (135, 195, 365). The intracellular efficiency of HIV-1 gene expression and replication is due in part to the ability of HIV-1 to utilize host signaling pathways to mediate its own transcriptional regulation. The promoter-proximal enhancer region of the HIV-1 LTR contains two NF- κ B binding sites (-109 to -79) (148, 210, 293, 359) whose functional significance in inducible HIV-1 gene expression was demonstrated by mutational analysis in transient transfection assays using HIV LTR or HIV enhancer reporter constructs in the presence of inducers such as TNF α and IL-1 (16, 107, 125, 219, 251, 342, 365, 429). Although NF- κ B proteins play a central role in HIV-1 long terminal repeat (LTR) driven transcription, these κ B sites are not absolutely required for viral growth (70, 290) **Figure 5. HIV-1 Tat protein and regulatory elements in HIV-1 LTR.** The viral LTR is composed of three regions designated U3, R and U5. U3 region includes the enhancer (two NF- κ B binding sites), the core promoter containing three Sp-1 binding sites and TATA box and the upstream modulatory domain which contains binding sites for a number of cellular factor binding sites. Transcription starts at the U3/R border and R region encodes the transactivation response element, TAR. HIV-1 Tat protein binds to the TAR element in the nascent RNA and enhances viral transcription. It is composed of five domains. Domain III and IV are important for its transactivation potential and RNA binding activity, respectively. Domain II is rich in cysteines which are important for Tat function.



Recently, HIV-1E, a naturally occurring subtype of HIV-1 that contains a single NF- κ B binding site in the enhancer region, has been shown to display reduced $TNF\alpha$ responsiveness, which further demonstrates the importance of NF-kB in HIV-1 gene expression (290). Sp-1, which binds to three sites adjacent to the NF- κ B sites in the core promoter region of the HIV-1 LTR, has been shown to be important for basal as well as HIV-1 Tat induced transcription of the HIV-1 LTR (38, 161). In addition, NF-KB activity was further enhanced by synergistic transactivation with the transcription factor Sp-1 (326, 329, 401). Sequences upstream of the enhancer region have been defined as the negative regulatory element (NRE) because elimination of this region increases basal and induced HIV-1 LTR activity in transfected cells or in vitro (261, 262, 313, 358, 399). In contrast, a region between -130 and -201 was shown to be important for viral replication in peripheral blood lymphocytes (PBLs) and some T cell lines (210). This region contains binding sites for USF-1 (E-box), which is a bHLHZip protein and Ets proteins (EBS), as well as for the DNA bending transcription factor LEF-1 (lymphoid enhancer binding factor-1). Both Ets-1 and LEF-1, expressed highly in T cells, were shown to be able to relieve nucleosomal repression of the HIV-1 LTR in conjugation with Sp-1 suggesting an important role of these transcription factors in the distal region of HIV-1 LTR (71, 235, 395, 418, 437). Moreover, cooperative binding and synergistic transactivation of the HIV-1 LTR between USF-1 and Ets-1 has recently been shown to occur at the distal enhancer region of the HIV-1 LTR (400). NFAT binding sites were also shown to be involved in HIV-1 gene expression upon T-cell activation (399). The functional importance of other upstream transcription factor binding sites for COUP, AP-1 and Myb and binding sites downstream of transcription start site for UBP-2 and CTF/NF1 is not currently known, except for upstream binding protein/leader binding protein (UBP-1/LBP-1) which was shown to inhibit HIV-1 gene expression by interfering with TFIID binding to the TATA element (201).

3.2.2 HIV-1 Tat

A small nuclear protein, Tat is a 101 amino acids arginine-rich RNA-binding protein that is absolutely required for productive HIV-1 replication (190). HIV-1 Tat protein enhances LTR-derived gene expression and is required for high-level expression of all viral genes (87). Pleiotropic effects of Tat on cellular gene expression have also been well documented; modulation of cytokine secretion, inhibition of antigen-induced lymphocyte proliferation, downregulation of MHC (Major histocompatibility complex) class I surface expression and decrease in manganese-dependent superoxide dismutase activity (58, 176, 316, 340, 341, 422, 430, 446, 447). Furthermore, Tat has been shown to be involved in promoting or inhibiting apoptosis and acts as a growth factor for Kaposi's sarcoma cells (109, 215, 240, 267, 296, 304, 305, 445, 472). Among these pleiotropic effects of Tat, transcriptional activity of Tat on the HIV-1 LTR will be discussed in this section. Tat can be separated into five functional domains (Figure 5B). Cysteine-rich domain II is important for Tat function as well as domain III and IV, which are essential for its transactivational capacity and RNA binding activity (102, 134, 344, 391). However, domain I has a minimal effect and domain V is dispensable for its transcriptional function. Unlike other transcription activators, Tat acts by binding to RNA through its RNA binding domain, composed of basic amino acids, not to DNA, but to a 59-base stem-loop RNA structure called the transactivation response (TAR) sequence (Figure 5C), which is located at the 5' ends of all nascent HIV-1 transcripts causing a substantial increase in transcript levels (39, 93, 130, 195, 366, 367). The core secondary stem-loop structure including the bulge region (Figure 5, nucleotides +18 to +44) is critical for Tat-TAR interactions, Tat-mediated transactivation as well as HIV replication (39, 93, 213, 367, 390). The bulge region in TAR (+23 to +25) serves as the primary binding site for Tat, and the loop sequences (+30 to +35) also contribute to this interaction (366, 367, 390). Certain cellular factors such as TRP-185 and p68 also bind to TAR RNA and facilitate interactions with promoter elements such as TATA, Sp1 and
the HIV-1 enhancer, stimulating transcription initiation and stabilizing elongation complexes (37, 38, 199, 270, 393).

The optimal activity of Tat to induce transcriptional initiation and elongation, requires its association with two classes of cellular proteins, Tat-associated kinases (TAKs) and Tatassociated histone acetyltransferases (TAHs) (189, 194, 195, 227). TAKs, which include RNA polymerase II (RNAPII) C-terminal domain (CTD) kinases, a basal transcription factor II H (TFIIH) and a positive transcriptional elongation factor b (P-TEFb), induce processive transcription of RNAPII from the HIV-1 LTR promoter by phosphorylating the CTD of RNAPII (79, 86, 129, 131, 312, 322, 438, 461, 477). Kinases responsible for CTD phosphorylation are CDK7 found in the cyclin-dependent kinase-activating kinase (CAK) complex of TFIIH and CDK9/PITALRE in P-TEFb complex. CDK7 has been shown to be responsible for phosphorylating the CTD of the largest subunit of RNAPII in the preinitiation complex during its transition from initiation to promoter clearance while CDK9 phosphorylates RNAPII during transcriptional elongation as well as initiation/reinitiation (86, 131, 144, 269, 274, 300, 460, 477). CDK9 is recruited to the TAR element by indirect interaction with Tat, and this association is mediated by cyclin T (Figure 6), therefore forming a ternary complex (327, 438). Association between Tat and TFIIH has also been demonstrated (86, 131, 322). Therefore, two CTD kinases which are important for initiation, promoter clearance and elongation gain access to the HIV-1 LTR through Tat interaction. Tat has also been shown to interact with TAHs, which contain p300/CBP and P/CAF capable of acetylating histores and therefore causing the activation of chromatinized HIV-1 (34, 175, 271, 272). Thus, Tat gains access to the integrated HIV-1 LTR (394, 426, 428). Furthermore, acetylation of Tat by p300/CBP and PCAF has recently been demonstrated to be important for Tat binding to the TAKs and dissociation of Tat from TAR RNA that occurs during early transcription elongation (209). Figure 6 describes the current model for Tat-mediated HIV-1 LTR activation.

Figure 6. Model for transcriptional activation of the HIV-1 LTR by HIV-1 Tat and cellular transcription factors. Tat which is expressed from integrated HIV-1 genome possibly by cellular activation and/or taken up by the cells associates with CBP/p300 (1) therefore causing the activation of chromatinized HIV-1, which can also occur by cellular activation, for example, TNF α stimulation. Now, Tat/CDK7/TFIIH (2) and Tat/CDK9/CycT (3) complexes gain access to the HIV-1 LTR, and initiate transcription by phosphorylating CTD of RNAPII. Tat/CDK9/CycT complex binds to the TAR element in nascent viral transcripts. (4) Basal transcription factors such as Sp-1 may further activate HIV-1 transcription by bringing CBP/p300 which acetylates Tat and regulates its activity, as well as through interaction with TFIID complex (141, 285, 339). (5) NF-xB upon cellular activation even further increases HIV-1 transcription by bringing CBP/p300 to the HIV-1 LTR. CBP/p300 also interacts with TFIIB (188). By interacting with many cellular factors, Tat can increase HIV-1 transcription, along with transcription factor which are activated by cellular events.



Specific Research Aims

The primary objective of the research presented in this thesis was to elucidate the effects of transdominant mutants of $I\kappa B\alpha$ (TD-I $\kappa B\alpha$) on NF- κB regulated genes and HIV-1 replication in Jurkat T cells. To accomplish this, the work has been divided into three specific research aims:

1) To examine the effect of TD-1kB α on the synergistic activation of HIV-1 LTR by HIV-1 Tat protein and TNF α .

2) To study the effect of inducible TD-I κ B α expression on *de novo* HIV-1 replication in Jurkat T cells.

3) To analyze the $I\kappa B\alpha$ promoter by *in vivo* genomic footprinting in Jurkat T cells inducibly expressing TD-I $\kappa B\alpha$.

This work presents the effects of TD-I κ B α on HIV-1 replication. The experiments performed focus on T cells which are the main targets for HIV-1 infection as well as cells of the monocytic lineage. NF- κ B activity was carefully examined at the same time due to the fact that the HIV-1 LTR is largely regulated by NF- κ B. This work further investigates the effect of TD-I κ B α on stimulus induced transcriptional activation of the I κ B α gene promoter. Based on these experiments, we demonstrate that TD-I κ B α effectively blocks HIV-1 replication in T cells, furthermore inducer-mediated regulation of I κ B α gene expression is dependent on NF- κ B and Sp-1 binding sites in the proximal region of I κ B α promoter.

CHAPTER II

MATERIALS AND METHODS

Plasmids.

1) Expression vectors. Plasmids SVK3-I κ B α and SVK3-I κ B α (3C) encoding wild type $I\kappa B\alpha$ and $I\kappa B\alpha(3C)$ respectively were described elsewhere (174, 250). $I\kappa B\alpha(3C)$ is a full length human $I\kappa B\alpha$ in which serine 283, threonine 291 and threonine 299 were substituted for an alanine residue. Substitutions S32A/S36A in mutant IkBa (2N) and substitutions S32A;S36A;S283A; T291A;T299A in mutant $I\kappa B\alpha$ (2N + 3C) were generated by overlap PCR mutagenesis using Pfu DNA polymerase. The resulting mutated $I \times B \alpha$ cDNAs were inserted in the expressing vector SVK3 (Pharmacia) and the plasmid pREP-9 CMVt (26). Mutations were confirmed by sequencing. The plasmids expressing wild type and R52O,R53O mutant of Tat, HIV LTR ΔB and ΔB -ACU, as well as the plasmid containing the HIV-1 proviral DNA (pSVC21 BH10) were previously described (82, 93, 366). CMVt-rtTA contains the Moloney murine leukemia virus-based pBABE vector backbone, which contains a puromycin (puro) resistance gene under the control of the CMV promoter. Construction of the plasmid consisted of the consecutive insertion of three components into the polylinker site: the doxycycline-responsive promoter CMVt from the CMVtBL vector (a kind gift from A. Cochrane), the rtTA gene from the pUHD172-Ineo plasmid (398), and the polyA fragment from the pSVK3 vector. neo CMVt BL was constructed in two steps. First, an intermediary plasmid (neo BL) was generated by ligation of a 3 kb XhoI/EcoRI fragment from the pMV7 vector (contains the neomycin (neo) resistance gene) to a 3.8 kb XhoI/EcoRI fragment from the CMV BL vector (contains the poly A site and the ampicillin (Amp) resistance gene). Second, a 450 bp XhoI (blunt)/NotI fragment of CMVt BL (contains the CMVt promoter) was cloned into the EcoRI (blunt)/NotI sites of neo BL. CMVt-IxBa 2N was constructed by cloning an EcoRV (blunt)/BamHI IxB α 2N mutant cDNA fragment downstream of CMVt at the EcoRI (blunt, filled with Klenow enzyme)/BamHI site of neo CMVt BL. SVK3-IkBa 2NA4 was constructed by replacing a XhoI fragment of SVK3-IkBa 2N with a XhoI fragment from SVK3-I κ Ba Δ 4. CMVt-I κ Ba 2N Δ 4 was constructed by cloning an EcoRI/BamHI I κ B α 2N Δ 4 mutant cDNA fragment from SVK3-I κ B α 2ND4 downstream of CMVt at the EcoRI/BamHI site of neo CMVt BL.

2) Reporter plasmids. HIV LTR CAT plasmids ptzIIICAT, -109/-79, IIIA23 and IIIAA were a kind gift from Dr. Eric Cohen (for a schematic map, see Fig 8). 0.4SK-pGL3 Luc was obtained by subcloning the 0.4 kb fragment of $I\kappa B\alpha$ promoter (a kind gift of Dr. A. Israël) into Kpnl/SacI-digested pGL3. The plasmids carrying respectively point mutations into the $\kappa B1$ or Sp1 or in both sites were obtained by the subcloning of polymerase chain reaction-amplified fragments into Kpnl/Sacl-digested pGL3. Briefly, these constructs were obtained in two steps by a procedure previously described (225). The first round of amplification used 0.4SK-pGL3 Luc as template, 5'-CACGCGTAAGA GCTCCACCG-3' (SacI primer) as 3'-primer and 5'-GGAAATTCaaCGAGCCTGAC-3' (small nucleotides indicate point mutations) as 5'-primer for kBl site mutagenesis or 5'-CCTGACCaaGCCCCAGAGAA-3' as 5'-primer for Sp1 site mutagenesis. The amplified fragments were used as the 3'-primer in a second polymerase chain reaction using 0.4SK-pGL3 Luc as template and 5'-CTATCGATAGGTACCGGGCC-3' (KpnI primer) as 5'-primer. In each case, the final products were purified, digested by KpnI and SacI, and inserted between these sites in the pGL3 polylinker. The construct carrying both $\kappa B1$ and Sp1 mutations was similarly obtained using Sp1-mutated IkB α promoter as template. The promoter constructs carrying internal deletions or insertions were obtained by the ligation of two separately amplified fragments, one digested by Sacl, the other by KpnI, to KpnI/SacI-digested pGL3. Thus, $\Delta 8$ -IkBa plasmid was constructed by ligation of two fragments amplified with 5'-CCCCGCCCAGAGAAATC-3'/SacI primers and KpnI/5'-GGGGAATTTCCAAGCCAGT-3' primers, in the presence of 0.4SK-pGL3 Luc as template. The +5 and +9- $I\kappa B\alpha$ plasmids were similarly constructed using 5'-TGCAGCTGACCCCGCCCCAGAGAAA-3'/SacI primers (inserted nucleotides are underlined) and KpnI/5'-GCTCGGGGGAATTTCCAAGCCA-3' primers and with 5'-GCA

<u>GCATCG</u>CTGACCCCGC CCCAGAGAAA-3'/SacI primers and KpnI/5'-GCTCG GGG AATTTCCAAGCCA-3' primers, respectively. The correct sequences of the constructs presented were confirmed by DNA sequence analysis.

Cell culture and generation of IxBa expressing cell lines. Cell lines inducibly expressing wild type IxB α or IxB α (3C), tTA-IxB α (wt) and tTA-IxB α (3C) respectively, were described elsewhere (26). tTA-3T3 cells were transfected with pREP9-CMVt-IkBa (2N) or (2N + 3C) plasmids. Cells which inducibly expressed $I\kappa B\alpha$ (2N) or (2N + 3C) were selected and maintained in DMEM media containing 10% calf serum, 300 ug/ml Hygromycin B and 400 µg/ml G418 (Gibco BRL). Jurkat cells were transfected with CMVt-rtTA plasmid by the DEAE-dextran method. The precipitated CMVt-rtTA plasmid (15 µg) was resuspended in TS solution (8 mg/ml NaCl, 0.38 mg/ml KCl, 0.1 mg/ml Na₂HPO₄·7H₂O, 3.0 mg/ml Tris, 0.1 mg/ml MgCl₂, 0.1 mg/ml CaCl₂, pH 7.4) and subsequently DEAE-dextran (Pharmacia) was added. For transfection, 1x10⁷ cells in exponential phase were washed once in TS, resuspended with the DNA solution and incubated at room temperature for 20 min and then incubated at 37°C for 30 min in 10 ml with RPMI 1640 medium supplemented with 10% fetal bovine serum (FBS), 2 mM glutamine, 10 µg/ml gentamicin (Schering Canada, Pointe Claire, Quebec) and 0.1 mM chloroquine (Sigma Chem. Co.) after which they were centrifuged and resuspended in fresh medium. Cells were selected beginning at 24h after transfection in RPMI 1640 medium containing 10% FBS, 2 mM glutamine, 10 µg/ml gentamicin and 2.5 µg/ml puromycin (Sigma). Resistant cells carrying the CMVt-rtTA plasmid (rtTA-Jurkat cells) were then transfected with CMVt-Neo, CMVt-2N and CMVt-2N∆4 plasmids by DEAEdextran. Cells were selected beginning at 24h after transfection for approximately 4 weeks in RPMI containing 10% FBS, 2 mM glutamine, 10 µg/ml gentamicin, 2.5 µg/ml puromycin and 400 µg/ml G418 (Life Technologies, Inc.). Initially, pools of transformants corresponding to rtTA-, rtTA-neo-, rtTA-IkBa-2N-, rtTA-IkBa-2NA4

expressing Jurkat cells were analyzed for inducible I κ B α expression; subsequently, 6-10 individual clones from each transformant pool were selected for further analysis. To analyze growth kinetics, rtTA-neo-, rtTA-I κ B α -2N-, rtTA-I κ B α -2N Δ 4-expressing Jurkat cells were cultured in the presence of 1 μ g/ml Dox for various times at an initial cell density of 1x10⁵ cells/ml and then counted every other day. All cell lines grew well in the above medium with doubling times of 50 ± 4h. Values obtained are the average of two experiments.

Analysis of HIV-1 LTR transcription in reporter gene experiments. Jurkat cells or rtTA-TD-I κ B α Jurkat cells were transiently transfected by DEAE -dextran method as above with precipitated DNAs (0.5 to 8 μ g), representing either HIV-LTR or HIV-enhancer containing CAT reporter plasmids with or without pSVexTat plasmids (wt Tat or R52Q,R53Q Tat mutant) (93). At 32 h after transfection, Jurkat cells were induced with 5 ng/ml TNF α (Boeringer Mannheim). At 16 h after induction, cells were harvested and lysed. rtTA-Neo or rtTA-2N Δ 4 were incubated with or without Dox in the presence of 10 ng/ml TNF α (Boeringer Mannheim) or PMA (100ng/ml, ICN)/PHA (1 μ g/ml, ICN) at 24 h after transfection and subsequently harvested at 24 h after treatment. Extracts (10 to 400 μ g) were assayed for CAT activity during 10 min - 8 h, depending on the experiment. The percent acetylation was determined by ascending thin layer chromatography as previously described (132) and quantified using the BioRad Gelscan Phosphoimager and the Molecular Analyst (BioRad) software program.

Analysis of apoptosis. To identify apoptotic cells, cells were treated with TNF α after 24h culture in the absence or presence of 1 µg/ml Dox, and stained using the TUNEL assay (Boehringer Mannheim) and the Hoescht dye 33258. The mixture was then viewed under UV illumination using a Leica fluorescent microscope. To calculate percent apoptosis, a minimum of 200-400 cells were counted. Apoptosis was also analyzed by

DNA fragmentation assay. A total of $3X10^6$ cells were collected, resuspended in 0.25 ml TBE containing 0.25 % NP-40 and 0.1 mg/ml RNAse A and incubated for 30 min at 37°C. Extracts were then treated with 1 mg/ml proteinase K for 30 min at 37°C. DNA preparations (30 µl) were loaded on 1.8 % agarose gel; DNA fragmentation was visualized under UV light.

Western blot analysis. Cells were washed with phosphate-buffered saline (PBS) and lysed in Western Lysis Buffer (WLB) containing 10 mM Tris-Cl pH 8.0, 60 mM KCl, 1 mM EDTA, 1 mM dithiothreitol (DTT), 0.5 % Nonidet P-40 (NP-40), 0.5 mM phenylmethysulfonyl fluoride (PMSF), 10 µg/ml leupeptin, 10 µg/ml pepstatin, and 10 μ g/ml aprotinin. After incubation on ice for 10 min, protein extracts were collected by centrifugation at 14000 rpm for 15 min at 4°C. Equivalent amounts of whole cell extract (20 µg) were subject to SDS-polyacrylamide gel electrophoresis (SDS-PAGE) in a 10% or 15 % polyacrylamide gel. After electrophoresis, the proteins were transferred to Hybond transfer membrane (Amersham Pharmacia Biotech) in a buffer containing 30 mM Tris, 200 mM glycine and 20% methanol for 1 h. The membrane was blocked by incubation in PBS containing 5 % dried milk for 1h and then incubated overnight with anti-IkBa MAD10B (187), -p24 (ID Laboratories), -actin (Sigma) monoclonal or anti-p65 (328) polyclonal antibodies in 5 % milk/PBS, at dilutions of 1:500 or 1:1000. These incubations were done at 4°C overnight. After four 10min washes with PBS, membranes were incubated with a peroxidase-conjugated secondary goat anti-rabbit or anti-mouse antibody (Amersham Pharmacia Biotech) at a dilution of 1:1000. The reaction was then visualized with the enhanced chemiluminescence detection system (ECL) as recommended by the manufacturer (Amersham Pharmacia Biotech or NEN™ Life Science, Boston, MA).

Immunoprecipitation. rtTA-Neo and rtTA-2N Δ 4 Jurkat cells were induced TNF α (10 ng/ml) and PMA (50 ng/ml) for various times in the presence or absence of Dox and lysed in TNN buffer (20 mM Tris-HCl, pH 7.5, 200 mM NaCl, 0.5 % NP-40, 2 mM PMSF, 5 µg/ml Leupeptin, 5 µg/ml Pepstatin, 0.5 mM Spermidine, 0.15 mM Spermine and 5 µg/ml Aprotinin). Cell lysates (500 µg) were precleared with preimmune sera. Precleared lysates were incubated with 10 µl of p65 antibody (328) or IxB α antibody and 30 µl of protein A-Sepharose beads (Pharmacia Biotech, Upsalla, Sweden) for 1 h at 4°C. Beads were washed five times with TNN buffer and the immunoprecipitates were eluted by boiling the beads 5 min in SDS loading dye. Eluted proteins were electrophoresed on 10 % SDS-polyacrylamide gel electrophoresis and detected by using anti-goat p65 antibody (SantaCruz Biotechnology, Santa Cruz, CA) and MAD10B IxB α antibody.

Nuclear extracts. Cells were washed in Buffer A [10 mM HEPES, pH 7.9; 1.5 mM MgCl₂; 10 mM KCl; 0.5 mM dithiothreitol (DTT); and 0.5 mM phenylmethylsulfonyl fluoride (PMSF)] and were resuspended in Buffer A containing 0.1 % NP-40. Cells were then chilled on ice for 10 min before centrifugation at 14000 rpm. Pellets were then resuspended in Buffer B (20 mM HEPES, pH 7.9; 25 % glycerol; 0.42 M NaCl; 1.5 mM MgCl₂; 0.2 mM EDTA; 0.5 mM DTT; 0.5 mM PMSF; 5 μ g/ml leupeptin; 5 μ g/ml pepstatin; 0.5 mM spermidine; 0.15 mM spermine; and 5 μ g/ml aprotinin). Samples were incubated on ice for 15 min before being centrifuged at 14000 rpm. Nuclear extract supernatants were diluted with Buffer C (20 mM HEPES, pH 7.9; 20% glycerol; 0.2 mM EDTA; 50 mM DTT; and 0.5 mM PMSF).

Electrophoretic mobility Shift Assay (EMSA) Nuclear extracts were incubated for 20 min at room temperature with 3^{2} P-labeled probes corresponding to the PRDII region of the IFN- β promoter and κ B1, Sp1, κ B1/Sp1 sites from I κ B α promoter either in NF- κ B DNA binding buffer (20 mM HEPES, pH 7.9, 5 % glycerol, 0.1 M KCl, 0.2 mM EDTA,

pH 8.0, 0.2 mM EGTA, pH 8.0, 1 mM dithiothreitol) or in NF-kB/Sp1 DNA binding buffer (20 mM HEPES, pH 7.9, 100 mM KCl, 20 % Glycerol, 0.1 mM EDTA, 0.25 mM ZnSO₄, 0.05 % NP-40, 1mM dithiothreitol), together with 5 or 0.5 µg of poly(dI-dC) (Amersham Pharmacia Biotech), respectively. Oligonucleotides used are as follow: PRDII: 5'-GGGAAATTCCGGGAAATTCC-3'; KB1: 5'-GATCTTGGAAATTCCCCGA-3'; Sp1: 5'-TCGAGACCCCGCCCCAG-3'; consensus Sp1: 5'-ATTCGATCGGGGGGGG GGCGAG C-3'; mutated Sp1: 5'-ATTCGATCGGTTCGGGGGGGGGGGGG-3'; KB1/Sp1: 5'-T CGATTGGAAATTCCCCGGCCTGACCCCGCCCCAG-3'; mutkB1/Sp1: 5'-TCGATTG TCAATTCCCCGAGCCTGACCCCGCCCCAG-3'; kB1/mutSp1: 5'-TCGATTGGAAAT TCCCCGAGCCTGACCAAGCCCCAG-3'; +5 xB1/Sp1: 5'-TCGATTGGAAATTCCCC GAGCTGCAGCTGACCCCGCCCCAG-3'. Underlining delineates the Sp1 site, and bold face letters indicate mutations in either xB1 or Sp1. Recombinant proteins (GST-NF-kB fusion proteins (251, 333) and Sp1(Promega Inc.) were also incubated with the probes in a different DNA binding buffer (10 mM Tris-HCl pH 7.5, 50 mM NaCl, 1 mM DTT, 0.1 mg/ml BSA, 50 µM MgCl₂, 1 mM ATP, 5 µg/ml poly dI-dC). The resulting protein-DNA complexes were resolved by 5-6 % Tris-glycine or Tris-borate-EDTA gels and exposed to X-ray film. To demonstrate the specificity of protein-DNA complex formation, 125-fold molar excess of unlabeled oligonucleotide was added to the nuclear extract before adding labeled probe. Supershift analysis was performed by incubating anti-p65, anti-p50, anti-c-Rel and anti-Sp1 antibodies (Santa Cruz Biotechnology Inc) with nuclear extracts for 20 min at room temperature.

RT-PCR analysis of HIV RNA. Total RNA was isolated from rtTA-Neo and rtTA- $2N\Delta4$ Jurkat cells infected with HIV in the presence or absence of Dox using RNeasy Mini Kit (QIAGEN) and treated with 1U RNase free DNase (RQ1 DNase; Promega Biotec, Madison, WI) for 30 min at 37°C, phenol:chloroform:iso-amylalcohol extracted, ethanol precipitated. RT was performed on 2 µg of RNA and 0.2 pmol random hexamers

using 200 U of MMLV reverse transcriptase (BRL Burlington, Ont.) in buffer containing 50 mM Tris HCl, pH 8.3, 75 mM KCl, 10 mM dithiothreitol, 3 mM MgCl₂, 500 nM dNTP, 0.1 mg/ml BSA, 272.5 U/ml RNase Inhibitor (Pharmacia Biotech). PCR assays were performed using 7 μ l of RT product, in PCR buffer containing 100 mM Tris HCl, pH 8.4, 500 mM KCl, 15 mM MgCl₂, 200 mM dNTP, 15 pmol γ^{-32} P labeled primers, and 1.25 U Taq DNA polymerase (Pharmacia Biotech). Nucleotide sequences of primers used are as follows : M667, 5'-GGCTAACTAGGGAACCCACTG-3'; M668, 5'-CAGGT CCCTGTTCGGGGGGCC-3'; LA45, 5'-GCCTTAGGCATCTCCTATGGC-3'; LA41, 5'-T GTCGGGTCCCCTCGTTGCTGG-3'; M669, 5'-GTGTGCCCGTCTGTTGTGTGACTC TGGTAAC-3';LA23, 5'- GCCTATTCTGCTATGTCGACACCC-3'. The PCR reaction mixture was subjected to 24-30 cycles of denaturation for 1 min at 95°C, annealing for 2 min at 61°C and polymerization for 2 min at 72°C. PCR products were then ethanol precipitated and analyzed on a 6 % denaturing polyacrylamide gel. Primers for glyceraldehyde phosphate dehydrogenase (GAPDH) were used as previously described (88) to normalize all reactions.

RNAse Protection Assay. A 221 bp XbaI-PstI fragment was obtained by PCR amplification with $I\kappa B\alpha$ cDNA clone (cloned into pSVK3) using specific primers containing restriction enzyme sites corresponding to positions 824-839 (5'ATCATCTAGAAACAGAGTTACCTACC3') and 1030-1045 (5'ATCACTGCAGTA ACGTCAGACGCTGG3'); the XbaI-PstI fragment of the PCR product was cloned into the XbaI-PstI site of the pDP18-T7/T3 transcription vector (Ambion, Austin, TX) to generate pDP18CU-/CTERM. ³²P-labeled antisense RNA probe was transcribed by using *ln Vitro* Transcription Kit (Pharmingen, San Diego, CA) and RNase protection carried out using RPA Kit (Parmingen). A β -actin antisense probe (pTRI- β -actin; Ambion, Inc) was synthesized by the same protocol and used in the same reaction with IkB α probe. 5-10 µg of total RNA extracted using RNeasy Mini Kit (QIAGEN, Valencia,

CA) from unstimulated or stimulated rtTA-Neo or rtTA-2N Δ 4 Jurkat cells was used. The resulting protected RNAs were resolved by 5 % denaturing gel and exposed to X-ray film.

Analysis of HIV-1 protein and RNA synthesis in a single cycle infection model. Cos-1 cells were transfected with 10 µg of HIV-1 proviral DNA (pSVC21 BH10) and 1, 5 or 10 µg of 1 κ B α expressing plasmid : either SVK3-I κ B α -I κ B α (2N), -I κ B α (3C), or -I κ B α (2N + 3C). In all experiments, the total amount of DNA transfected was completed to 20 µg with unrelated DNA (pUC8). DNA was introduced in cells by lipofection (LipofectamineTM) according to manufacturer's instructions (Promega inc.). Three days after transfection, the media and the cells were collected. The relative amount of virion protein p24 present in the media was determined by ELISA (357). Proteins were extracted from a portion of the collected cells by resuspending them in WLB buffer. Proteins were analyzed by immunoblotting as described above using I κ B α monoclonal antibody, human sera from a HIV-1 seropositive individual or actin monoclonal antibody (ICN). Total RNA was extracted from the remaining cells using an RNeasy kit (Qiagen) according to manufacturer's instructions. RNA was subjected to Northern blot analysis using ³²P labeled, random-primed HIV-1 proviral DNA or β -actin cDNA probes (see below).

Northern blot analysis. Total RNA (10-20 μ g) was electrophoresed in a 1.2 % denaturing formaldehyde agarose gel and transferred to a nylon membrane (Hybond-N; Amersham) with a Vacu-Gene blotting system (Pharmacia). RNA was cross-linked to the membrane in a UV Stratalinker 2400 (Stratagene) and prehybridized overnight in Prehybridization solution: 25 mM KPO₄ pH 7.4, 5X SSC (750 mM NaCl, 75 mM sodium citrate pH 7.0), 50% deionized formamide, 50 μ g/ml salmon sperm DNA (Boehringer Mannheim) and 5X Denhardt's solution containing 0.5 % (w/v) Ficoll 400 (Sigma), 0.5

% (w/v) polyvinylpyrrolidine, and 0.5 % (w/v) BSA at 42°C in a hybridization oven. The HIV-1 proviral cDNA probes were the 2 and 2.2 kbp Hind-III fragments derived from pSVC21 BH10. The β -actin cDNA used as probes was the 1 kbp Pst-1 fragments derived from p β -actin plasmid. Probes were labeled to approximately 1 x 10⁹ cpm/µg with the Oligolabeling kit (Pharmacia) and [α -³²P]CTP. Hybridization occurred overnight at 42-50°C in Prehybridization solution supplemented with 10 % (w/v) dextran sulfate (Pharmacia) and approximately 50 million cpm of labeled probe. The blots were washed, wrapped in plastic and exposed to X-OMAT film (Kodak) at -80°C.

Analysis of HIV-1 multiplication. rtTA-neo, rtTA-I κ B α -2N, rtTA-I κ B α -2N Δ 4 expressing Jurkat cells after preincubation with or without Dox for 24 h were infected with HIV-IIIB, derived from the HXB2D molecular clone of HIV-1 (117) in serum-free medium for 2 h at a MOI of 0.01 pfu/ml and then grown in complete medium for 36 days. Cell supernatants (precleared by centrifugation at 3000 rpm for 30 min at 4°C) were collected every four days and analyzed for virus reverse transcriptase (RT) activity as previously described (233). The relative amount of virion protein p24 present in the media was determined by ELISA (357). Proteins were extracted from a portion of the collected cells by resuspending them in WLB. Proteins were analyzed by immunoblotting as described above using I κ B α MAD10B monoclonal antibody, p24 specific antibody (ID Labs) or actin monoclonal antibody (ICN).

Reverse transcriptase analysis. Cell culture supernatants were clarified by centrifugation at 3000 RPM for 30 min. A 50 μ l aliquot of the supernatant was incubated in 50 mM Tris-HCl pH 7.9, 5 mM MgCl₂, 150 mM KCl, 0.05% Triton X-100, 0.3 mM glutathione (reduced) 0.5 mM [Ethylenebis(oxyethylenenitrilo)]-tetraacetic acid (EGTA). 50 μ g/ml poly rAdT (Pharmacia), and 10 mCi tritiated thymidine triphosphate (³H-TTP; ICN Biomedicals) for 22 h at 30°C. Reverse transcription was stopped by adding 2 ml of

0.01M sodium pyrophosphate in 1 N HCl, 2 ml of ice cold 10% trichloroacetic acid (TCA) and placing the tubes on ice. The resulting precipitates were then collected on Whatman GF/C filters and washed several times with cold 5 % TCA and once with 70 % ethanol. Filters were air dried, then counted by liquid scintillation fluorography.

In vivo genomic footprinting. Jurkat cells (10^8) were harvested and resuspended in 1 ml of RPMI 10 % FBS containing 20 mM HEPES (pH 7.3). The methylation reaction was performed in presence of 10 µl of concentrated dimethyl sulfate (Aldrich Chemical Company, Milwaukee, USA) for 1 min. The reaction was then quenched by 2 washes in cold PBS containing 2 % β-mercaptoethanol. Genomic DNA extraction was performed as previously described (3). Briefly, cells were lysed in 2 ml of Tris buffer pH 7.5 containing 10 mM NaCl, 10 mM EDTA and supplemented with 100 µl of Proteinase K (20 mg/ml), 100 µl SDS (20 %), 100 µl NP40 (10 %) and incubated at 50°C overnight. Proteins were precipitated by adding 1.2 ml of NaCl 5M and centrifuged 40 minutes at 8000 rpm. Cleared supernatant was ethanol precipitated to obtain genomic DNA; the pellet was resuspended in 200 µl H₂0 with 20 µl of piperidine (Aldrich Chemical Company) and incubated 30 minutes at 90°C to provide cleavage of methylated G (or A) residues. The DNA control (Naked DNA) was first extracted from cells, then submitted to DMS treatment and subsequently to piperidine cleavage to allow methylation and cleavage to all G residues of the sequence. For each sample, 2 µg of DNA were submitted to LM-PCR using Vent DNA Polymerase (New England Biolabs, Mississauga, USA) as described (133, 291). PCR amplification step was 2 minutes for the first cycle and was progressively increased to 10 minutes in the last cycle. A total of 18 cycles were performed for DNA amplification. The third primer was radiolabeled by end-labeling using T4 polynucleotide kinase (Pharmacia Biotech) and $[\gamma^{32}P]ATP$ (ICN). Two more PCR cycles were performed to radiolabeled elongated DNA. The final labeled PCR product was analyzed on a 5 % Hydrolink[™] Long Ranger sequencing gel (Baker, Phillipsburg, USA) in 0.6X TBE at 65 W, and exposed from 12 to 36 hours with a BioMax sensitive film (Kodak, New-York, USA). For the LM-PCR, several set of oligonucleotides were used (see Fig 22C):

For the non-coding strand:

primer 1: 5'- CTCATCGCAGGGAGTTTCT -3', $T_m 55^{\circ}C$ primer 2: 5'- CCCAGCTCAGGGTTTAGGCTTCTTT -3', $T_m 63^{\circ}C$ primer 3: 5'- GGGTTTAGGCTTCTTTTTCCCCCTAGCAG -3', $T_m 66^{\circ}C$ For the coding strand: primer 1B: 5'- ACTGCTGTGGGGCTCTGCA -3', $T_m 63^{\circ}C$ primer 2B: 5'- TAAACGCTGGCTGGGGATTTCTCTG -3', $T_m 63^{\circ}C$ primer 3B : 5'- TGGGGATTTCTCTGGGGCGGGGTCAGGCT -3'. $T_m 71^{\circ}C$

Luciferase Assay. Jurkat T cells were transiently transfected by the DEAE-dextran method with 1 μ g of 0.4SK/pGL3 (wild type IkB α promoter) luciferase reporter plasmids or mutant 0.4SK/pGL3 (mutkB1, mutSp1 and mutkB1/Sp1) along with pRL-TK (for transfection normalization, Promega Inc.). At 30h after transfection, cells were induced with TNF α or PMA/PHA. At 16h after induction, cells were harvested, lysed by 1X Passive Lysis Buffer and then luciferase activity was analyzed by Dual-LuciferaseTM Reporter Assay System (Promega Inc.) as specified by the manufacturer. The background obtained from mock transfected cells was subtracted from each experimental value. The experiments were performed in triplicate in 24-well plates, and the average fold induction was calculated.

CHAPTER III

TRANSDOMINANT MUTANTS OF IκBα BLOCK TAT-TNFα SYNERGISTIC ACTIVATION OF HIV-1 GENE EXPRESSION AND VIRUS MULTIPLICATION

Experiments using HIV-1 LTR reporter constructs in lymphoid cells showed that mutation of NF- κ B motifs reduced gene expression in the presence and absence of the HIV-1 Tat protein (1, 12, 37, 38, 118). This prompted us to analyze the effect of transdominant mutant I κ B α (TD-I κ B α) on the Tat-TNF α synergistic activation of the HIV-1 LTR and HIV-1 multiplication in a single cycle infection model.

Tat-TNF α Synergism requires Tat binding to the TAR element. To determine the specific conditions required for Tat-TNF α synergistic activation of HIV-1 LTR driven reporter constructs in Jurkat T cells, titration of wt Tat expression plasmid and/or recombinant TNF α was initially performed (data not shown). In subsequent experiments, Tat plasmid was used at a concentration of 2 μ g, while TNF α was used at a concentration of 5 ng/ml. Tat stimulated the HIV-1 LTR CAT reporter plasmid approximately 10-fold while TNF α treatment alone induced reporter gene expression about 5-fold (Figure 7A). Addition of both activators produced a true synergistic stimulation of the HIV-1 LTR, resulting in a 50-70 fold induction of gene expression (Figure 7A). Previous studies demonstrated that efficient transactivation of HIV-1 gene expression by Tat required physical interaction between Tat and the TAR element (93). The R52Q,R53Q point mutations of the HIV-1 Tat protein abrogated Tat binding to the TAR element and gene transactivation. To test whether the Tat-TNF α synergism defined in the above model system required Tat-TAR association, the R52Q,R53Q mutant of Tat (designated TatRQ) was used together with TNFa to stimulate expression of the HIV-1 LTR driven CAT reporter (Figure 7B). The combination of $TNF\alpha$ treatment and TatRQ co-expression was only weakly effective (5-fold induction) in mediating activation of the HIV-1 LTR (Figure 7B), compared to wt Tat plus $TNF\alpha$ (Figure 7A). Similarly, mutations within the TAR element (ΔB and ΔB -ACU) that altered the Tat protein binding site (93, 366) also were not activated by Tat-TNFa treatment (Figure 7C and 7D). These results thus reflect Figure 7. Tat-TNF α activation of the HIV LTR requires Tat binding to the TAR element. Jurkat T cells were co-transfected with 5µg of ptzIIICAT (A and B) and 2µg of pSVexTat (A) or Tat (R52Q,R53Q) (B) expression plasmids; cells were also transfected with 2µg of LTR- Δ B (C) or LTR- Δ B-ACU (D) and 2µg of pSVexTat. At 32h after transfection, cells were incubated for an additional 16h in the presence or absence of TNF α . CAT activities were assayed using whole cell extracts (50µg for 30min). Cells transfected only with ptzIIICAT in the absence of activators were used as negative control. The results are the average of three experiments.



a requirement for Tat-TAR interactions in the synergistic transactivation of the HIV-1 LTR.

Tat-TNF α Synergism Requires Intact NF- κ B Sites. To characterize the region of the HIV-1 LTR involved in synergistic activation, HIV-1 LTR deletion mutants were transfected into Jurkat cells and stimulated with Tat, TNF α or Tat plus TNF α . As expected, the intact LTR-CAT construct (plasmid ptzIIICAT) was strongly inducible by both activators (Figure 8), with an 18 fold induction with Tat-TNF α . In contrast, the -109/-79 plasmid, a construct lacking the NF-kB sites, had only baseline level of activity and was not transactivated by TNF α . Surprisingly, this construct was not inducible by wt Tat expression plasmid, even though it contained an intact TAR element. Nevertheless, the combination of Tat and TNF α was able to stimulate the -109/-79 plasmid about 5fold. The III $\Delta 23$ construct which was deleted for the upstream modulatory sequences of the HIV-1 LTR (upstream of -167) was stimulated by both activators as efficiently as the wild LTR-CAT plasmid, indicating that the upstream elements in the -423 to -167 domain of the LTR did not play a complementary role in Tat-TNF α activation. The plasmid III ΔA was deleted for all of the LTR sequences upstream of -57 and was not activated significantly by either inducer alone, although a residual 4-fold induction of the III ΔA plasmid was observed with Tat-TNF α . This experiment indicates that strong synergistic activation of the HIV-1 LTR by the combination of Tat and TNF α required intact NF- κ B sites. The fact that some activation could occur in the absence of the enhancer element (in constructs -109/79 and IIIA) suggests that TNF α may be able to potentiate Tat activity at the TAR element independently of the NF-kB sites.

Stability of the $I\kappa B\alpha$ Mutants. Recent experiments have defined specific sites of inducer mediated and constitutive phosphorylation in the $I\kappa B\alpha$ regulatory protein (summarized in Figure 2). In particular, mutation of the N-terminal phosphorylation sites

Figure 8. Maximum Tat-TNF α synergism requires intact NF- κ B sites. Jurkat T cells were co-transfected with 5µg of ptzIIICAT, -109/-79, III Δ 23, or III Δ A in the absence or presence of pSVexTat (2µg). TNF α was added at 32h after transfection and incubated for an additional 16h. Whole cell extracts were prepared, normalized for total protein, and assayed for CAT activity (50µg for 30min).



Inducer

at Ser-32 and Ser-36 in the signal response domain of $I\kappa B\alpha$ prevented inducer mediated phosphorylation and subsequent proteasome-dependent degradation of $I\kappa B\alpha$ (53, 54, 72). Also, triple point mutation of $I\kappa B\alpha$ in the C-terminal residues S283, T291 and T299 abrogated constitutive phosphorylation in vivo by casein kinase II and increased the intrinsic stability of $I\kappa B\alpha$, but did not affect inducer mediated degradation of $I\kappa B\alpha$ (250). IkBa expression plasmids were generated that produced IkBa proteins singly mutated in Ser-32, Ser-36, in both S32 and S36 [I κ B α (2N)], in the three C-terminal sites [I κ B α (3C)] and in all five regulatory phosphorylation sites $[I\kappa B\alpha (2N+3C)]$. The inducer mediated turnover of these proteins was analyzed in stably transfected NIH 3T3 cells (26, 250) at different times after treatment with cycloheximide and TNFa (Figure 9A). Immunoblot analysis using an $I\kappa B\alpha$ specific antibody was able to distinguish between the endogenous murine $I\kappa B\alpha$ and the exogenously expressed human $I\kappa B\alpha$ (Figure 9A, lane 1). Cycloheximide was added to eliminate the complicating effects of *de novo* synthesis of IkB α after induction. The endogenous murine IkB α , human wt IkB α and IkB α (3C) all degraded rapidly in response to TNF α addition with a T1/2 of much less than 15 min (Figure 9A, lanes 2-6), indicating that triple mutation of S283, T291 and T299 did not affect inducer mediated degradation of $I\kappa B\alpha$. In contrast, both S36A (Figure 9A) and S32A mutations (data not shown) stabilized $I\kappa B\alpha$; both point mutations increased the T1/2 of IxB α to approximately 90-120 min (Figure 9A, lanes 2-6). Double point mutated IxB α (2N) and $I\kappa B\alpha$ (2N+3C) were extremely stable in the presence of TNF α and cycloheximide, with a $T_{1/2}$ of greater than 4h (Figure 9B). This experiment demonstrates the increased stability of point mutated $I\kappa B\alpha$ molecules and suggests that both $I\kappa B\alpha$ (2N) and $I\kappa B\alpha$ (2N+3C) should be stable transdominant mutants of the NF- κB response.

Inhibition of Tat-TNF α Activation of the HIV-1 LTR by IxB α Transdominant Mutants. To examine the effect of wt and mutated forms of IxB α on Tat-TNF α synergistic activation of HIV-1 LTR directed gene expression, the different forms of Figure 9. Inducer mediated degradation of $I\kappa B\alpha$. tTA-I $\kappa B\alpha$ (wt), tTA-I $\kappa B\alpha$ (2N), tTA-I $\kappa B\alpha$ (S36A), tTA-I $\kappa B\alpha$ (3C) and tTA-I $\kappa B\alpha$ (2N+3C) cells were treated with TNF α (5ng/ml) and cycloheximide (50 μ g/ml) for 0 (lane 1), 15 minutes (lane 2), 1h (lane 3), 2h (lane 4), 3h (lane 5) or 4 h (lane 6). (A) Endogenous murine and exogenous human I $\kappa B\alpha$ were detected in whole cell extracts (15 μ g) by immunoblotting using affinity purified AR20 antibody. (B) Levels of I $\kappa B\alpha$ were quantified by laser densitometry and represented graphically.



IkB α were co-transfected into Jurkat cells together with the reporter construct and the wt Tat expression plasmid. Expression of both wild type IkB α and IkB α (3C) reduced Tat-TNF α activation in a dose dependent manner from a level of about 70-fold transactivation to 15-30 fold induction (Figure 10). However, neither wt IkB α nor IkB α (3C) completely inhibited HIV-1 LTR mediated expression. Expression of the S32 mutant of IkB α (or S36) dramatically reduced Tat-TNF α activation to 10-20 fold stimulation. Strikingly, the IkB α (2N) and IkB α (2N+3C) mutants were able to eliminate Tat-TNF α transactivation at low concentrations of inhibitory plasmid; 1 µg of IkB α (2N) or IkB α (2N+3C) reduced LTR-directed reporter gene expression down to only 5-fold stimulation. At higher concentrations, Tat-TNF α transactivation of HIV-1 LTR driven gene expression was completely suppressed by the transdominant IkB α mutants (Figure 10).

Inhibition of HIV-1 protein and RNA synthesis in a single cycle infection model. To examine the ability of the $I\kappa B\alpha$ mutant proteins to interfere with HIV-1 multiplication, HIV-1 proviral DNA (pSVC21 BH10) was transfected together with the increasing amounts of wt $I\kappa B\alpha$ or mutant $I\kappa B\alpha$ -expressing plasmid into Cos-1 cells. This single cycle infection model permits a single round of virus multiplication and release of infectious HIV-1 but re-infection does not occur because of the absence of the CD4 receptor on Cos-1 cells. At three days post-transfection, high levels of transfected $I\kappa B\alpha$ accumulated in Cos-1 cells (Figure 11B, lane 3-14) compared to the endogenous level of primate $I\kappa B\alpha$ (Figure 11B, lanes 1 and 2). Using a human antiserum that recognizes HIV-1 structural proteins, a dramatic reduction in the amounts of viral specific p24 core antigen. p55 precursor for virion core proteins, and gp120 envelope glycoprotein was observed in cells expressing $I\kappa B\alpha$ (2N) (Figure 11A, lanes 6-8). In other experiments using the single cycle infection model, we found that wt $I\kappa B\alpha$, $I\kappa B\alpha$ (3C) and $I\kappa B\alpha$ (2N+3C) were also effective in blocking a round of HIV-1 replication, but $I\kappa B\alpha$ (2N) was consistently more effective in a dose dependent manner. Analysis of the intracellular Figure 10. Transdominant IxB α mutants inhibit Tat-TNF α activation of the HIV LTR. In Jurkat cells, pTZIIICAT (2µg) was co-transfected with pSVexTat and different amounts (1, 2, 4 µg) of pSVK-wt IxB α , pSVK-IxB α (S32A), pSVK-IxB α (2N), pSVK-IxB α (3C), pSVK-IxB α (2N+3C), and treated with TNF α (5ng/ml) for 16h beginning at 32h post-transfection. The level of HIV-1 LTR driven reporter gene expression was determined by CAT assay on the whole protein extracts of the cells. Positive control (+Tat/TNF α) was obtained by co-transfection with HIV-1 LTR CAT (2µg) and pSVexTat (2µg), and induction with TNF α (5ng/ml) for 16h. The negative control (lane -) was obtained by transfection with the HIV-1 LTR reporter construct only. The results represent the average of three independent experiments.



accumulation of viral mRNA also confirmed that $I\kappa B\alpha$ and the transdominant negative forms of $I\kappa B\alpha$ differentially inhibited HIV-1 multiplication (Figure 12). Expression of $I\kappa B\alpha$ inhibited HIV-1 proviral transcription in a dose dependent manner (Figure 12A, lanes 3-14). In particular, $I\kappa B\alpha$ (2N) was the strongest inhibitor of HIV-1 transcript accumulation (Figure 12A, lanes 6-8). Complementary results were obtained when the level of p24 antigen release into the supernatant was measured by an enzyme-linked immunosorption assay (ELISA)-based viral antigen capture assay (Figure 11D). Together these results indicate that $I\kappa B\alpha$ (2N) inhibited HIV-1 transcript levels, intracellular viral protein accumulation and release of virions into the supernatant. Surprisingly, additional mutations within the C-terminal phosphorylation sites in I $\kappa B\alpha$ (2N+3C) reduced the inhibitory capacity relative to $I\kappa B\alpha$ (2N) (Figure 11A, lanes 12-14 and Figure 12A, lanes 12-14), suggesting an important role for the intact C-terminal PEST domain in the inhibition of HIV-1 multiplication. Figure 11. Inhibition of viral protein expression by trans-dominant $I\kappa B\alpha$ mutants. Cos-1 cells were transfected with HIV-1 proviral DNA (pSVC21 BH10: 10 µg) and viral protein expression was inhibited by co-transfecting either 1 µg (lane 3, 6, 9, and 12), 5 µg (lane 4, 7, 10 and 13) or 10 µg (lane 5, 8, 11, and 14) of plasmid expressing wt I $\kappa B\alpha$ (lane 3-5), I $\kappa B\alpha$ (2N) (lane 6-8), I $\kappa B\alpha$ (3C) (lane 9-11) or I $\kappa B\alpha$ (2N+3C) (lane 12-14). Three days after transfection, cells were collected and analysed by immunoblotting for expression of HIV proteins (A), I $\kappa B\alpha$ (B) and β-actin (C). Bands corresponding to the viral envelope glycoprotein gp120, the p55 polyprotein precursor for virion core proteins , and the viral capsid protein p24 are indicated. D) The release of HIV-1 p24 antigen into the supernatant of infected cells was measured by p24 ELISA; the results represent the average of two independent experiments.



Figure 12. Inhibition of viral transcription by trans-dominant I κ B α mutants. Cos-1 cells were transfected with HIV-1 proviral DNA (pSVC21 BH10: 10 μ g) and either 1 μ g (lane 3, 6, 9, and 12), 5 μ g (lane 4, 7, 10 and 13) or 10 μ g (lane 5, 8, 11, and 14) of plasmids expressing wt I κ B α (lane 3-5), I κ B α (2N) (lane 6-8), I κ B α (3C) (lane 9-11) or I κ B α (2N+3C) (lane 12-14). Three days after transfection cells were collected and RNA was extracted. (A) Viral transcripts were detected by northern blot analysis; the HIV-1 proviral cDNA probes were the 2 and 2.2 kbp Hind-III fragments derived from pSVC21 BH10. Positions of the 9 kb, 4.5 kb and 2 kb transcripts are indicated. (B) The blot in (A) was stripped and reprobed with a β -actin probe to illustrate the relative amount of RNA present in each lane. The β -actin cDNA used as probe was the 1 kbp Pst-1 fragment derived from p β -actin plasmid.



1 2 3 4 5 6 7 8 9 10 11 12 13 14
CHAPTER IV

INDUCIBLE EXPRESSION OF IκBα REPRESSOR MUTANTS INTERFERES WITH NF-κB ACTIVITY AND HIV-1 REPLICATION IN JURKAT T CELLS

Inhibition of HIV-1 gene expression by transdominant repressors of $I\kappa B\alpha$ (TD-I $\kappa B\alpha$) in a single cycle infection using COS-1 cells (25) lead us to examine the effect of TD-I $\kappa B\alpha$ on *de novo* HIV-1 infection in Jurkat T cells which are more physiologically relevant. Jurkat T cell lines that inducibly express TD-I $\kappa B\alpha$ were generated and examined for the effect of doxycycline (Dox)-inducible expression of TD-I $\kappa B\alpha$ on NF- κB DNA binding activity, NF- κB dependent gene expression and *de novo* HIV-1 multiplication. The time course of *de novo* HIV-1 infection in TD-I $\kappa B\alpha$ -expressing Jurkat cells was altered by Dox induction of TD-I $\kappa B\alpha$, resulting in a dramatic transcriptional inhibition of HIV-1 multiplication, as measured by p24 antigen, reverse transcriptase and viral RNA analyses.

Dox inducible expression of TD-IkBa down regulates endogenous IkBa expression. In order to examine the consequences of overexpression of TD-IkBa on NF-kB dependent gene expression and virus multiplication, Jurkat T cell lines were generated that inducibly expressed two forms of TD-I κ B α . One form was I κ B α (2N) and the other form of I κ B α (2N Δ 4) also contained the S32A, S36A mutations like IxB α (2N), as well as a 22 amino acid deletion of the C-terminal portion of $I\kappa B\alpha$ (26, 250), a region of the PEST domain that is dispensable with regard to binding of NF- κ B subunits and I κ B α degradation (Figure 13A). Starting with Jurkat T cells selected for expression of the reverse tetracycline transactivator protein rtTA (146), expressed under the control of the CMVt autoregulatory promoter (Figure 13A), we isolated pools and clones of rtTA-Jurkat cells expressing $I \kappa B \alpha$ (2N) and $I \kappa B \alpha$ (2NA4). The first pool of $I \kappa B \alpha$ -2NA4 cells was disappointing because of the high level of leakiness of the transgene (Figure 13B, lane 6), compared to endogenous IkBa (Figure 13B, lanes 1-4). However, analysis of IkBa expression revealed an interesting modulation of endogenous $I\kappa B\alpha$ protein level when IxBa (2N Δ 4) was Dox-induced for 24h. The level of endogenous IxBa was decreased about four-fold in Jurkat cells expressing $I\kappa B\alpha$ (2N Δ 4) compared to the $I\kappa B\alpha$ levels in either Jurkat or rtTA-Jurkat cells (Figure 13B, lanes 1-4 and lane 6). Dox induction

Figure 13. Schematic summary of the TD-IkBa-expressing CMVt-IkBa vectors and inducibility of TD-IkBa-expressing Jurkat cells. (A) The five ankyrin repeats of IkBa are indicated by the open boxes. Two phosphorylation sites at Ser-32 and Ser-36 (indicated by triangles) in the N-terminal region of IkBa required for inducer mediated degradation of IkBa. Within the highly acidic C-terminal region, several potential casein kinase II (CKII) phosphorylation sites are clustered around S-283, T-291 and T-299. IxB α -2N Δ 4 contains a 22aa carboxy terminal deletion of IxB α -2N in which Ser-32 and Ser-36 are mutated to Ala. (B) Jurkat, rtTA-Jurkat and rtTA-IkBa-2NA4 Jurkat cells were collected at 24h after doxycycline (Dox) addition and the effect of Dox on $I\kappa B\alpha$ expression was examined by immunoblotting using the IkBa MAD10B antibody. (C) rtTA-IxB α -2N Δ 4 cells were incubated with Dox for different intervals (0-48h) and then treated with calpain inhibitor (100µM) for 30 min and subsequently induced with TNF (10ng/ml) for 5 min; expression of $I\kappa B\alpha$ was analyzed by immunoblotting using the $I\kappa B\alpha$ MAD10B antibody. (D) rtTA-l κ B α -2N Jurkat cells were harvested after 0 to 48h Dox addition and similarly analyzed by immunoblotting for IkBa expression. Phosphorylated $I\kappa B\alpha$ (P- $I\kappa B\alpha$), endogenous $I\kappa B\alpha$ ($I\kappa B\alpha$), and $I\kappa B\alpha$ - $2N\Delta 4$ ($2N\Delta 4$) are indicated by arrows.





resulted in five fold increase in IkB α (2N Δ 4) expression after 24h and an almost complete inhibition of endogenous IxB α expression (Figure 13B, lane 5). To characterize this inhibition further, a representative clone of $I\kappa B\alpha$ (2NA4) Jurkat cells was Dox induced for 3h-48h and then treated with TNF α (10 ng/ml) for 5 min as an inducer of IkB α phosphorylation, following a 30 min pretreatment with calpain inhibitor I (100 μ M) to block inducer mediated degradation of $I\kappa B\alpha$ (24, 26). The different forms of $I\kappa B\alpha$ were resolved by 15% SDS-PAGE; both endogenous $I\kappa B\alpha$ and the slower migrating phosphorylated form of $I\kappa B\alpha$ (P-I $\kappa B\alpha$) were detected by immunoblotting (Figure 13C, lanes 1 and 2). In the $I_{\kappa}B\alpha$ (2NA4) Jurkat clone without Dox addition, the three forms of $I\kappa B\alpha$ were detected (Figure 13C, lane 3); Dox addition for 3 to 6h resulted in a 3-5 fold increase in $I \kappa B \alpha$ (2NA4) (Figure 13C, lanes 4-6), and a progressive decrease in the endogenous IxB α forms such that by 24 and 48h after Dox addition, endogenous IxB α was undetectable (Figure 13C, lanes 4-8). Because of the S32A, S36A mutation in $I\kappa B\alpha$ (2N Δ 4), this form of IkB α was not phosphorylated as a consequence of TNF α addition (53, 54, 416). Additionally, a clone of $I\kappa B\alpha$ (2N) Jurkat cells was analyzed that demonstrated properties similar to the $I\kappa B\alpha$ (2NA4) Jurkat cells, although it was not possible to distinguish the endogenous from the transfected IkBa forms (Figure 13D, lanes 1,2). With this clone, the level of leakiness of the TD-I κ B α was significantly lower than that observed with IkB α (2N Δ 4), since the amounts of IkB α in rtTA-Jurkat and IkB α (2N) Jurkat in the absence of Dox were similar (Figure 13D, lanes 1,2). Nevertheless, Dox induction resulted in a 20-25 fold increase in the overall level of $I\kappa B\alpha$ in these cells (Figure 13D, lanes 2-7). Based on these results, we have isolated pools and clones of Jurkat cells inducibly expressing TD-I κ B α under the control of the Tet-responsive promoter. Furthermore, Dox induction of TD-I κ B α resulted in the inhibition of endogenous $I\kappa B\alpha$, consistent with the fact that the $I\kappa B\alpha$ gene is tightly regulated by an NF-kB dependent mechanism (228).

Growth of TD-IKBa expressing cells and induction of apoptosis. All stably transfected TD-I κ B α expressing clones grew well in 10% serum and growth was not dramatically retarded as a consequence of Dox addition or in the case of $I\kappa B\alpha$ (2N) or $I\kappa B\alpha$ (2NA4) Jurkat cells, by upregulation of TD-I κ B α expression (doubling time of 50h ± 4h). Based on recent observations that NF-kB may play a protective role in apoptotic cell death (28, 423, 433), the response of control and TD-I κ B α -expressing Jurkat cells to TNF α -induced apoptosis was examined by TUNEL assay. At 16h after TNFa (10 ng/ml) treatment in Dox induced cells, 65-80 percent of the TD-I κ B α -expressing cells were undergoing apoptotic cell death whereas in Dox-induced TD-IkBa-expressing cells without TNFa treatment, less than 2 percent of the cells were apoptotic (Table 2). Similarly, $TNF\alpha$ treatment alone resulted in 2 percent apoptosis in TD-1kBa-expressing cells and 6 percent apoptotic cells in rtTA-Neo Jurkat cells (Table 2). Dox induction of TD-I κ B α expression resulted in an increased sensitivity to $TNF\alpha$ -induced apoptosis, as detected by DNA fragmentation analysis at 8 or 16h after TNF α addition in the TD-I κ B α -expressing cells but not in the control rtTA-Neo cells (data not shown). It appears that Dox induction of TD- $I_{\kappa}B\alpha$ expression, does not lead to apoptosis per se, but rather dramatically sensitizes Jurkat cells to TNF α -induced apoptosis. This observation may explain the observed selection against cells that constitutively express TD-I κ B α (see below).

Inhibition of NF- κ B DNA binding activity and gene expression by TD-I κ B α . The induction of NF- κ B DNA binding activity in control and TD-I κ B α -expressing cells was examined following treatment of cells with several different inducers (Figures 14). Treatment of rtTA-neo-Jurkat, a control cell line stably transfected with the empty neo CMVt BL (Figure 14A) or rtTA-Jurkat (data not shown) with TNF α or PMA/PHA for 4h resulted in a strong induction of NF- κ B DNA binding activity, irrespective of Dox treatment for 6 to 48h (Figure 14A, lanes 5-14). In contrast, TNF α induction of NF- κ B activity in I κ B α (2N Δ 4) Jurkat cells (Figure 14B, lanes 5, 6) was completely blocked by

Table 2. TD-I κ **B** α sensitizes Jurkat cells to TNF α -induced apoptosis. rtTA-Neo-, I κ B α -2N-, and I κ B α -2N Δ 4-expressing Jurkat cells were treated with Dox (1 μ g/ml) for 24h and then induced with TNF α (10ng/ml) for 16h. Cells were fixed and stained for TUNEL (Boehringer Mannheim) and with Hoechst 33258. The percentage of total cells staining positive by TUNEL assay was determined by counting 200-400 cells per sample. The values are presented as a percentage of positive cells by TUNEL divided by the total number of Hoechst 33258 stained nuclei.

TNF α Induced Apoptosis in TD I κ B α -expressing Jurkat cells

Trea	tment		Cell lines	
Dox	ΤΝFα	rtTA-Neo	ΙκΒα-2Ν	ΙκΒα-2ΝΔ4
-	-	<2	<2	<2
+	-	<2	<2	<2
-	+	6.9	2.3	2.5
+	+	6.4	65.9	79.1

Figure 14. NF- κ B DNA binding activity in control and TD-I κ B α -expressing Jurkat T cells treated with TNF or PMA/PHA. rtTA-Neo (A), I κ B α -2N Δ 4 (B, D, E), rtTA-2N (C) Jurkat cells were incubated with Dox for different times as indicated in the Figure and subsequently induced by TNF (10ng/ml) or PMA/PHA (100ng/ml and 1ug/ml, respectively) for 4h. EMSA was performed on nuclear extracts (5µg) prepared from cells. I κ B α immunoblot analysis (E) was performed on whole cell extracts (20µg) prepared from I κ B α -2N Δ 4 cells induced by Dox for different times and subsequently treated with PMA/PHA for 4h. Endogenous I κ B α and transfected I κ B α -2N Δ 4 are indicated by arrows. Control lanes (C) in panels A,B,C,and D represent the competition of NF- κ B-DNA complex formation using a 125-fold excess of unlabeled PRDII probe.



the induction of $I\kappa B\alpha$ (2NA4) for 6h or longer (Figure 14B, lanes 6-9); the strong induction of NF-kB binding activity by PMA/PHA was also more than 95 percent inhibited by Dox activation of $I\kappa B\alpha$ (2NA4) (Figure 14B, lanes 10-14). Similarly, Dox induction of $I\kappa B\alpha$ (2N) also inhibited completely the induction of NF- κB binding activity by TNF α (Figure 14C, lanes 2-6) and PMA/PHA (Figure 14C, lanes 7-12). In a subsequent experiment, the kinetics of activation of $I\kappa B\alpha$ (2NA4) and the inhibition of NF-kB binding activity were examined (Figure 14D and E). Surprisingly, as early as 1h after Dox addition, expression of IxB α (2N Δ 4) was upregulated (Figure 14E, lanes 1 and 2) and NF- κ B DNA binding activity was inhibited (Figure 14D, lanes 1 and 2). Interestingly, comparison of the levels of $I\kappa B\alpha$ (2NA4) and endogenous $I\kappa B\alpha$ revealed that constitutive expression of $I\kappa B\alpha$ (2NA4) was dramatically decreased with time in culture (compare lane 6 in Figure 13B and lane 1 in Figure 14E), whereas the cells remained highly inducible in response to Dox addition (Figure 14E, lanes 2-9). TD-I κ B α expressing Jurkat cells were also resistant to induction of NF-kB binding activity by double stranded RNA (poly I:C) treatment (data not shown). Thus, overexpression of TD- $I\kappa B\alpha$ blocks the induction of NF- κB DNA binding activity by multiple inducers. Also, continued growth in culture selects for Jurkat cells that display low constitutive expression of TD-IkBa, possibly due to an increased sensitivity of TD-IkBa expressing cells to apoptosis.

To complement the observation that overexpression of TD-I κ B α inhibited NF- κ B binding activity, the effect of TD-I κ B α on NF- κ B dependent reporter gene expression was also examined. A CAT reporter gene driven by the SV40 minimal promoter, linked to the HIV-1 -109 to -79 region of the LTR, was transfected into I κ B α (2N Δ 4) expressing Jurkat cells together with a control plasmid mutated in the two NF- κ B binding sites of the HIV-1 LTR (363). As shown in Figure 15A, treatment of these cells at 24h after transfection with PMA/PHA (24h) resulted in a 4 fold stimulation of reporter gene activity above background level with the wild type but not mutated promoter; Dox addition

Figure 15. Inhibition of Tat-TNF, Tat, or PMA/PHA induced HIV-1 LTR and HIVenhancer activation by $I\kappa B\alpha$ mutants. (A) rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells were transfected with HIV-enh (\Box) or HIV-enh mut CAT (\Box) reporter plasmid (10 μ g); at 24h after transfection cells were treated with PMA/PHA or PMA/PHA + Dox for an additional 24h. (B) rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells were transfected with pTZIIICAT (10 μ g) and in some cases with pSVexTat (10 μ g); at 24h after transfection some cells were treated with TNF α (10ng/ml) alone, with TNF α + Dox (\blacksquare) or with Dox alone (\boxdot). The level of HIV-1 LTR driven reporter gene expression was determined by CAT assay on the whole cell extracts (200 μ g), assayed for 2h. The negative control (lane -) was obtained by transfection with the HIV-1 LTR reporter construct only without TNF induction.



simultaneously with PMA/PHA inhibited NF- κ B dependent induction of reporter gene activity. The HIV-1 LTR-CAT reporter plasmid was also transfected into TD-I κ B α expressing Jurkat cells and the effect of TD-I κ B α induction on the Tat-TNF α synergistic activation of the HIV-1 LTR was examined (25) (Figure 15B). In this experiment, Tat-TNF α activation of the LTR represented an 80-fold activation of gene activity that was inhibited more than 5-fold with Dox-induced TD-I κ B α expression; the residual LTR-reporter gene activity likely represents NF- κ B independent activation of the HIV-LTR. Co-expression of Tat protein also stimulated the HIV-1 LTR about 10-fold; somewhat surprisingly, expression of the TD-I κ B α also inhibited induction of the HIV-1 LTR mediated by Tat alone (Figure 15B).

Inhibition of de novo HIV-1 multiplication in TD-IkBa expressing Jurkat cells. Given the involvement of NF-kB in the early transcriptional control of HIV-1 LTR gene expression (reviewed in (365), the impact of TD-IkBa expression on the course of de novo HIV-1 protein synthesis and virus production was next examined. Control and TD-IkBaexpressing Jurkat cells after preincubation with or without Dox for 24h were infected with the HIV-1 strain III B (derived from the molecular clone HXB2D) at an MOI of 0.01 pfu/ml and HIV-1 infection was monitored by RT assay, p24 ELISA, and p24 antigen accumulation over periods varying from 16 days to 36 days depending on the infection. Both RT assay (Figure 16A) and p24 ELISA analysis (Figure 16B) demonstrated that continuous Dox induced expression of $I\kappa B\alpha$ -2NA4 resulted in dramatic delay in the onset of HIV-1 multiplication. In control rtTA-Neo-Jurkat cells, RT and p24 expression were detected as early as 8 days post-infection (p.i.), whereas in $I_{\kappa}B\alpha$ -2N Δ 4 cells infection was first detected at day 12; addition of Dox at different times during the infection delayed the onset of detectable HIV-1 multiplication until 16-20 days (Figure 16A and B). The most effective inhibitory regimen was Dox addition 24h before infection (day -1) and subsequent Dox addition to the medium at days 8, 18, and 24. One addition of Dox at day Figure 16. Suppression of HIV-1 infection in $I\kappa B\alpha - 2N\Delta 4$ Jurkat cells. rtTA-Neo and rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells were infected with HIV-IIIB for 2h at an MOI of 0.01 pfu/ml. Cells were then grown for 36 days and HIV-1 infection was monitored by A) RT assay (200µl) and (B) p24 ELISA (50µl). Symbols: • rtTA-Neo + Dox; • rtTA-2N $\Delta 4$ - Dox; • rtTA -2N $\Delta 4$ - Dox (+Dox12, Dox addition 12 days after infection); • rtTA-2N $\Delta 4$ + Dox (Dox addition 24h before infection); • rtTA-2N $\Delta 4$ + Dox (continuous addition of Dox -1, 8, 18, 24 after infection).



-1 or addition of Dox at day 12 also effectively blocked the onset of HIV-1 replication. However, with these treatments, breakthrough of HIV-1 multiplication was observed at day 36, as detected by RT and p24 ELISA. On the other hand, intermittent replenishment of Dox in the medium dramatically repressed HIV-1 RT and p24 expression throughout the course of infection (Figure 16A and B).

The intracellular accumulation of p24 antigen was also monitored during the course of de novo HIV-1 infection, together with the expression of $I\kappa B\alpha$ and β -actin (Figure 17). p24 accumulation was weakly detected as early as 4 day p.i. (Figure 17A, lane 2); high level expression was detected thereafter throughout the course of infection (Figure 17A, lanes 3-9) in HIV-1 infected rtTA-Neo-Jurkat cells. Also with the analysis of HIV-1 replication in Jurkat cells, a decrease in the level of $I\kappa B\alpha$ was detected during the exponential phase of virus multiplication at days 12 to 20 (Figure 17A, lanes 4-6), reflecting the HIV-1 mediated degradation of IkBa, an effect that contributes to constitutive NF-kB DNA binding activity in HIV-1 infected cells (12, 96, 275, 363, 364). In the $I \times B \alpha$ -2NA4 expressing cells, the appearance of p24 antigen was delayed until day 12 after infection and peaked at day 20-24 p.i. (Figure 17B, lanes 4-7). In the TD-I κ B α expressing cells, the decrease in $I\kappa B\alpha$ was also delayed until later times after infection. Again, the basal level of $I\kappa B\alpha$ transgene was significantly reduced relative to endogenous $I\kappa B\alpha$, reflecting the ongoing selection of low background expressing cells (Figure 14E). However, addition of Dox to the infected cell culture at day 12 p.i. resulted in a dramatic increase in IxB α -2N Δ 4 expression (Figure 17C, lanes 4 and 5); this time of addition was not sufficient to inhibit the appearance of p24 antigen at day 12 (Figure 17C, lane 4). However, induction of TD-IkBa completely inhibited endogenous IkBa expression by day 16 (Figure 17C, lane 5) and partially blocked the subsequent intracellular accumulation of p24 antigen (compare Figure 17B and 5C, lanes 5-9). Addition of Dox to TD-IkBa expressing Jurkat cells 24h before infection (Figure 17D) or intermittent Dox addition at days -1, 8, 18, and 24 (Figure 17E) delayed the onset of detectable p24 antigen until day

Figure 17. Inhibition of viral p24 protein expression by $I\kappa B\alpha$ -2N $\Delta 4$ mutant. rtTA-Neo and rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells were incubated in the presence or absence of Dox and then infected with HIV-IIIB for 2h at an MOI of 0.01 pfu/ml. Cells were collected every fourth day for 36 days and analyzed by immunoblotting. rtTA-Neo Jurkat cells (panel A) and rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells (panel D and E) were treated with Dox for 24 hours prior to infection or not treated (panel B). rtTA-I $\kappa B\alpha$ -2N $\Delta 4$ Jurkat cells (panels B and C) were infected without Dox pretreatment, but Dox was added 12 days after the infection (panel C). Dox was also intermittently added at 8, 18, and 24 days after infection in panel E. Endogenous I $\kappa B\alpha$ (wtI $\kappa B\alpha$), I $\kappa B\alpha$ -2N $\Delta 4$ (2N $\Delta 4$), ReIA(p65), viral p24 and actin proteins were detected by immunoblotting as described in Material and Methods and are indicated by arrows.

A) rtTA-Neo Jurkat



rtTA-2N∆4 Jurkat



20 p.i. (Figure 17D and E, lane 6). In contrast to the results obtained by RT and p24 ELISA assays, both one time addition and intermittent addition of Dox delayed the accumulation of intracellular p24 antigen to an equivalent extent. Overall, Dox induction of TD-I κ B α expression resulted in a 10-20 fold decrease in the production of p24 antigen (Figure 17), as well as inhibition of HIV-1 virion release (Figure 16). Similar results were obtained using the I κ B α -2N expressing cells (data not shown), thus demonstrating a dramatic inhibitory effect of TD-I κ B α expression on the course of *de novo* HIV-1 infection in Jurkat T cells.

Decreased levels of HIV-1 mRNA in TD-IkBa expressing Jurkat cells. In order to link the inhibition of HIV-1 multiplication with NF- κ B inhibitory effects of TD-1 κ B α , the effects of TD-IkBa induction on HIV-1 induced NF-kB binding activity was evaluated by mobility shift analysis. Virus induced activation of NF-kB was blocked by TD-lkBa expression (data not shown), thus complementing the results described in Figure 14, and confirming that TD-IkBa interfered with HIV-induced NF-kB binding. To further characterize the block in HIV-1 multiplication, accumulation of HIV-1 viral RNA species was evaluated by semi-quantitative RT-PCR, using the primers and procedures described previously (468). The primer pair M667/M668 detected total viral RNA with fragment of 161 bp; M669/LA23 identified a fragment of 214 bp which represented singly spliced (env) and doubly spliced tat/rev RNA; and LA41/LA45 amplified a fragment of 123 bp corresponding to doubly spliced tat/rev RNA (Figure 18A). Viral RNA species in rtTA-Neo-Jurkat and rtTA-2N Δ 4-Jurkat cells were detected at different times after *de novo* HIV infection in the presence or absence of Dox-induced TD- $I\kappa B\alpha$ (Figure 18B). In rtTA-Neo Jurkat cells, HIV mRNA transcripts were detected as early as 2-4 days after infection (Figure 18B, lanes 2, 3, 7 and 8) and their levels increased at days 6 and 10 post-infection (Figure 18B, lanes 4, 5, 9 and 10), regardless of Dox addition. In rtTA-2NA4 Jurkat cells, without Dox addition, a low level of full length viral RNA was Figure 18. Suppression of HIV-1 transcription in $I \ltimes B\alpha$ -2N Δ 4 expressing Jurkat cells. (A) A schematic representation of full-length and spliced mRNAs (*env*, *tat/rev*) of HIV-1 with specific primers used for RT-PCR analysis. M667/M668 detects both full-length and spliced mRNAs and generate a 161bp fragment. The primer pair M669/LA23 detects only spliced mRNA (*env*, *tat/rev*) and produces a 214bp fragment. *tat/rev* mRNA is detected by LA41/LA45 primer pair and a 123bp fragment is generated following PCR. (B) RT-PCR analysis of HIV-1 RNA. rtTA-Neo and rtTA-I κ B α -2N Δ 4 Jurkat cells were incubated in the presence or absence of Dox and then infected with HIV-IIIB for 2h at an MOI of 0.01 pfu/ml. Cells were collected 2, 4, 6 and 10 days after infection and total RNA (2 µg) was analyzed by RT-PCR. All results are normalized to the levels of GAPDH. A)



M667 M668 (161bp) : Full length, env. tat/rev M669 LA23 (214bp) : env. tat/rev LA41 LA45 (123bp) : tat/rev

B)



detected at day 2 (Figure 18B, lane 12, upper panel) and by day 4 unspliced and spliced viral RNA was detected (Figure 18B, lane 13) and accumulated thereafter at days 6 and 10 (Figure 18B, lanes 14 and 15). However, with Dox induction of TD-I κ B α , viral RNA levels were reduced (Figure 18B, lanes 17-20). Full length RNA was detected at day 2 (Figure 18B, lane 17, upper panel) but the overall levels of unspliced and spliced RNA were decreased at days 6 and 10, relative to the levels detected in the absence of Dox or in rtTA-Neo cells. Strikingly, doubly spliced tat/rev mRNA was not detected in rtTA-2N Δ 4 Jurkat cells treated with Dox (Figure 18B, lanes 18-20, lower panel). These results demonstrate a transcriptional inhibitory effect of TD-I κ B α .

CHAPTER V

IDENTIFICATION BY *In Vivo* GENOMIC FOOTPRINTING OF AN NF-κB/Sp1 TRANSCRIPTIONAL SWITCH THAT REGULATES THE IκBα PROMOTER

In Jurkat T cells that inducibly express TD-I κ B α (222), endogenous I κ B α protein expression was blocked by TD-I κ B α . We now demonstrate that inducer dependent induction of the I κ B α gene transcription was blocked by TD-I κ B α expression at the transcriptional level. To further analyze the autoregulatory control of I κ B α expression, dimethylsulfate genomic footprinting was used to determine the pattern of protein-DNA interactions at the I κ B α locus in stimulated Jurkat T cells and TD-I κ B α expressing cells. These studies permit the first *in vivo* characterization of I κ B α transcriptional autoregulation by NF- κ B and identify the promoter proximal NF- κ B/Sp1 transcriptional switch as an essential component in the regulation of the I κ B α promoter.

Tet-induced TD-IκBα blocks expression of IκBα gene. As shown previously (222), endogenous IκBα protein expression was abolished after TD-IκBα induction for 24h (Figure 19A, lane 7-11). To determine whether IκBα gene transcription was downregulated by TD-IκBα, rtTA-IκBα (2NΔ4) Jurkat cells were treated with TNFα or PMA in the presence or absence of Dox and endogenous IκBα and TD-IκBα mRNA were analyzed by RNase protection analysis with a 276 nt 3' cDNA probe that specifically recognized the C-terminus of endogenous IκBα mRNA as well as the truncated IκBα (2NΔ4) mRNA (Figure 19B). After 10 min of TNFα or PMA/PHA induction, 20 and 40 fold increases in IκBα mRNA were detected, respectively (Figure 19B, lanes 2 and 5); subsequently the level of IκBα mRNA declined with time in rtTA-IκBα (2NΔ4) Jurkat cells (Figure 19B, lanes 4 and 7). In TD-IκBα expressing cells, endogenous IκBα mRNA induction was decreased 5-fold by Dox addition, whereas high level expression of the IκBα (2NΔ4) transgene was easily detected by RNase protection (Figure 19B, lanes 8-14). These results indicate that Dox-induced TD-IκBα expression interfered with the induced but not the basal level of endogenous IκBα mRNA transcription. **Figure 19. Tet-induced TD-I**κ**B**α **inhibits endogenous I**κ**B**α **expression.** (A) rtTA-Neo (lanes 1-6) and rtTA-IκBα(2NΔ4) Jurkat cells (lanes 7-12) were incubated with Dox (1 μ g/ml) for different times (0, 10 min, 4h, 48h). Endogenous IκBα (top arrow) and TD-IκBα (bottom arrow) were detected by immunoblotting using MAD10B antibody. (B) Schematic representation of C-terminal IκBα probe used in RNase protection analysis. rtTA-IκBα(2NΔ4) Jurkat cells were treated with TNFα (10 ng/ml, lanes 2-4, 9-11) or PMA (50 ng/ml) plus PHA (1µg/ml) (lanes 5-7, 12-14) for different times (0, 10 min, 4h, 24h) in the absence (lanes 1-7) or presence (lanes 8-14) of Dox (1 µg/ml, 24h). Endogenous IκBα and TD-IκBα mRNA were detected using the 276nt 3'cDNA probe by RNase protection assay. Arrows indicate β-actin, IκBα (221nt band) and IκBα(2NΔ4) (155nt band) from top to bottom. The results shown are representative of at least three independent experiments.

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					_	-			• •					-	-ΙκΒα
									•						-2N∆4
		1	2	3 4	5	6		7	8	9	10	11	12		IKBO
B		-	-	•••	÷	Ū		·	U	-					
wt Ix	εΒα	mR	NA												
3 Ni A /	4 [1.4]		- DNI										IAAA	AA	AAA
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			Un	digest	ed p	robe	(27	6 nt.	.) =						
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			-Dox							+Do	X			_	
_		TNI	Fα	PM	API	<u>IA</u>			TN	Fα_	PN	/A /	PHA	<u> </u>	
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A

TD-IκBα **inhibits** NF-κB **binding to** κB1 **site of the** IκBα **promoter**. Using Jurkat T cells inducibly expressing TD-IκBα (222), the effect of TD-IκBα on TNFα and PMA induced NF-κB binding activity was studied by EMSA using the κB1 site of the IκBα promoter as a probe. Treatment of rtTA-Neo Jurkat with TNFα or PMA/PHA resulted in a strong induction of NF-κB binding activity, irrespective of Dox treatment (Figure 20AB, top panel, lanes 1-4, 6-9). In contrast, TNFα or PMA/PHA induced NF-κB binding activity in rtTA-IκBα (2NΔ4) Jurkat cells was completely blocked by Dox induction of TD-IκBα (Figure 20AB, bottom panel, lanes 6-9), while NF-κB binding activity was observed in rtTA-IκBα (2NΔ4) Jurkat cells without Dox-treatment (Figure 20AB, bottom panel, lanes 1-4). To identify the subunit composition of the NF-κB complexes, supershift analysis of extracts from rtTA-Neo Jurkat cells treated with PMA for 4h was performed using anti-p65, -p50, -p52 and -c-rel antibodies. Complexes were shifted with p65 or p50 antibodies but not with p52 or c-rel antibodies (data not shown). Therefore, NF-κB DNA binding activity was completely blocked by expressing TD-IκBα.

p65 is tightly bound to TD-1kBa. Co-immunoprecipitation studies were performed with anti-p65 (Figure 21AB) and anti-1kBa antibodies (Figure 21C) to determine whether TD-1kBa could associate with p65 *in vivo* during the course of TNFa or PMA/PHA induction. In unstimulated rtTA-Neo Jurkat cells, p65 complexed with 1kBa in the presence or absence of Dox (Figure 21AB, lanes 1 and 5). In unstimulated rtTA-1kBa (2N Δ 4) Jurkat cells in the absence of Dox pretreatment, p65 was associated with both endogenous 1kBa and TD-1kBa (Figure 21AB, lane 10), while in Dox-treated TD-1kBa expressing cells, p65 was mainly associated with TD-1kBa (Figure 21AB, lane 14), due to downregulation of endogenous 1kBa expression. TNFa or PMA/PHA stimulation induced degradation of 1kBa which reappeared after 60 min in control Jurkat cells (Figure 21AB, lanes 2-4, 6-8) in the presence or absence of Dox; in rtTA-1kBa (2N Δ 4) Jurkat cells in the absence of Dox the same loss and reappearance of endogenous 1kBa was observed (Figure 21AB, Figure 20. TD- $l\kappa B\alpha$ blocks NF- κB binding to $\kappa B1$ site of the $l\kappa B\alpha$ promoter. (A) Nuclear extracts from rtTA-Neo (top panel) and rtTA- $l\kappa B\alpha(2N\Delta 4)$ Jurkat cells (lower panel) treated with TNF α (10 ng/ml) for the indicated times in the absence (lanes 1-5) or presence (lanes 6-9) of Dox pretreatment (1 µg/ml, 24h) were subjected to an EMSA using the $\kappa B1$ probe. (B) Nuclear extracts from rtTA-Neo (top panel) and rtTA $l\kappa B\alpha(2N\Delta 4)$ Jurkat cells (lower panel) treated with PMA (50 ng/ml) / PHA (1µg/ml) for the indicated times in the absence (lanes 1-5) or presence (lanes 6-9) of Dox pretreatment (1 µg/ml, 24h) were subjected to an EMSA using the $\kappa B1$ probe. Control lanes C (lane 5 in A and B) represent the competition of NF- κ B-DNA complex formation using a 125fold excess of unlabeled $\kappa B1$ probe.



Figure 21. TD-I κ B α is tightly bound to RelA(p65). rtTA-Neo (lanes 1-8) and rtTA-I κ B α (2N Δ 4) (lanes 9-17) Jurkat cells were treated with TNF α (10 ng/ml) (A) or PMA (50 ng/ml) / PHA (1 μ g/ml) (B) for various times in the absence (lanes 1-4, 9-13) or presence (lanes 5-8, 14-17) of doxycycline (1 μ g/ml) for 24h. Cell lysates were immunoprecipitated with p65 specific antibody and immunoblot analysis was performed using the anti-I κ B α and anti-p65 antibodies. Arrows indicate p65, I κ B α and I κ B α (2N Δ 4) from top to bottom. Control lane P (lane 9) represents an immunoprecipitation with rabbit preimmune sera. (C) rtTA-I κ B α (2N Δ 4) Jurkat cells were treated with PMA (50ng/ml) / PHA (1 μ g/ml) for various times in the absence (lanes 1-5) or presence (lanes 6-9) of Dox (1 μ g/ml. 24h). Cell lysates were immunoprecipitated with I κ B α and I κ B α (2N Δ 4) from top to bottom. Control lane P (lane 1) represents an anti-I κ B α antibodies. Arrows indicate p65, I κ B α antibodies.

IP Ab : p65

TNFα

rtTA-Neo Jurkat										_	<u> </u>	t <u>TA</u>	<u>-2N</u>	<u>I∆4 Jurkat</u>					
	-Dox			+Dox							-]	Dox		+Dox					
0	10	30	60	0	10	30	60		P	0	10	30	60	0	10	30	60		
-	-		-	_				← p65 →					-	-			-		
-		-		-	, .,,	-	•	$ = i\kappa B\alpha - $									-		
1	2	3	4	5	6	7	8	ΙκΒα	9	10	11	12	13	14	15	16	17		

B

С

IP Ab : p65

PMA

<u>rtTA-Neo Jurkat</u>											r	tTA	-2N	<u>ΙΔ4</u>	Ju	<u>rka</u>	<u>t</u>	
	-Dox			+Dox							-	Dox		+Dox				
0	10	30	60	0	10	30	60		P	0	10	30	60	0	10	30	60	
-					-			← p65 →		-		-				~~~		
-			-	-	-		-	 IκBα → 2N∆4 → 				_		-	-		-	
1	2	3	4	5	6	7	8	ΙκΒα	9	10	11	12	13	14	15	16	17	

 $IP Ab : I \kappa B\alpha$ PMA $rtTA-2N\Delta 4 Jurkat$ -Dox +Dox P 0 10 30 60 0 10 30 60 -p65 $-I \kappa B\alpha$ I 2 3 4 5 6 7 8 9

A

lanes 11-13). In contrast, in TD-I κ B α expressing Jurkat cells, immunoprecipitation with anti-p65 antibody resulted in the co-immunoprecipitation of predominantly I κ B α (2NA4) (Figure 21AB, lanes 14-17), indicating that the degradation-resistant TD-I κ B α was tightly associated with p65 throughout induction. The reciprocal immunoprecipitation with anti-I κ B α antibody was also performed (Figure 21C). Both endogenous and TD-I κ B α were immunoprecipitated from rtTA-I κ B α (2NA4) expressing cells in the absence of Dox addition together with p65 (Figure 21C, lanes 2-5), whereas following Dox treatment, only TD-I κ B α and associated p65 were identified (Figure 21C, lanes 7-9). Therefore, inhibition of NF- κ B DNA binding activity and endogenous I κ B α transcription in TD-I κ B α inducible cells is due to the tight association between the NF- κ B transactivator p65 and TD-I κ B α which is resistant to inducer-mediated degradation.

In vivo genomic footprinting of the $I\kappa B\alpha$ promoter. In order to analyze the inducibility of $I\kappa B\alpha$ gene transcription, genomic footprinting analysis was performed in Jurkat and $I\kappa B\alpha$ (2NA4) expressing Jurkat cells. Following stimulation by either TNF α or PMA/PHA, living cells were submitted to DMS (dimethyl sulfate) treatment which methylates G residues and to a lesser extent A residues; genomic DNA was then extracted and submitted to piperidine treatment to cleave methylated residues. Then, piperidinecleaved DNA was amplified by ligation-mediated PCR using specific primers for $I\kappa B\alpha$ promoter as detailed in Figure 22C. A G specific sequence ladder was also generated as reference and analyzed by sequencing.

Footprinting primers were initially designed to analyze *in vivo* protein-DNA interactions occurring in the proximal -10 to -170 region of the I κ B α promoter (primers 1, 2, 3 for the non-coding strand, and 1B, 2B, 3B for the coding strand, Figure 22C). In resting Jurkat T cells, the proximal G residues of the κ B1 site at -53 to -56 were cleaved and easily detected by comparison with the G ladder revealing no induction in the absence of

Figure 22. In vivo footprinting of the proximal IxB α gene promoter in Jurkat T cells. (A) Non-coding strand and (B) coding strand analysis. Naked DNA was treated *in vitro* by DMS (lane 1). Cells were either non-stimulated (lane 2), treated by PMA/PHA (lane 3) or by TNF α (Lane 4) for 40 min and then were treated with DMS. Genomic DNA was extracted and treated with piperidine. All DNA samples were amplified by LM-PCR and visualized on Long-RangerTM sequencing gel. (C) Sequence of the IxB α promoter. Major consensus sites for protein binding such as the NF- κ B sites and sites of Ets-1, Sp1 and AP2 are enclosed in boxes. The mRNA start site and TATA box are also shown. Arrows correspond to primers used in genomic footprinting. Primers 1, 2, and 3 were designed to characterize the non-coding strand and primers 1B, 2B, and 3B for the coding strand.





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АОЗАСТИТСЕ АОССАСТСОВ СОСТСАТСАА АЛАОТТСССТ ОТССОТОАСС СТАЛОВОСТС АТСОСАВОВА ОТПСТЕСОВ ТОЛАССССАВ СТСЛОООТИТ ТССТОЛАЛОВ ТСООТБАОСС ОСОЛОТАЮТТ ТТЕСЛАООЗА СЛОВСАСТОВ ВАТСАССАЛА ТААСОТЕСТ САЛАВЛОСТ АСТНОВОТС ВАОТСССАЛА KB like -150 -159 -225 KB3 -216 9 0 אספרדוכדדד דרככככדאה כיפאספרמא אסככאפדריד כידידיזכדסה דכיפאכדסה דוספאאאדדכ כיכלאסככדה אלככיסככיכ INGB & _

(D)

.28

KB like AP2

. 16 Spl

-53

-44

CC -

-103 .96 -63 Ets-1 **kB**l •

СС ОССАВСЯ ТТТАТАРОСС ОСООСООСТО САМАВСССАС АВСАОТССОТ ОССОССОТСС ОО СООТСОС АЛАТАРССОС СОССОССАХ ОТСТСОООТС ТСОТСАВОСА СООСООСЛОВ -25 -23 TATA box

+1

С

-125
stimulation (Figure 22A, lanes 1 and 2). In the absence of stimulation, an interaction was detected at the Sp1 site located between -44 to -36 bp, adjacent to the κ B1 site (Figure 22A, lanes 1 and 2). In response to PMA/PHA or TNF α induction for 40 min, the κ B1 site was strongly protected by protein-DNA interactions, resulting in very limited cleavage of the -54G, -55G and -56G residues and a hypersensitive cleavage at the -53G residue (Figure 22A, lanes 3 and 4). Similarly, modifications of the pattern of the Sp1 site were observed; with naked DNA or DNA from unstimulated cells, cleavage of -44G, -43G, -42G and -41G was detected as well as -39G, -37G, -36G (Figure 22A, lanes 1 and 2), while following induction, the G residues of the Sp1 site were protected with the exception of the -42G residue which was hypersensitive to cleavage (Figure 22A, lanes 3 and 4).

Changes in the coding strand methylation pattern of the κ B1 site were also detected using specific primers, although PCR amplification was difficult to obtain because of the GC rich nature of the region, allowing only the detection of κ B1 and Ets but not Sp1 sites (see Figure 22C). The two G residues of the κ B1 site located at -63 and -62 were methylated on naked DNA (Figure 22B, lane 1 and 2). Following stimulation of Jurkat T cells with PMA/PHA or TNF α , only the -63G residue was methylated and cleaved, whereas the -62G residue was protected from methylation (Figure 22B, lanes 3 and 4), thus demonstrating protection of the κ B1 site on both coding and non-coding strands. Two other potential binding sites in the -10 to -110 region - AP2 and Ets-1 - were identified *in vivo* (Figure 22 AB): hypermethylation of the -24G and -25G residues was observed at the AP2 site in both unstimulated and stimulated cells (Figure 22A, compare lane 1 to lanes 2-4). Similarly, methylation of the -99A residue at the Ets-1 site appeared slightly enhanced in resting and stimulated cells (data not shown); for both sites induction specific changes in promoter occupancy were not detected.

Scanning analysis of the methylation pattern of the [-20 to -70] IxBa promoter region. Since the modifications at the Sp1 site were more discrete than those detected at the $\kappa B1$ site, changes in the methylation pattern of the [-20 to -70] region of $I\kappa B\alpha$ promoter which includes the AP2, Sp1 and κ B1 sites were analyzed by densitometry scanning (Figure 23). A representative autoradiography is presented in Figure 23A. Comparison of non-stimulated and naked DNA patterns revealed increased methylation of the -42G residue and a slight decrease in -41G methylation at the Sp1 site whereas no significant differences in methylation were observed for the bordering -20G and -66G residues, indicating an even methylation pattern in the scanned region (Figure 23B). These data indicate that the Sp1 site was constitutively occupied in resting Jurkat T-cells. Similarly, hypermethylation of -24 and -25G residues in non-stimulated Jurkat cells suggests a constitutive binding at the AP2 site. In contrast, no binding was detected on the $\kappa B1$ site in unstimulated conditions. Following stimulation by either TNF α , as shown in Figure 23C, or PMA/PHA (data not shown), protection of the Sp1 site was modified as observed by a strong decrease in methylation at residues -36, -37, -39, -41, -43 and -44 G; only the -42G residue remained methylated. As clearly seen in Figure 2A, inducible binding at the kB1 site is characterized by decreased methylation of the -54, -55 and -56 G residues as well as a very strong increase in -53G methylation, detected as a broad peak by densitometric scanning (Figure 23C). Interestingly, methylation of -48 and -49G residues which are located between Sp1 and kB1 sites was also significantly decreased after stimulation, indicating that the inducible changes at the kB1 and Sp1 sites affect the whole region delimited by these two sites (Figure 23C). In contrast, no significant modifications of -66G and -21G residues were observed after stimulation, thus restricting the inducible region to the Sp1 and κ B1 sites.

Together, these results demonstrate the *in vivo* occupancy of the -63 to -53 kB1 site of the IkB α promoter after stimulation with either PMA/PHA or TNF α and also indicate that the

Figure 23. Scanning analyses of *In vivo* footprinting of the proximal $I \times B \alpha$ gene promoter in Jurkat T cells. Methylation patterns observed on the [-20 to -70] region of non-coding strand of $I \times B \alpha$ promoter with naked DNA, or from non-stimulated or TNF α stimulated cells for 4 h, presented in (A) were analysed by densitometry scanning using Scan Jet 4c Hewlett Packard scanner and NIH Image 1.60 software. Comparison of profiles obtained with naked DNA versus DNA from resting Jurkat T cells (B) or with DNA from resting cells versus TNF α stimulated cells (C) correspond to profiles obtained in at least three independent experiments. Open arrows represent constitutive modifications whereas filled arrows correspond to inducible changes. Arrows pointing up or down represent increased or decreased methylation on G residues. The sequence of the scanned region, where the methylated G residues are in capital letters, is indicated below each graph.



Sp1 site located 10 bp downstream from the κ B1 site may play a role in the inducible transcription of the I κ B α promoter.

Footprinting analysis of the $I\kappa B\alpha$ **upstream promoter**. The potential role of other upstream NF- κ B sites that may play a role in $I\kappa B\alpha$ inducibility (185, 228), including κ B2 and κ B3 sites - was also evaluated. No significant modification of the patterns was observed in the region corresponding to the κ B2 site at -319 to -310 or in the putative κ B site at -34 to -24, located downstream of κ B1. However, the A residue at position -222 in the κ B3 site appeared methylated in unstimulated cells as well as in TNF α induced cells, suggesting constitutive protein binding to this site (data not shown). These data indicate that although other κ B sites in the $I\kappa B\alpha$ promoter are recognized *in vitro* by NF- κ B complexes (185, 228) and *in vivo* by constitutive binding complexes, they are not modified *in vivo* after stimulation of Jurkat T-cells. Only the κ B1 site appears to be targeted by inducible NF- κ B binding proteins as detected by *in vivo* genomic footprinting (Figure 22).

NF- κ B protection of the κ B1 site is blocked in TD-I κ B α expressing cells. Next, control Jurkat (Neo) and TD-I κ B α (2N Δ 4) expressing cells were treated with TNF α or PMA/PHA for 40 min, following 24h of Dox induction (Figure 24) and then subjected to genomic footprint analysis using non-coding specific primers 1, 2 and 3. In control cells, the 4G ladder was easily identified (Figure 24, lanes 1-3), and following TNF α or PMA/PHA addition, the characteristic hypersensitive cleavage of -53G was detected (Figure 24, lanes 4-7). In I κ B α (2N Δ 4) expressing cells, TD-I κ B α induction resulted in complete inhibition of inducible binding complexes to the κ B1 site in a Dox-dependent manner; TNF α or PMA/PHA stimulation in the absence of Dox-induced TD-I κ B α resulted in a footprint at the κ B1 site that was indistinguishable from that of stimulated Jurkat cells (Figure 24, lanes 4-7,10,12, and 14), whereas in the presence of Dox-induced TD-I κ B α Figure 24. In vivo footprint of the IxB α gene promoter in rtTA-Neo and Tetinducible TD-IxB α expressing cells. Non-coding strand analysis was performed with rtTA-Neo (lanes 2 to 7) or rtTA-IxB α (2N Δ 4) Jurkat cells (lanes 8 to 14), either unstimulated (lanes 2, 3, 8, 9 and 14), stimulated by TNF α (10 ng/ml, lanes 4, 5, 9 and 10) or stimulated by PMA/PHA (respectively 50 ng/ml and 1 µg/ml, lanes 6, 7, 12 and 13) for 40 min. Naked DNA was methylated *in vitro* (lanes 1). Where indicated (+), cells were pretreated by doxycycline (1 µg/ml, 24h).



the observed footprint pattern resembled unstimulated control Jurkat cells (Figure 24, lanes 2, 3, 8, 9, 11 and 13). Although less clearly resolved, the pattern of methylation and cleavage of the adjacent Sp1 site was also sensitive to Dox induction. For example, in TD-I κ B α inducible cells, PMA/PHA treatment resulted in protection of the Sp1 site with the exception of -42G (Figure 24, lane 12), whereas Dox-induction resulted in protection of the Sp1 site, characteristic of unstimulated control Jurkat cells (Figure 24, lane 13, compare with lanes 2, 3 and 8). These results further indicate that binding of complexes to the Sp1 site may be coordinately regulated by the adjacent κ B1 site in a TD-I κ B α inducible manner.

Prolonged NF-κB binding and temporal switch in the composition of NF-κB complexes at κB1 site. To determine the kinetics of the *in vivo* occupancy of **κB1** and Sp1 sites of $I\kappa B\alpha$ promoter, control Neo (Figure 25A) and TD-IκBα expressing cells (Figure 25B) were analyzed at different times after stimulation by TNFα or PMA/PHA. Surprisingly, the same protection of the **κB1** site was observed from 10 min to 24h following TNFα or PMA/PHA treatment in both cell types (Figure 25A, lanes 4-15, Figure 25B lanes 4, 6, 8, 10, 12 and 14). In TD-IκBα expressing cells pretreated with Dox, the pattern of methylation and cleavage of the **κB1** site remained characteristic of unstimulated cells (Figure 25B, lanes 5, 7, 9, 11, 13 and 15), regardless of the time of TNFα or PMA/PHA stimulation. Prolonged protection of the adjacent Sp1 site was also observed from 10 min to 24h in stimulated control or TD-IκBα expressing cells (Figure 25A, lanes 4, 5, 7, 10, 12, 14, 15, Figure 25B, lanes 4, 8, 12). Again, Dox induction of TD-IκBα expression resulted in a methylation pattern at the Sp1 site that was characteristic of unstimulated cells (Figure 25B, lanes 5, 7, 9, 13).

To identify the subunit composition of the NF- κ B complexes during I κ B α induction, EMSA supershift analysis of extracts from rtTA-Neo Jurkat cells treated with PMA/PHA Figure 25. Kinetics of protein-DNA interactions on the proximal I κ B α promoter. Non-coding strand analysis of (A) rtTA-Neo Jurkat T cells and (B) rtTA-I κ B α (2NA4) Jurkat T cells. For both panels, naked DNA was methylated *in vitro* (lane 1). Cells were either unstimulated (lanes 2 and 3), stimulated by TNF α (10 ng/ml, lanes 4 to 9) or by PMA/PHA (respectively 50 ng/ml and 1 µg/ml, lanes 10 to 15). The time of cell harvesting following TNF α or PMA/PHA stimulation is indicated above the lanes. Where indicated (+), cells were pretreated by doxycycline (1 µg/ml, 24h).





for 10 min, 4h and 24h was performed using [-66 to -51] κ B1 probe and anti-p65, -p50 and -c-Rel antibodies. All PMA/PHA-induced complexes were shifted with anti-p50 antibodies regardless of the time of stimulation (Figure 26, lanes 5-7). Interestingly, at early times of induction - 10 min and 4h - , majority of the NF- κ B complex detected contained p65 subunit (Figure 26, lanes 8-10), whereas at later times - 24h - c-Rel constituted the main partner of p50 subunit (Figure 26, lanes 11-13). Thus, induction of I κ B α gene transcription appears to require the p50-p65 NF- κ B heterodimer during activation, while downregulation may be due in part to p50-c-Rel heterodimer binding to κ B1 site. This temporal switch in NF- κ B complexes composition is likely to be responsible for the prolonged protection of the κ B1 site observed by *in vivo* genomic footprinting.

p65 and Sp1 bind together to the κ B1/Sp1 site of $l\kappa$ B α promoter. To assess Sp1 binding to the NF- κ B/Sp1 region, EMSA analysis was performed using probes encompassing the [-44 to -36] Sp1 site, the [-63 to -36] κ B1 site or both κ B1 and Sp1 sites (κ B1/Sp1 probe from the [-65 to -34] region of the $l\kappa$ B α promoter). PMA treatment of Jurkat cells resulted in a 10-fold increase in the intensity of the Sp1-binding complex (Figure 27A, upper panel, lanes 1 and 2); complex formation was blocked in competition reactions by both Sp1 and κ B1/Sp1 binding sites (Figure 27A, upper panel, lanes 3 and 7), but not by the κ B1 site alone (Figure 27A, lane 6). This complex was further identified as an Sp1 binding activity by its competition in the presence of the consensus Sp1 sequence, whereas only partial inhibition was observed when a mutated Sp1 sequence was used as competitor (Figure 27A, upper panel, lanes 4 and 5). As control, no inhibition of NF- κ B binding to κ B1 was detected in the presence of the Sp1 site of the I κ B α promoter, consensus Sp1 or mutated Sp1 sequences (Figure 27A, middle panel, lanes 2-5). Identification of the complexes detected by κ B1/Sp1 probe was further determined by supershift analysis (Figure 27B). As expected, anti-p50 and anti-p65 Figure 26. Switch in the composition of NF- κ B complexes bound to κ B1 site of the I κ B α promoter. Supershift analysis was performed with nuclear extracts from rtTA-Neo Jurkat cells treated with PMA/PHA for different times indicated above each lane, using anti-p65 (lanes 5-7), anti-p50 (lanes 8-10) and anti-c-Rel (lanes 11-13) antibodies with an κ B1 probe ³²P- γ ATP labeled. Arrows indicate the positions of complexes corresponding to p50/p65 and p50/c-Rel heterodimers, respectively.



Figure 27. NF-κB and Sp1 bind to the -63 to -36 region of the IκBα promoter. (A) EMSA analysis was performed with different radiolabeled oligonucleotide probes: Sp1 (upper panel), κB1 (middle panel) and κB1/Sp1 (lower panel). Nuclear extracts prepared from Jurkat cells were either unstimulated (lane 1) or treated with PMA (50 ng/ml) for 2h (lanes 2 to 7). Competition was performed in the presence of a 125-fold excess of unlabeled oligunucleotide: Sp1 site of IκBα promoter (lane 3), Sp1 consensus (cons. Sp1, lane 4), mutant Sp1 (mut. Sp1, lane 5), κB1 (lane 6) and κB1/Sp1 (lane 7). To facilitate detection of simultaneous binding of NF-κB and Sp1, EMSA buffer conditions were modified as described in the Materials and Methods and the amount of extract used in the binding reactions was varied between 150ng and 3μg; the binding reactions shown in this figure used 150ng of Jurkat nuclear extract and 500ng of poly dI:dC. (B) Complex composition was analyzed by supershift analysis. PMA-induced nuclear extracts were incubated with anti-p65 (lane 3), anti-p50 (lane 4) and anti-Sp1 (lane 5) antibodies.



Antibodies	•	•	p65	p5 0	Sp1
Competition	-	+	-	•	-
				_	
				* #	· .



antibodies abolished p65/p50 binding to κ B1/Sp1 probe, whereas anti-Sp1 antibodies reacted against Sp1-containing complex (Figure 27B, lanes 3, 4 and 5). The faster migrating band observed with κ B1/Sp1 probe (Figure 27A, lanes 1, 2, 5 and 6) is likely to be a degradation product of Sp1-containing complex generated during nuclear protein extraction; this band is competed by Sp1-related oligonucleotides (Figure 27A, lanes 3, 4 and 7) but is not affected by anti-Sp1 antibodies (Figure 27B, lane 5). This EMSA analysis failed to reveal a complex formed by both endogenous Sp1 and NF- κ B bound to the κ B1/Sp1 probe.

To determine whether Sp1 and p65/p50 bind to their recognition sites (kB1/Sp1) cooperatively in the $I\kappa B\alpha$ promoter, an EMSA was performed with different amounts of recombinant p65/p50 or Sp1 using the kB1/Sp1 probe from the [-65 to -34] region of the IkB α promoter. In the absence of Sp1, p65 and p50 bound to the kB1/Sp1 probe in a dose-dependent manner (Figure 28A, lanes 2, 3, 5-7). In the presence of the same amount of Sp1, no cooperative binding was observed between Sp1 and p65-p50 with increasing amounts of p65-p50 (Figure 28A, lanes 8, 9 and 10). However, at high concentration of p65/p50, an additional complex of slower mobility was observed that also appeared with increasing concentrations of Sp1 when a fixed amount of p65 and p50 was used (Figure 28A, 11-13). This complex was composed of p65 and Sp1 since incubation with specific antibodies eliminated complex formation (Figure 28B). Similarly, anti-p50 antibody removed the p50 containing complexes (Figure 28B, lane 3) while anti-p65 antibody shifted the complexes containing p65 (Figure 28B, lane 2). Anti-Sp1 antibody also disrupted complex formation by removing either Sp1 binding alone or Sp1/p65 heterodimers (Figure 28B, lane 4). Therefore, while Sp1 and p65/p50 do not bind cooperatively to the $\kappa B1/Sp1$ site, both Sp1 and p65 bind together to the $\kappa B1/Sp1$ sites of $I\kappa B\alpha$ promoter. The discrepancy between EMSA performed with Jurkat nuclear extracts and recombinant proteins regarding the formation of NF-kB/Sp1 complex could **Figure 28.** NF- κ B and Sp1 can co-occupy κ B1/Sp1 site of I κ B α promoter. (A) EMSA was performed with recombinant p65 (GST-Np65), p50 (GST-p50) and Sp1 (rhSp1) proteins using radiolabeled κ B1/Sp1 site ³²P- γ ATP labeled. Each recombinant p65 (2 ng), p50 (2.73 ng) and Sp1 (3ng) were used alone in lanes 2-4. Increasing amounts of p65 (0.5, 1 and 2 ng) combined with increasing amounts of p50 (0.65, 1.3 and 2.73 ng) were incubated in the absence (lanes 5-7) or in the presence (lanes 8-10) of Sp1 (3 ng). Increasing amounts of Sp1 (1. 3 and 5 ng) were also tested with the same amount of p65 (1 ng) and p50 (1.3 ng) in lanes 11-13. Shifted complexes are indicated by arrows. (B) Combinations of recombinant p65 (2 ng), p50 (2.73 ng) and Sp1 (3 ng) proteins were incubated with radiolabeled κ B1/Sp1 oligonucleotides in the presence or absence of specific antibodies for p65, p50 and Sp1 proteins. The composition of the complexes was analyzed by supershift analysis using anti-p65, anti-p50 or anti-Sp1 antibodies (lanes 2-4).



B

anti-p65	-	+	-	•
anti-p50	-	-	+	-
anti-Spl	-	-	-	+
Np65		-	+	
p50		-	+	
Spl			+	
		÷.		
		i.		



be due to limiting amount of one of the component in nuclear extract, thus excluding detection of this complex. This hypothesis is consistent with the weakness of the Sp1/p65 complex detected in the presence of high amount of recombinant proteins, compared to the p50- and/or p65-containing complexes (Figure 27A, lane 13).

IkBa gene expression is dependent on both NF-kB and Sp1 binding. The functional role of the NF- κ B and Sp1 sites in I κ B α gene transcription was next examined in Jurkat cells by transient co-transfection with luciferase reporter constructs driven by the wild type $I\kappa B\alpha$ promoter (0.4SK) (228) or mutated versions of the $I\kappa B\alpha$ promoter (Figure 29). Treatment of transfected Jurkat cells with TNFa or PMA/PHA resulted in a 4- and 10fold stimulation of gene activity, respectively. Deletion or point mutation of the $\kappa B1$ site of the IkBa promoter (ΔkB and mutkB1) abrogated TNFa and PMA/PHA induced gene activation relative to the wild type promoter (Figure 29A). Strikingly, point mutation of the Sp1 site (mutSp1) also dramatically decreased induction of IkBa gene expression and also slightly decreased basal level promoter activity. As expected, mutation of both kB1 and Sp1 sites also completely inhibited gene activity. As shown in Figure 29B, EMSA analysis demonstrated that impairment of transactivation was due to lack of NF- κ B binding (Figure 29B, lanes 4-6) or Sp1 binding (Figure 29B, lanes 7-9) to kB1/Sp1 sites. From these results, both $\kappa B1$ and Sp1 sites are required for full induction of $I\kappa B\alpha$ promoter. To further analyze whether activation requires direct contact between NF-kB and Sp1, mutant luciferase reporter plasmids containing deletions or insertions between κ B1 and Sp1 sites were tested (Figure 29C). Interestingly, the introduction of 5 nucleotides or 9 nucleotides between the $\kappa B1$ and Sp1 sites which alters the helical relationship between the two sites decreased but did not eliminate $I\kappa B\alpha$ inducibility (Figure 29C). When eight nucleotides ($\Delta 8$) between $\kappa B1$ and Sp1 sites were deleted, transcriptional inducibility was nearly completely abolished. Together, these results indicate that both $\kappa B1$ and Sp1 sites are required for full induction of $I\kappa B\alpha$ promoter.

Figure 29. Both xB and Sp1 are required for full TNFa or PMA induced IxBa promoter activity. (A) Jurkat cells were transfected with 1 μ g of luciferase reporter plasmid containing wild type (0.4SK), mutant kB1 ($\Delta \kappa B$, mutkB1), mutant Sp1 (mutSp1) or mutant kB1/Sp1 (mutkB1/Sp1) IkBa promoter. Twenty four hours after transfection, cells were treated with TNFa (10 ng/ml) or PMA (50 ng/ml) or left untreated for an additional 16h. Transfection efficiency was normalized by Renila luciferase (See Materials and Methods). The experiments were performed in triplicate and the average fold induction was calculated. (B) EMSA analysis was performed with different radiolabeled oligonucleotide probes : $\kappa B1/Sp1$, mutated $\kappa B1/Sp1$ (mut $\kappa B1$) and kB1/mutated Sp1 (mutSp1) using uninduced or PMA-induced Jurkat nuclear extract (50 ng/ml PMA for 2h). (C) Luciferase assays were performed as shown in (A) using 1µg of reporter plasmids containing eight nucleotide deletion ($\Delta 8$), five nucleotide addition (+5) and nine nucleotide addition (+9) between $\kappa B1$ and Sp1 sites of $I\kappa B\alpha$ promoter. Transfection efficiency was normalized by Renila luciferase (See Materials and Methods). The experiments were performed in triplicate and the average fold induction was calculated.









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CHAPTER VI

GENERAL DISCUSSION

CONTROL OF NF-κB REGULATED GENE EXPRESSION AND HIV-1 REPLICATION BY MUTANTS OF Ικ**B**α

1.0 SUMMARY OF RESULTS

NF- κ B plays an important role in stimulation of HIV-1 transcription after T-cell activation, and the HIV-1 LTR is the target of several signal transduction pathways involving both cellular and HIV-1 Tat protein. NF- κ B binding sites in HIV-1 LTR have been shown to be indispensable for LTR-driven gene expression in the absence or presence of the HIV-1 Tat protein (160, 165, 258, 293, 411).. Therefore, activators of NF- κ B such as TNF α and PMA, have been shown to induce HIV-1 LTR-mediated gene expression and viral replication (1, 160, 336-338). Synergistic activation of HIV-1 LTR-driven gene expression was observed by the concerted action of NF- κ B and Tat (42, 43, 258, 446). Therefore, antagonistic effects on these two regulatory factors would adversely affect the level of HIV-1 LTR-mediated activation of viral genes and of viral replication.

1.1 Inhibition of HIV-1 Gene Expression and Virus Multiplication by Transdominant Mutants of $I \ltimes B \alpha$

Different forms of $I\kappa B\alpha$ mutated in distinct regulatory phosphorylation sites, were examined for the effects on the Tat-TNF α synergistic activation of the HIV-1 LTR in Jurkat cells. Transactivation of the HIV-1 LTR was dependent upon both functional Tat-TAR interaction and the presence of NF- κ B binding sites in the -100 enhancer region of the HIV-1 LTR. Co-expression of wt I κ B α or mutants of I κ B α inhibited Tat-TNF α synergism in a dose dependent manner. Interestingly, the transdominant mutants I κ B α (2N) or I κ B α (2N+3C) were at least five times more effective than wt I κ B α in inhibiting HIV-1 LTR directed gene expression. Moreover, I κ B α (2N) but surprisingly not I κ B α (2N+3C) was more effective in blocking HIV-1 protein and RNA synthesis in a single cycle infection model than wt I κ B α or I κ B α (3C). The observation that mutations in the C-terminal PEST domain of I κ B α decreased the inhibitory potential of I κ B α (2N) is surprising and indicates that an intact C-terminus is required for maximal inhibition of HIV-1 multiplication by $I\kappa B\alpha(2N)$. This effect of the C-terminal domain was not apparent in assays measuring inhibition of LTR transactivation and may thus reflect a distinct functional activity for the I $\kappa B\alpha$ C-terminus.

To further characterize the impact of TD-IkB α on the course of *de novo* HIV-1 infection, Jurkat T cell clones were engineered to inducibly express two transdominant repressor forms of $I\kappa B\alpha$ under the control of a Tet-responsive promoter and first, the effects of inducible expression of TD-I κ B α on NF- κ B activation were tested. Dox inducible expression of $I\kappa B\alpha$ -2N and $I\kappa B\alpha$ -2N $\Delta 4$ was detected as early as 1h after Dox addition and blocked the induction of NF- κ B DNA binding by multiple inducers including TNF α , PMA/PHA and dsRNA; expression of TD- $l\kappa B\alpha$ also repressed the expression of the endogenous $I\kappa B\alpha$ gene, consistent with the observation that the $I\kappa B\alpha$ gene contains multiple NF- κ B binding sites in its promoter and is tightly regulated by NF- κ B (228); NF- κB dependent reporter gene activity was also inhibited following the induction of TD-IkBa. Finally, induced expression of the TD-IkBa successfully inhibited de novo HIV-1 infection in Jurkat cells as measured by RT assay, p24 antigen accumulation and viral RNA analysis by RT-PCR. During these studies, the levels of CD4 and fusin were also measured by flow cytometry to determine if TD-1 κ Ba expression repressed cell surface expression of the HIV-1 co-receptors (113); no modulation of either CD4 or fusin levels was observed after 48-96h of Dox-induced TD-I κ Ba expression (data not shown). Thus, HIV-1 infection was not inhibited at the level of virus attachment and entry.

Our results are complementary to a number of recent experiments which have addressed the role of NF- κ B transcription factors in HIV-1 regulated gene expression (42, 43, 258, 446). Westendorp *et al.* demonstrated that HIV-1 Tat protein amplified the activity of TNF α with regard to TNF α -induced activation of NF- κ B and TNF α mediated cytotoxicity via the formation of reactive oxygen intermediates (446). Tat suppressed the expression of Mn-dependent superoxide dismutase (Mn-SOD) which normally functions as part of the cellular response to oxidative stress, thus shifting the cellular redox state towards prooxidative conditions. Under these conditions, higher levels of NF- κ B binding activity that contribute to stimulation of HIV-1 LTR directed gene expression were observed (data not shown). Under conditions of maximal Tat-TNF α synergism, I κ B α was nonetheless able to interfere with NF- κ B induction, by sequestering NF- κ B in the cytoplasm in a concentration dependent manner (data not shown). I κ B α molecules mutated in the N-terminal signal response phosphorylation sites S32 and/or S36 did not undergo rapid inducer mediated degradation (Figure 9) and were at least five times more effective in blocking LTR-directed gene expression. Our experiments furthermore extend a recent study demonstrating that I κ B molecules inhibited Tat-mediated transactivation of the HIV-LTR (155).

Biswas *et al.* showed that Tat protein provided a low level of activation of the viral LTR, even in absence of a functional TAR element (42, 43), thus confirming the earlier described TAR-independent mode of Tat action (1, 17, 411). The TAR-independent mode of Tat action was proposed to occur through the transcriptional activation of TNF α which would in turn stimulate NF- κ B binding activity (43, 446). These observations are reminiscent of a study demonstrating that interleukin-2 (IL-2) secretion was upregulated at the transcriptional level by the addition of extracellular Tat to activated T cells. The response element in the IL-2 promoter also mapped to the NF- κ B site at positions -206 to -195 (447). As was observed in our study, Biswas *et al* found that mutations in the NF- κ B motifs decreased Tat activation dramatically, indicating that maximal stimulation of the LTR directed gene expression required Tat-TNF α cooperation (43).

A systematic comparison of HIV-1 LTR activity in human CD4+ primary T cells and a transformed lymphoblastoid cell line J-Jhan demonstrated strikingly different requirements for maximal LTR activation (1). In unstimulated CD4 T lymphocytes, a low basal level of LTR activity was detected, whereas in the lymphoblastoid cell line a high spontaneous level of LTR activity was found that was essentially independent of the NF- κ B responsive elements. In contrast, in primary lymphocytes there was an absolute dependence upon the NF- κ B sites for initiation and Tat-mediated amplification of HIV-1 transcription. These results are in keeping with differences in the permissiveness to HIV replication of primary versus established cell types. In lymphoblastoid cell lines, HIV infection resulted in active replication in the absence of other stimuli, whereas in primary T cells, replication (1). In our study we also found that HIV LTR-directed gene activity required both Tat-TAR transactivation and NF- κ B induction, indicating that our Jurkat cell model may reflect more closely the quiescent state of primary T cells, rather than the activated state of other lymphoblastoid cell lines.

NF- κ B sites in the HIV-1 LTR were recently demonstrated to be important in enhancing the growth of primary HIV-1 isolates; nonetheless, the virus was still able to grow slowly in the absence of NF- κ B sites (70). Similarly, in our study, conditional inhibition of NF- κ B in Jurkat T cells by an I κ B α repressor significantly interfered with virus multiplication, but could not suppress HIV-1 growth indefinitely. Although the above studies suggest a transcriptional role for I κ B α in the inhibition of HIV-1 LTR gene expression, I κ B α may act at a distinct level in the HIV-1 life cycle - at the posttranscriptional level of Rev function (452, 453). HIV Rev contains an RNA binding domain, required for interaction with Rev response element (RRE) present in HIV-1 RNA, and an effector domain required for RNA-bound Rev to function in export. The Rev effector domain contains a nuclear export signal (NES) and interacts with the recently identified nuclear NES receptor, CRM1 (119, 127, 315, 405). I κ B α also contains two putative NES elements at the N- and C-terminus, which are from amino acid 45 to 55 and from 265 to 277 respectively, matching the NES consensus within Rev which could be functionally replaced with the I κ B α -derived NES (9, 124, 193). Furthermore, newly synthesized I κ B α can localize to the nucleus, dissociate NF- κ B-DNA complexes and translocate back to the cytoplasm (8, 9, 193, 466). Thus, an additional function of I κ B α is to serve as a shuttle protein to export NF- κ B from the nucleus. Nuclear export of I κ B α has been shown to be mediated by CRM1 (193, 352). One possible explanation for the inhibitory activity of TD-I κ B α in HIV-1 infection is that the stable form of I κ B α competes effectively with HIV Rev for the nuclear export pathway utilized by CRM1.

HIV-1 infection also causes constitutive activation of NF-κB DNA-binding activity in infected cells (365). A direct temporal correlation exists between HIV infection and the appearance of NF-κB DNA-binding activity in myeloid cells (12, 96, 275, 325, 363, 364), which may in turn prime or stimulate cytokine release (113). Cytokine release from HIV-1 infected cells may contribute to the elevated levels of TNFα, IL-1, IL-6, TGFβ and IFNγ, present in the sera of AIDS patients in late stage disease. In addition, elevated IFNα/β activity is also present in the sera of AIDS patients in late stage disease and serves as a marker for poor prognosis (365). Preliminary data shows that TD-IκBα also interferes with TNFα- and PMA-induced inflammatory cytokines (data not shown), therefore suggesting the possibility of inhibitory effects of TD-IκBα on HIV-1 infection at the level of expression of HIV-1-induced inflammatory cytokines.

Recently, NF- κ B activation was shown to play a protective function in the response to TNF α -, ionizing irradiation- and daunorubicin-induced apoptosis (28, 222, 423, 433). Since apoptosis has been suggested to be one of the major mechanisms of CD4+ T cell depletion in HIV-1 infected patients (6, 18, 217, 413) and TNF α plasma levels correlate with disease

progression (365), the role of NF- κ B in HIV-1 induced apoptosis was examined in HIV-1 infected myeloid cells and was also shown to protect HIV-1 infected myeloid cells from apoptosis (94). These studies demonstrated that constitutive NF- κ B activation is required to counteract a persistent apoptotic signal resulting from HIV-1 infection; thus, a previously unrecognized role for constitutive NF- κ B activation in HIV-1 infected cells is to protect from virus-mediated apoptotic cell death. Similarly, activation of TD-I κ B α sensitized Jurkat cells to TNF α -induced cell death (Table 2). However, HIV-1 induced apoptosis was not enhanced by TD-I κ B α in Jurkat T cells (data not shown) and, recently, Quinto *et al.* have shown that potent and stable attenuation of recombinant HIV-1 virus engineered to express TD-I κ B α was not due to an increase in HIV-1 induced apoptosis (343). Further studies are required to see whether a protective role of NF- κ B on HIV-1 induced apoptosis in T cells is also valid as observed in myeloid cells (94).

Thus, given the multiple functions of the NF- κ B transcription factors and $I\kappa B\alpha$ inhibitory proteins, Dox-induced TD- $I\kappa B\alpha$ expression may interfere with HIV-1 multiplication at several levels (Figure 30): LTR-mediated transcription, Rev-mediated export of viral RNA, inhibition of HIV-1 induced pro-inflammatory cytokines, and increased sensitivity of HIV-1 infected cells to apoptosis. A transcriptional role for $I\kappa B\alpha$ in the inhibition of HIV-1 LTR driven gene expression was well characterized in our studies.

1.2 Identification by *In Vivo* Genomic Footprinting of an NF-κB/Sp1 Transcriptional Switch that Regulates the IκBα Promoter

TD-I κ B α expression was shown to inhibit endogenous I κ B α at the protein level as well as to interfere with NF- κ B binding and HIV-1 multiplication in Jurkat cells (222). This led us to study further the autoregulatory control of I κ B α transcription by using an *in vivo* genomic footprinting analysis of the I κ B α promoter. We demonstrated that induction of Figure 30. Potential mechanisms of TD-I κ B α mutants-mediated inhibition of HIV-1 multiplication. TD-I κ B α would be capable of sequestering of newly synthesized NF- κ B in uninduced cells as well as inhibition of released NF- κ B in the cytoplasm, and removal of DNA bound NF- κ B in the nucleus in induced cells by TNF α or virus (I), therefore inhibiting HIV-1 LTR transcription. TD-I κ B α is also able to compete with HIV-1 rev protein for the usage of nuclear export pathway which occurs through CRM1 (II). It is also possible that production of virus-induced and NF- κ B regulated cytokine such as TNF α can be inhibited by TD-I κ B α (III).



endogenous IkBa after TNFa or PMA/PHA treatment is suppressed by TD-IkBa at the transcriptional level. Tet-induced TD-IkBa expression blocked NF-kB binding activity at the proximal -63 to -53 kB1 site of the $lkB\alpha$ promoter. This inhibition was shown to be due to the tight association between transactivator p65 and TD-I κ B α as revealed by coimmunoprecipitation studies. Similar data were recently obtained in thymocytes isolated from transgenic mice expressing either non-degradable $I\kappa B\alpha$ or $I\kappa B\beta$ (11, 48, 168). In vivo genomic footprinting revealed multiple protein-DNA interactions in the region of the IkBa promoter between -250 to +100 bp in Jurkat T cells; protection of Sp1, AP2, Ets-1 and $\kappa B3$ sites in unstimulated cells, indicate that these sites participate in basal level $I\kappa B\alpha$ transcription. In response to stimulation of Jurkat T cells by PMA/PHA or TNF α , changes in methylation of the kB1 site and the adjacent Sp1 site were observed, whereas no inducible changes were detected at $\kappa B3$ or the other sites (data not shown). The protection observed at $\kappa B1$ and Sp1 sites was sustained from 10 min to 24h, and together with the EMSA results demonstrated that binding of p50-p65 heterodimer correlated with transcriptional induction of the $I\kappa B\alpha$ gene; at later times, the switch in composition of the NF-kB complexes to predominantly p50-c-Rel heterodimers correlated with transcriptional downregulation. Deletion and point mutagenesis of the IkB α promoter demonstrated that both the $\kappa B1$ and Sp1 sites were absolutely required for $I\kappa B\alpha$ promoter induction, whereas only Sp1 was involved in basal transcription of this promoter. These results further demonstrated a strict spacing requirement between xB1 and Sp1 sites for full activation of the $I\kappa B\alpha$ promoter. Together, these studies allowed us to propose a model for $I\kappa B\alpha$ transcriptional regulation in Jurkat T cells summarized in Figure 31. In this model, downregulation of $I\kappa B\alpha$ transcription, occurring at later times of induction, is associated with a switch in the composition of NF-kB complexes bound to the kB1 site, from p50-p65 to p50-c-Rel heterodimers. This mechanism is in agreement with inhibition of p65-mediated transcription of the HIV-1 LTR and IL-2Ra promoters by c-Rel (105). Similarly, c-Rel protein, shown to be induced by PMA or TNF α with delayed Figure 31. Schematic representation of the protein-DNA interactions regulating the I κ B α promoter. I κ B α promoter organization, including κ B1 to κ B3 as well as Sp1, Ets-1 and AP2 binding sites, is described in the upper part of the figure. In resting Jurkat T cells, protection are observed at the κ B3, Ets-1, Sp1 and AP2 sites which are likely responsible for basal I κ B α transcription. At early time of induction of cells by PMA/PHA or TNF α , the κ B1 site (-63 to -53) is occupied by p65/p50 heterodimers. At later time, a switch in complex composition to p50-c-Rel heterodimer is correlated with downregulation of I κ B α transcription. NF- κ B specific binding and I κ B α gene transcription is blocked by Tet-induced expression of TD-I κ B α , via sequestration of p65 in the cytoplasm. Protection observed at the adjacent Sp1 site (-44 to -36) is also modulated in response to stimulation and is likewise modified by Tet-induced TD-I κ B α expression. Binding to the Sp1 site may be related to the occupancy of the κ B1 site by inducible NF- κ B complexes. No changes were observed on κ B3, Ets-1, and AP2 sites during cell activation.



kinetics compared to p65 (105), may also inhibit $I\kappa B\alpha$ transcription by competition with p50/p65 for occupancy of the $\kappa B1$ binding site (Figure 31).

The EMSA and genomic footprinting data are consistent with inhibition of IkBa promoter activity identified by deletion of the κ B1 site (228); the κ B2 and κ B3 sites appear to play no role in the inducibility of the $I\kappa B\alpha$ promoter at least in Jurkat T cells stimulated by PMA/PHA or TNF α . Our results are also in agreement with the mutagenesis analysis performed by Ito *et al.* (185), showing a predominant role for the $\kappa B1$ site. This analysis had also suggested that full activation of the $I\kappa B\alpha$ promoter also required another κB -like site located downstream of kB1 between nucleotides -34 to -24, as well as the upstream κ B2 site. In the present study, no inducible *in vivo* protein-DNA interactions were observed at either of these sites. Although a role for $\kappa B2$ and $\kappa B3$ sites cannot be excluded, our *in vivo* data clearly demonstrate that $\kappa B1$ and Sp1 sites play the major role in the inducibility of the $I \ltimes B \alpha$ promoter in Jurkat T cells. Furthermore, in vivo genomic footprinting experiments performed with the U937 promonocytic cell line revealed the same in vivo protection pattern as observed with Jurkat T cells - only the Sp1 site was protected before stimulation and both Sp1 and κ B1 sites were targeted by inducible complexes after induction (data not shown). Thus, a common mechanism of IkBa regulation involving the NF-kB/Sp1 transcriptional switch is likely active in multiple cell types, including T cells and monocytes/macrophages.

Many genes regulated by NF- κ B also contain adjacent Sp1 sites and direct interaction between NF- κ B proteins and Sp1 has been demonstrated (329); a recent study also identified *in vitro* binding of Sp1 to the κ B sites located on promoters such as the IL-6 and P-selectin (171). We have demonstrated binding of p50-c-Rel and p50-p65 heterodimers to the κ B1 site in response to cell induction, as well as binding of Sp1 to its own site in I κ B α promoter. Furthermore, the Sp1 protection observed was reversed with TD-I κ B α activation (Figure 31). This coordinate change suggests that the binding of NF- κ B inducible complexes to the κ B1 site may also facilitate an increased Sp1 binding affinity to the adjacent Sp1 site. Interestingly, the residues at position -48 and -49, located between the NF- κ B and Sp1 sites became more sensitive to methylation/cleavage, suggesting that the protein-DNA conformation of the entire NF- κ B/Sp1 region is modified after stimulation (Figure 23).

Sp1 binding to its consensus site prior to stimulation indicates that it may contribute to basal transcription of the I κ B α gene. Interestingly, a different methylation and cleavage pattern was observed at the Sp1 site after stimulation. Direct Sp1 conformational changes and/or alterations in Sp1 binding affinity may be induced after stimulation via Sp1 post-translational modification. Sp1 has been described as a zinc finger phosphoprotein which upon cell activation undergoes specific phosphorylations and dephosphorylations that regulate its DNA binding activity and its interactions with other proteins (10, 355, 377). Following cell stimulation, Sp1 can be phosphorylated by casein kinase II, protein kinase A and by a recently described 60 kDa kinase, activated in response to Neu differentiation factors (NDFs) (5). The inducible change at the Sp1 binding site in response to Jurkat T cells stimulation may reflect such Sp1 modifications leading to increased binding on DNA.

The critical role of the $\kappa B1$ site and the adjacent Sp1 site in the inducibility of the $I\kappa B\alpha$ promoter is further supported by the conservation of these two sites in the murine and porcine homologs of the $I\kappa B\alpha$ promoter (74, 90). Moreover, not only are the exact sequences conserved, but also the 10 bp spacing between both sites is maintained between species. This distance, corresponding to one helical turn of DNA, may permit a physical interaction between proteins bound to the Sp1 site and the p65-p50 complex on the same face of chromatin *in vivo*, as shown for the HIV-1 LTR promoter (329).
Although no cooperativity in the binding of NF- κ B and Sp1 was observed by EMSA, transfection studies using hybrid I κ B α promoters in which nucleotides between κ B1 and Sp1 sites were inserted or deleted, revealed a strict spacing requirement for maximal inducibility of I κ B α promoter. Deletion of the 8 nucleotides between both sites or insertion of 5 or 9 nucleotides significantly lowered I κ B α promoter inducibility. The fact that addition of an half helical turn, or a complete helical turn led to a similar decrease in I κ B α gene inducibility, argues against a direct physical interaction between NF- κ B and Sp1, and rather suggests a requirement for the interaction of NF- κ B and/or Sp1 with basal transcription factors such as TAFs or with the transcription machinery for maximal induction of I κ B α promoter. Sp1 has been found in a multiprotein complex containing CBP/p300, although a direct interaction has not been shown, and the NF- κ B p65 subunit is able to interact with the N- and C-terminal region of the coactivator p300, resulting in gene activation of E-selectin and VCAM-1 (138, 317, 330). Further studies are required to characterize the association of NF- κ B and Sp1 with TAFs, TBP or CBP/p300, and their role in I κ B α regulation.

As shown above by luciferase assays as well as others (31, 74, 185, 228) basal expression of $I\kappa B\alpha$ gene is not regulated by NF- κB . However, we observed a gradual disappearance of endogenous $I\kappa B\alpha$ upon an inducible expression of TD- $I\kappa B\alpha$. Therefore, RNase protection assay was performed using total RNA isolated from TD- $I\kappa B\alpha$ expressing cells treated with Dox up to 72h. There was no or very little decrease in the amount of endogenous $I\kappa B\alpha$ mRNA (data not shown). Similar results by Beg *et al.* indicated that no difference was observed in the basal levels of $I\kappa B\alpha$ RNA expression in both wt and $p65^{-/-}$ embryonic fibroblasts yet, $I\kappa B\alpha$ protein levels were decreased in $p65^{-/-}$ embryonic fibroblasts (31). This may be due to a decreased stability of $I\kappa B\alpha$ in the absence of p65 as observed in a number of studies (26, 348, 389, 407) As shown by coimmunoprecipitation studies (Figure 21), endogenous p65 was mainly associated with

TD-IkBa after 24h of Dox treatment, due to an increased amount of TD-IkBa. These experiments revealed the presence of TD-I κ B α in latent NF- κ B complex containing the transactivating subunit p65. Unbound endogenous $I\kappa B\alpha$ thus is rapidly degraded in the free form and a decreased steady-state levels of endogenous $I\kappa B\alpha$ become undetectable by Western Blot Analysis. Similar data was obtained in thymocytes isolated from transgenic mice expressing $I\kappa B\alpha$ (ΔN), another constitutive repressor of $I\kappa B\alpha$ lacking Nterminal signal response domain (48, 53). In contrast, decreased levels of endogenous $I\kappa B\alpha$ were not observed in thymocytes which were also isolated from transgenic mice expressing similar transdominant mutants of $I\kappa B\alpha$ (mlkB α) (168). However, this may be due to different levels of transgene expression. In our Jurkat T cell model, there was significantly more TD-IkBa than endogenous IkBa and TD-IkBa can be further increased by Dox treatment while almost equal levels of $mI\kappa B\alpha$ were observed compared to endogenous $I \kappa B \alpha$ in thymocytes expressing m $I \kappa B \alpha$ (2, 168, 222). Thymocytes isolated from these mice similarly responded to NF-kB inducers as analyzed by Western Blot analysis, co-immunoprecipitation and DNA binding assays. Therefore, our in vitro Jurkat T cell system can reflect the *in vivo* transgenic mice model on NF-kB/IkB signaling studies.

2.0 FUTURE DIRECTIONS

The experiments presented in this thesis analyze the effects of TD-I κ B α on HIV-1 replication. Both transient and stable transfection of TD-I κ B α efficiently inhibited HIV-1 multiplication in a single cycle infection model and in *de novo* HIV-1 infection. This inhibitory effect of TD-I κ B α resulted in part from cytoplasmic sequestration of NF- κ B which has been shown to be an important host transcription factor for HIV-1 LTR activity.

1) As shown in our experiments, inhibition of Tat-mediated HIV-1 LTR transcription by TD-I κ B α has also been verified by others (157). Therefore, it would be interesting to see how TD-I κ B α inhibits Tat-mediated HIV-1 LTR transcriptional activity. One possible explanation for the inhibitory effect of TD-IkBa on Tat-mediated HIV-1 LTR transcription can be made based upon the observation that NF- κ B p65 interacts with p300/CBP which has been shown to activate Tat by acetylation (138, 209, 330, 476). However, Tat has also been shown to interact with p300/CBP (34, 175, 271, 272). Therefore, it is not clear whether acetylation of Tat is performed by p300/CBP that is associated with Tat or by p300/CBP that is associated with p65. To differentiate these two possible mechanisms, one can use GAL4 luciferase reporter in which only GAL4 DNA binding sites are introduced to upstream of TAR element without the upstream regulatory elements. These two elements would be sufficient because intact Tat- or Tat-TNF α synergistic activation was observed using III $\Delta 23$ construct which contains only the enhancer and the TAR elements (Figure 8). The question above would be answered by introducing GAL4-p300/CBP or GAL4 DNA binding domain (negative control) along with HIV-1 Tat and GAL4-TAR hybrid luciferase.

Some research has suggested that Tat can also induce NF- κ B activation (47, 84, 97, 220). This effect of Tat on NF- κ B activation was shown by extracellular, not intracellular, Tat. In addition, we performed the reporter assay using NF- κ B specific luciferase (HIVenh/pGL3) and observed no effect of intracellular Tat introduced by a transient transfection (data not shown). Whether extracellular Tat-mediated NF- κ B activation occurs through signal transduction involving an unidentified HIV-1 Tat receptor is not currently known. Experiments are in progress to assess the effect of exogenous Tat on NF- κ B activation using the inducible TD-I κ B α expressing Jurkat cells. Tat has also been involved in some other signal transduction pathways involving PKC and PI3K (84, 284, 296). Interestingly, these kinases have recently been shown to be involved in IKK

activation (197, 224, 310, 356, 378). Therefore, once we get the system in which extracellular Tat activates NF- κ B, it would be also interesting to see the involvement of the recently identified IKKs as well as upstream kinases on this extracellular Tatmediated NF- κ B activation by using transdominant mutants of these kinases. It has also been suggested that Tat-mediated NF- κ B activation was proposed to occur through the transcriptional activation of TNF α gene expression by Tat which would in turn activate NF- κ B via autocrine or paracrine effect of TNF α (43, 446).

2) Unexpected results were obtained with $I\kappa B\alpha$ (2N+3C) in a single cycle infection. $I\kappa B\alpha$ (2N) was significantly more effective in inhibiting HIV-1 multiplication than IkBa (2N+3C) (Figure 11 and 12). The only difference between these two mutants were at the C-terminal region. This many suggest the importance of the C-terminal region on posttranscriptional inhibitory effect on HIV-1 because both mutants could effectively inhibit HIV-1 LTR transcription induced by Tat and TNFa (Figure 10). The posttranscriptional inhibitory effect of $I\kappa B\alpha$ on HIV-1 rev function was previously suggested by Dr. Gary Nabel's group (452, 453). This inhibitory effect of IkBa may be through the competition with HIV-1 rev protein for the usage of nuclear export pathway which occurs through CRM1 (193, 352). First of all, we have to further verify whether I κ B α (2N+3C) mutants are less effective in blocking HIV-1 replication compared I κ B α (2N) in cell types other than Cos-1 cells. Therefore, we tried to generate Jurkat T cells that are inducibly expressing wt and mutants of $I\kappa B\alpha$. Unfortunately, only three cell lines (rtTA-Neo, 2N and 2NA4) were obtained which were used in this thesis. Because the generation of stable cell line is time-consuming and labor-intensive, we started to use the protein transduction method (431). It has been demonstrated that not only Jurkat T cells can be transduced but also many different cell types (294, 388). Introduction of these proteins to Jurkat cells and their subsequent HIV-1 infection would tell us whether the Cterminal region of $I\kappa B\alpha$ is also important in inhibiting HIV-1 multiplication in these cells. It would then be interesting to analyze the inhibitory effect of TD-I κ B α on HIV-1 Rev function at the posttranscriptional level through the nuclear export pathways.

3) A number of cytokine genes such as IL-2, Granulocyte colony-stimulating factor (G-CSF), TNF α , TNF β , Lymphotoxin β (LT- β) and β -interferon (IFN- β) are regulated by NF- κ B and HIV-1 infection causes constitutive activation of NF- κ B DNA binding activity (16, 24, 287, 319, 365). Therefore, it would be interesting to analyze the effect of TD-I κ B α on HIV-1-induced cytokine gene expression. In addition, preliminary data shows that the inducible expression of TD-I κ B α inhibited TNF α - and PMA-induced cytokine expression (data not shown).

4) There are a number of inhibitors of NF- κ B activity that act at the following levels: 1) through induction of I κ B α expression, 2) interference with NF- κ B nuclear transport 3) inhibition of NF- κ B DNA binding, 4) suppression of transactivational potential of NF- κ B (110). For example, cyclopentenone prostaglandins (cyPGs) have been shown to inhibit NF- κ B activation by preventing phosphorylation and degradation of I κ B α (360). Recently, it has been shown to inhibit IKK β activity through PPAR- γ independent mechanism (67, 361). Current problems with these inhibitors are that some of them can affect signaling pathways other than the NF- κ B signaling pathway. Also, the molecular mechanisms of action of these inhibitors is not well defined. However, TD-I κ B α specifically inhibits NF- κ B activity. On the other hand, overexpression of non-degradable I κ B α or I κ B β has caused problems such as spontaneous development of squamous cell carcinoma and malfunction of immune cells (48, 168, 425). Therefore, an ideal solution is to express TD-I κ B α conditionally. As our study demonstrated, inducible expression of TD-I κ B α inhibited HIV-1 replication, possibly at multiple different stages of viral life cycle (Figure 30).

A recent publication demonstrated that the HIV-1 protease expressed in HIV-1 infected cells cleaved a modified pro-caspase 3 (431). Upon cleavage by HIV-1 protease, caspase 3 became active and executed an apoptotic process, which lead to the elimination of infected cells only. Pro-caspase 3 in uninfected cells was not active, leaving uninfected cells unharmed. Modeling after this study, it will be interesting to introduce HIV-1 proteolytic cleavage sites into the N-terminal region of IkBa after the signal response domain. We propose that upon HIV-1 infection, this N-terminal region along with the signal response domain will be cleaved away by HIV-1 protease, creating N-terminally deleted IkBa (Δ N-IkBa) which behaves like TD-IkBa. Therefore, the HIV-1 protease induced TD-IkBa should eventually inhibit HIV-1 multiplication. In uninfected cells, modified IkBa containing HIV-1 protease cleavage sites will behave like wt IkBa. Therefore, these cells should function normally.

3.0 CONTRIBUTIONS TO ORIGINAL KNOWLEDGE

NF- κ B plays an important role not only in immune response, but also in viral pathogenesis of HIV-1. HIV-1 LTR expression involves a complex interaction between HIV-1 Tat protein and host transcription factors such as NF- κ B. Therefore, the effect of TD-I κ B α on Tat/TNF α synergistic activation of HIV-1 LTR was first analyzed. Use of Jurkat cell line inducibly expressing TD-I κ B α permitted a study on the effect of TD-I κ B α on *de novo* HIV-1 infection. We further examined the autoregulation of NF- κ B signaling by analyzing I κ B α promoter using *in vivo* genomic footprinting.

1) Transactivation of the HIV-1 LTR by Tat and TNF α is dependent on both functional Tat-TAR interaction and the presence of NF- κ B binding sites. Coexpression of wt I κ B α or mutants of I κ B α inhibits Tat-TNF α synergism in a dose-dependent manner. HIV-1 protein and RNA synthesis is inhibited by TD-I κ B α in a single cycle infection model and this occurs at the transcriptional level.

2) Jurkat cells are sensitized to TNF α induced apoptosis by inducible expression of TD-I κ B α . This may result from the inhibition of anti-apoptotic role of NF- κ B by TD-I κ B α . NF- κ B DNA binding activity and LTR transactivation is reduced by TD-I κ B α . Inducible expression of TD-I κ B α inhibits *de novo* HIV-1 infection at the transcriptional level.

3) Inducible expression of TD-I κ B α suppress endogenous wt I κ B α expression, which was due to tight interaction between TD-I κ B α and NF- κ B which prevented NF- κ B binding activity. *In vivo* genomic footprinting revealed stimulus-responsive protein-DNA binding to the κ B1 and Sp1 sites in the I κ B α promoter which was inhibited by inducible expression of TD-I κ B α . With time after stimulation, decreased levels of transcriptionally active p65/p50 and increased c-Rel/p50 heterodimers were detected at the κ B1 site. Both κ B1 and Sp1 sites were required for I κ B α promoter induction and a strict spacing between two sites was necessary for full activation.

CHAPTER VII

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