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**REGULATION OF RESISTANCE TO HIV-VPR  
INDUCED APOPTOSIS**

*By*

**Sasmita Mishra**

**A thesis submitted to the Faculty of Graduate Studies  
In partial fulfillment of the requirements for the degree of  
Doctor of Philosophy**

**Department of Biochemistry, Microbiology, and Immunology  
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# *Abstract*

Apoptosis of CD4<sup>+</sup> T cells and their eventual depletion constitute a hallmark of HIV infection and disease progression. However, monocytes/macrophages unlike CD4<sup>+</sup> T cells survive HIV replication and hence represent a major reservoir of virus. The mechanism underlying this resistance to HIV-mediated apoptosis in monocytic cells is not clear. It is believed that TNF- $\alpha$  which is produced during HIV infection may play a major role in inducing resistance in monocytes. In this study I investigated the molecular mechanisms involved in regulation of resistance to HIV-Vpr induced apoptosis in monocytic cells.

LPS and LPS induced TNF- $\alpha$  are known to induce resistance to monocyte apoptosis. However, the molecular mechanism regulating this process is not known. c-IAP2, one of the anti-apoptotic genes is known to be induced in monocytes in response to LPS. First of all, I demonstrated that LPS and TNF- $\alpha$  induced survival of human monocytic cells through the induction of the c-IAP2 gene. Further, I studied the involvement of MAPKs and PI3K signaling pathways in c-IAP2 induction by using specific pharmacological inhibitors. My results suggest that neither MAPKs nor PI3K is involved in c-IAP2 induction. Since calcium signaling pathway is considered to be one of the upstream signaling molecules in signaling cascade, I investigated its involvement in c-IAP2 induction in monocytic cell line. I showed that binding of LPS/TNF- $\alpha$  to their respective receptors induces calcium influx. Calcium is also known to activate calmodulin (CaM) which in turn activates various kinases and phosphatases. My results revealed that activation of CaM and CaM kinase II (CAMKII) is involved in c-IAP2 induction, whereas calcineurin, the protein phosphatase activated by CaM is not involved in this process. I have shown for the first time that LPS/TNF- $\alpha$  induced c-IAP2 and associated anti-apoptotic activity is regulated by CaM/CAMKII through the activation of NF $\kappa$ B.

Since TNF- $\alpha$  is believed to be involved in inducing resistance to HIV induced apoptosis in monocytes, further I used Vpr, one of the HIV proteins to induce apoptosis in monocytes. My results showed that HIV-Vpr induces apoptosis in monocytes and pretreatment of cells with either LPS/TNF- $\alpha$  induces resistance to Vpr mediated apoptosis. To determine the molecular mechanisms involved in Vpr induced apoptosis, I used the C-terminal synthetic peptide (Vpr52-96) which mimics the whole Vpr protein for induction of apoptosis. I also used the N-terminal (Vpr1-45 aa) peptide as control. I demonstrated that both the C-terminal and N-terminal peptides phosphorylate all the three MAPKs such as p38, ERK, and JNK MAPK; however, only C-terminal (Vpr52-96) peptide induced apoptosis is regulated selectively by JNK MAPK. To determine the involvement of pro- and anti-apoptotic genes in Vpr induced apoptosis, RNase protection assay was performed. My results revealed that in response to Vpr52-96, there was downregulation of Bcl2, whereas other pro and anti-apoptotic genes of Bcl2 family remained unchanged. I also demonstrated the involvement of c-IAP1, one of the inhibitor of apoptotic proteins (IAPs) in Vpr induced apoptosis. My results show that Vpr peptide-

induced apoptosis is mediated by down regulation of anti-apoptotic Bcl2 and c-IAP1 genes through JNK MAPK activation. Deregulation of the JNK pathway has been implicated in cancer and other diseases. Therefore, investigation of the molecular mechanisms that govern the role of the JNK pathway in apoptosis should provide insight into its biological functions and strategies to target this pathway for prevention and treatment of human diseases and cancer.

Finally, I demonstrated that pretreatment of cells with LPS or TNF- $\alpha$  induced resistance to Vpr52-96 mediated apoptosis. My results suggest that LPS induced resistance is mediated by endogenous production of TNF- $\alpha$  in monocytes. I also demonstrated that LPS/TNF- $\alpha$  mediated resistance is regulated by induction of c-IAP2 through NF $\kappa$ B by activation of CAMKII. However, pretreatment with Vpr followed by LPS or TNF- $\alpha$  stimulation no longer gave protection to Vpr induced apoptosis. Vpr peptide also inhibited LPS/TNF- $\alpha$ -induced calcium influx, activation of CAMKII, and c-IAP2 induction. Taken together, my results suggest that the c-IAP2 gene plays a critical role in LPS and TNF- $\alpha$ -induced resistance to HIV-Vpr-mediated apoptosis in human monocytic cells. Since the calcium/CAMKII pathway is involved in LPS/TNF- $\alpha$  induced resistance to Vpr mediated apoptosis, strategies based on manipulation of these molecules, which would suppress c-IAP2 induction may be useful in clearing virus reservoirs in monocytes.

## *Dedicated to*

*To my son, whose unbelievable strong wishes enable me to finish my work;*

*To my husband for his constant inspiration and cooperation throughout the study;*

*&*

*To my supervisor (Dr. Ashok Kumar), whose constructive suggestion and advice never made me look back,*

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---

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## List of Abbreviations

$\Delta\psi_m$	Transmembrane potential
$[Ca^{2+}]_i$	Intracellular calcium ions
aa	Amino acid
Ab	Antibody
AIDS	Acquired immunodeficiency syndrome
AIF	Apoptosis inducing factor
ANT	Adenine nucleotide translocator
Apaf1	Apoptotic protease activating factor 1
ATP	Adenine triphosphate
Bad	Bcl2 associated death promoter
Bak	Bc-2 antagonistic killer
Bax	Bcl2-associated X protein
bp	Base pair
Bcl2	B cell follicular lymphoma
BclXL	Bcl2-X long form
Bid	Bcl2 interacting domain
Bim	Bcl2 interacting mediator
BIR	Baculoviral inhibitory repeat
BH	Bcl2 homology
CAD	Caspase activated deoxyribonuclease
CaM	Calmodulin
CAMKII	Calmodulin kinase II
cAMP	Cyclic adenosine monophosphate
CARD	Caspase recruitment domain
Caspase	Cysteine aspartate proteases
Cdc2	Cyclin dependent kinase
cGMP	Cyclic guanosine monophosphate
c-IAP1	Cellular inhibitor of apoptosis1
c-IAP2	Cellular inhibitor of apoptosis2
cDNA	Complementary DNA
cpm	Counts per minute
CTL	Cytotoxic T lymphocyte
Cyt-c	Cytochrome-c
DD	Death domain
DED	Death effector domain
DXM	Dexamethasone
Endo G	Endonuclease G
ERK	Extracellular-related kinase
Fas	Fibroblast associated
FADD	Fas associated death domain
GM-CSF	Granulocyte macrophage – colony stimulating factor
GTP	Guanosine triphosphate
HAX1	Hematopoietic lineage cell specific protein 1- associated protein X-1

HIV	Human immunodeficiency virus
HRPO	Horseradish peroxidase
IAPs	Inhibitors of Apoptotic Proteins
ICAD	Inhibitor of caspase activated deoxyribonuclease
IFN	Interferon
IL	Interleukin
IM	Inner membrane
JAK	Janus associated kinase
JNK	c-jun N-terminal kinase
Kb	Kilobase
LPS	Lipopolysaccharide
LTR	Long terminal repeat
mAb	Monoclonal antibody
MALT	Mucosa associated lymphoid tissues
MAPK	mitogen-associated protein kinase
MAPKK	MAPK kinase
MAPKKK	MAPKK kinase
MAVS	Mitochondrial anti viral signaling protein
Mcl1	Myeloid leukemia cell differentiation protein
MEK	MAP kinase/ERK kinase
MMP	Mitochondrial membrane permeabilization
mRNA	Messenger RNA
NF $\kappa$ B	Nuclear factor $\kappa$ B
NK	Natural killer
NOXA	PMA-induced protein
NPC	Nuclear pore complex
nt	Nucleotides
OM	Outer membrane
PARP	Poly-(ADP-ribose)-polymerase
PBMC	Peripheral blood mononuclear cells
PI3K	Phosphatidylinositol 3 kinase
PIC	Preintegration complex
PMA	Phorbol 12-myristate 13-acetate
PTK	Protein tyrosine kinase
PTPC	Permeability transition pore complex
PUMA	p53- upregulated modulator of apoptosis
RPA	RNase protection assay
RT-PCR	Reverse transcription-polymerase chain reaction
SH2	Src-homology 2 domain
SEK	Stress activated protein/ERK kinase
Smac	Secondary mitochondrial activator of caspases
SOCS	Suppressor of cytokine signaling
SODD	Silencer of death domain
Th	T helper
TNF- $\alpha$	Tumor necrosis factor- $\alpha$
TNF- $\beta$	Tumor necrosis factor- $\beta$

TRADD	TNF receptor-associated death domain
TRAF	TNF-receptor associated factor
TRAIL	TNF-related apoptosis inducing ligand
VDAC	Voltage dependent anion channel
Vpr	Viral protein R
Vpr52-96	Vpr peptide containing 52-96 amino acids
Vpr1-45	Vpr peptide containing 1-45 amino acids
WHO	World health organization
XIAP	X linked inhibitor of protein
ZVAD	Z-Val-Ala-Asp-CH <sub>2</sub> F

**Chapter I**  
*General Introduction*

## **Introduction:**

Acquired Immunodeficiency syndrome (AIDS) is caused by human immunodeficiency virus (HIV), one of the viruses in the Retrovirus family [1]. It has been 25 years since AIDS was first identified and the latest report from WHO states that around 42 million people are living with HIV throughout the world (WHO, 2002). The main clinical features in HIV include an acute infection followed by a period of clinical latency which may last for 3-15 years before AIDS develop [2;3]. HIV primarily infects and replicates in immune cells such as T cells and monocytes/macrophages, which accounts for many of the major aspects of HIV pathogenesis [4].

The hallmark of AIDS is that HIV infects and kills CD4+ T cells, resulting in depletion of CD4+ T cells and eventually the patient dies of multiple infection and/or malignancies [5;6]. The major mechanism for CD4+ T cell depletion is apoptosis which can be induced by multiple pathways by various viral proteins [7]. Unlike T cells, monocytes/macrophages can harbor large quantities of the virus without being killed [8]. The factors involved in inducing resistance to HIV induced apoptosis in monocytes/macrophages are largely unknown. However, it is known that there is production of the proinflammatory cytokine tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) during HIV infection [9;10]. Since lipopolysaccharide (LPS) and LPS induced TNF- $\alpha$  prevent apoptosis in monocytes [10;11] and also induce anti-apoptotic genes such as cellular inhibitor of apoptotic protein (c-IAP2) [11], it is most likely that TNF- $\alpha$  is one of the factors inducing resistance to HIV induced apoptosis in monocytes/macrophages. Among various proteins involved in inducing apoptosis in HIV infection, Vpr plays an important role being packaged in great quantities into the virion nucleocapsid and is also expressed

late in the infection suggesting the importance of this protein throughout the viral life cycle [12;13]. Therefore, elucidating the molecular mechanisms involved in inducing resistance to HIV induced apoptosis in monocytes/macrophages may have broad implications related to host-pathogen interactions, viral persistence and survival of monocytic cells not only in HIV infection but also in infectious diseases caused by intracellular pathogens such as tuberculosis. For my Ph.D. research project, I have investigated the signaling pathways involved in HIV-Vpr induced apoptosis and the resistance induced by LPS in human monocytic cells. My results suggest that HIV-Vpr-induced apoptosis is mediated by down regulation of anti-apoptotic Bcl2 and c-IAP1 genes through JNK MAPK activation. Further, I demonstrated that the c-IAP2 gene plays a critical role in LPS and LPS induced TNF- $\alpha$  mediated resistance to HIV-Vpr-induced apoptosis through activation of calcium signaling pathways, particularly calmodulin kinase II (CAMKII) in human monocytic cells.

## **Background literature:**

### **HIV and apoptosis:**

The exact mechanism by which CD4<sup>+</sup> T cells are destroyed from HIV infected patients remains unclear. Several hypotheses have been proposed to explain this decline including 1) direct infection of T cells and apoptosis [3]; 2) bystander cell killing by viral proteins [14;15]; and 3) dysregulated cytokine production [16].

1) Direct infection of T cells by HIV leads to apoptosis which accounts only a small percentage of affected cells [14;17]. There are several viral proteins including structural protein such as Env, and accessory proteins such as Tat, Vpr, Vpu, and Nef are involved in infected cell death [18;19]. HIV has the property of inducing membrane

fusion that leads to syncytia formation [20]. Syncytia have short life span resulting in release of live virus potential for further infection. Besides that, continuous budding is also another feature of HIV infection which disrupts the plasma membrane [21]. Vpu induced membrane permeabilization [22], whereas Tat [23], Nef [24] and Env [25] specifically enhanced Fas mediated killing. Vpr is considered to have pro- and anti-apoptotic effects in the cell. The anti-apoptotic effect which includes upregulation of Bcl2 plays a key role during early infection resulting in productive infection [26]. However, in the late stage of infection which is associated with more quantity of Vpr production induces apoptosis in T cells [27]. CD4+ T cells are also killed by HIV specific cytotoxic T lymphocytes (CTL) [28].

2) HIV infected cells are killed by various means. However, more number of uninfected cells are killed than infected cells during HIV infection [14;15]. There are two mechanisms which induce cell death in uninfected bystander cells 1) apoptosis by HIV proteins; and 2) activation induced cell death [29]. HIV proteins such as gp120, Tat, Nef, Vpr, and Vpu released into the intracellular space have been shown to induce apoptosis in uninfected cells [29]. Soluble and membrane bound gp120 induces cross linking of the CD4 molecules followed by apoptosis by Fas dependent and independent manner [30]. Tat is found to be secreted from infected cell and has been shown to induce apoptosis in uninfected neurons and Th cells by upregulating caspase 8, and FasL [31;32]. Vpr is found to be present in serum and CSF [33] and induces apoptosis in T cells, and neurons [34;35]. It is mentioned earlier that some of the uninfected cells are killed and eliminated by activation induced cell death. It refers to high induction of Fas and FasL by HIV

infection on the uninfected cell surface resulting in apoptosis [36;37]. However, induction of apoptosis by HIV in monocyte is not clear.

3) Cytokines produced during HIV infection also play an important role in pathogenesis by modulating apoptosis. There is a shift in cytokine response predominantly type I cell mediated (IFN- $\gamma$ , TNF- $\alpha$ , and IL-12) to type II humoral immune response (IL-10) while HIV progresses [16]. It is presumed that type 1 cytokine is essential for cell survival in the early stage of infection whereas in the late stage of infection, type II cytokine helps in disease progression by inducing apoptosis.

### ***Apoptosis in monocytes:***

During the last several years, the main interest was focused on the tendency of peripheral blood lymphocytes to undergo apoptosis following HIV infection. However, other immune cell such as monocyte has received much less attention. This is because of the belief that monocytes survive during HIV infection which acts as a major reservoir of virus. However, there are few reports stating about monocyte apoptosis and their impaired function during HIV infection. Normally, during the process of apoptosis, monocytes/macrophages induce more production of anti-inflammatory cytokine IL-10 and decrease the production of inflammatory cytokines such as TNF- $\alpha$  and IL-12. This pattern of cytokine enhances monocyte/macrophage apoptosis [9]. However, in HIV infection, monocytes/macrophages do not undergo apoptosis most likely due to cytokines such as TNF- $\alpha$ , and nerve growth factor produced endogenously by HIV infection. It has been reported that TNF- $\alpha$  which is produced during HIV infection by monocytes and lymphocytes activates NF $\kappa$ B which in turn induces high level of HIV and TNF- $\alpha$  transcription [38]. This is supplemented with the evidence made by Wahl *et al.* where

they observed that coinfection of monocytes/macrophages with HIV and *Mycobacterium avium* facilitates HIV infection by multiple pathways [10]. *M. avium* activated NFκB which in turn activated TNF-α known to induce anti-apoptotic genes and confers cell survival. This hypothesis was supported by a recent study in which nerve growth factor was shown to act as an autocrine survival factor that rescued monocytic cells from the cytopathic effects of HIV [39]. Papasavvas *et al.* (2005) also demonstrated that exposure of monocytic cells to IL-13 significantly decreased spontaneous apoptosis [40].

Further, there is evidence to suggest that monocytic cells from HIV infected patients and *in vitro* infection of monocytic cell line U937 with HIV exhibit enhanced propensity to spontaneous apoptosis [41-43]. It has been observed that overexpression of BclXL, one of the anti-apoptotic genes induced resistance to HIV-1 mediated apoptosis and HIV-1 replication in U937 cells. Similarly, monocyte-derived macrophages obtained from HIV-infected patients express high levels of FasL that was correlated with high degree of apoptosis under *in vitro* as well as *in vivo* conditions in the lymphoid tissues [44]. It happened *in vivo* most probably due to switch in cytokine production. However, the mechanism involved in cytokine induced protection to HIV-Vpr mediated apoptosis is not clear. Manipulating these signaling molecules involved in resistance may help in inducing apoptosis in monocytes leading to clearance of HIV from reservoir.

### **Pathways of apoptosis:**

Apoptosis (In Greek meaning falling leaves), a self directed process of cell death was first described by Kerr, Wyllie, and Currie in 1972 [45]. It is a strictly regulated and conserved mechanism that is used to remove unwanted cells during embryonic development, morphogenesis, immune system function and maintenance of tissue

homeostasis [46;47]. Dysregulation of cell death pathways has been implicated in various pathological conditions including cancer, autoimmune and immunodeficiency diseases and neurodegenerative disorders [48;49]. The morphological changes that occur in cells during apoptosis are loss of cellular contact from matrix, cytoplasmic condensation, chromatin compaction, cell shrinkage leading to apoptotic body formation (plasma membrane blebbing) and absence of inflammatory response [45;46]. Apoptotic cells also expose phosphatidyl serine to their cell surface which is otherwise hidden in the plasma membrane resulting in phagocytosis of apoptotic cells [45;46]. The biochemical changes include activation of specific kind of proteases such as cysteine aspartate proteases known as caspases and activation of endonucleases leading to fragmentation of DNA [50-52]. Although a number of stimuli appear to trigger this apoptotic process, there are two major pathways of apoptosis: extrinsic or the death receptor pathway and the intrinsic or mitochondrial pathway [53-55] (Fig.1.1). There is also evidence to suggest that these two pathways cross talk in certain cell types [56;57]. Both the pathways lead to the activation of a complex array of caspases. Initiator caspases are caspase 2, 8, 9, and 10; whereas effector caspases are caspases 3, 7, and 6 [57;58]. Since initiator caspases are able to self activate and activate the downstream effector caspases, single apoptotic trigger is sufficient to cause apoptosis.

### ***Extrinsic Pathway of Apoptosis:***

The receptor mediated pathways are initiated by binding of death receptors such as fibroblast associated (Fas), tumor necrosis factor receptor (TNF-R) and TNF-related apoptosis inducing ligand receptor (TRAIL-R) to their respective ligands [53;57;59]. These proteins are integral membrane proteins with their receptor domains exposed at the

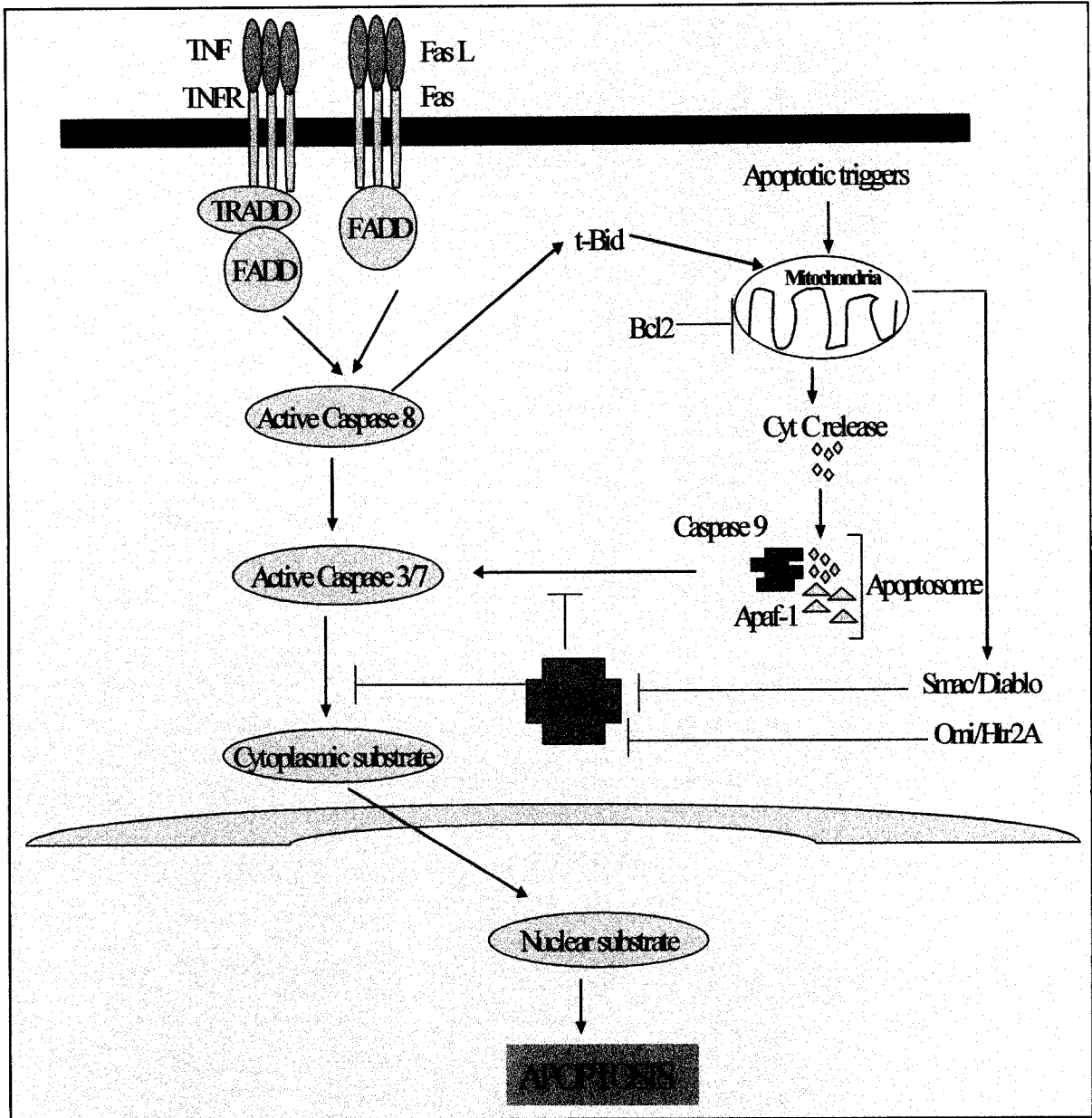
cell surface. The binding of complimentary death receptor to their respective ligands recruit procaspase 8 associated with its cofactor, FADD (Fas-associated protein with death domain) on the cytoplasmic side which becomes activated by proteolysis [60;61]. Further, activated caspase 8 promotes the cleavage of downstream effector caspases (caspases 3, 6, and 7) [62]. The effector caspases in turn activate a number of cytoplasmic and nuclear substrates including lamin B present on nuclear membrane, ICAD (inhibitor of caspase activated deoxyribonuclease) and PARP [poly (ADP-ribose) polymerase] [63]. The CAD-ICAD complex is located in the cytoplasm. After cleavage of ICAD, CAD translocates into the nucleus and degrades the chromosomal DNA leading to DNA fragmentation and cell death. PARP is a highly conserved protein that recognizes DNA strand break and implicated in DNA repair. It is a polypeptide of 118 kD and in the process of apoptosis it is cleaved into two fragments of 89 and 24 kD. PARP cleavage occurs early in the apoptotic process as a result of activity of caspase 3 and it is considered as one of the marker of apoptosis [64;65].

### ***Intrinsic Pathway of Apoptosis:***

The intrinsic pathway is initiated by various extracellular and intracellular stresses such as binding of glucocorticoids to nuclear receptors, physical agents such as heat, radiation, hypoxia, growth factor withdrawal, and oncogene induction [66-68]. Mitochondria are considered as the major organelles involved in this process. Mitochondria have two well defined compartments: the matrix surrounded by inner membrane (IM) and the intermembrane space surrounded by outer membrane (OM). The inner membrane contains ATP synthetase, and ANT (adenine nucleotide translocator), whereas the OM contains voltage dependent anion channel protein (VDAC), and

**Fig. 1.1: Pathways of apoptosis:**

Broadly, apoptosis is induced by two different pathways: receptor mediated and mitochondrial pathway. As shown in the figure, Fas ligands, which usually exist as trimers, bind to its receptor Fas on cytoplasmic membrane and induce receptor trimerization. Activated receptors recruit adaptor molecules such as FADD, which recruit procaspase 8 to the receptor complex, where it undergoes autocatalytic activation. Caspase 8 activates caspase 3, which leads to activation of various cytoplasmic and nuclear substrates responsible for DNA fragmentation. Caspase 8 also cleaves Bcl2 interacting protein (Bid) to truncated Bid (t-Bid) which translocates to mitochondria where it triggers cytochrome c release. However, Bcl2, one of the antiapoptotic proteins located in the mitochondrial membrane inhibits the release of cytochrome C. The released cytochrome c activates caspase 9 by binding to apoptotic protease activating factor-1 (Apaf-1) which in turn activates caspase 3. TNF also binds to TNFR and activate caspase 8 via recruitment of adapter molecules TNF receptor associated death domain (TRADD) and FADD. Caspase 8 in turn activates caspase 3. Stress such as drugs, irradiation, and growth factor withdrawal activates mitochondrial pathway. In response to death signal, mitochondria release cytochrome C and activate caspase 3 as described above. As shown in the figure, IAPs inhibit caspases, and Smac and Omi released from mitochondria block the activity of IAPs [69].



Bcl2 [54;70]. The intermembrane space contains cytochrome c, certain procaspases and apoptosis inducing factors (AIF), endonuclease G (Endo G) and secondary mitochondrial activator of caspases (Smac/DIABLO) [71;72]. IM permeabilization (MMP) leads to dissipation of the proton gradient, loss of transmembrane potential ( $\Delta\psi_m$ ), matrix swelling and rupture of outer membrane. On the other hand, OM permeabilization (MMP) leads to release of cytochrome c (Cyt C), AIF, Endo G, and Smac/DIABLO to cytoplasm [54;57;64;70]. However, this total process is very tightly regulated and controlled by a variety of Bcl2 (B cell follicular lymphoma) family of proteins [73;74].

Basically, the Bcl2 family of proteins are divided into 2 main groups: one group consists of anti-apoptotic proteins that share structural and functional homology with Bcl2 designated as BH (Bcl2 homology region) domains (BH1-4), the other one includes pro-apoptotic proteins that share less homology to Bcl2 (BH domains) [74;75]. Again the pro-apoptotic proteins are subdivided into two subgroups: the Bcl2-associated X protein (Bax)-like death factors and the BH3 only proteins. Mammalian anti-apoptotic proteins Bcl2, BclXL (Bcl2-X large form), Bclw, Mcl1 (myeloid leukemia cell differentiation protein) and A1 share 3 or 4 regions (BH1-4) of sequence similarity, whereas pro-apoptotic proteins, Bak (Bcl2 antagonistic killer), and Bax share 3 regions (BH1-3) [74;75]. The short BH3 only domain (9-16 aa) is present in Bad (Bcl2 associated death promoter), Bid (Bcl2 interacting domain), Bim (Bcl2 interacting mediator), Noxa (PMA-induced protein) and PUMA (p53- upregulated modulator of apoptosis) proteins and they are referred as BH3 only protein [74;76]. The BH3 only proteins and Bax like proteins can promote apoptosis by interacting with anti-apoptotic Bcl2 family of proteins. The anti-apoptotic proteins are normally localized in the mitochondrial outer membrane to

prevent release of Cyt C, in contrast pro-apoptotic proteins are localized either in the cytosol or in the cytoskeleton [75]. In response to death signals, there is induction of pro-apoptotic BH3 only proteins such as Bid, Bim, Bad, Noxa, and PUMA. During apoptosis, Bax which is present in monomer form in the cytoplasm is translocated into the OM along with Bak to form pore [70;77]. Depending on the trigger, Bim, which is present in microtubules is translocated into the OM [78]. Bad is normally sequestered in the cytoplasm in its phosphorylated form [79]. During the process of apoptosis, it is also dephosphorylated and translocates into the OM of mitochondria. NOXA and PUMA are activated by induction of p53 protein in response to DNA damage [75;80;81].

Based upon the trigger, all of these pro-apoptotic proteins interact with anti-apoptotic Bcl2 family of proteins such as Bcl2, BclXL and Mcl1 present on the mitochondrial membrane, triggers MMP, and dissipate  $\Delta\psi_m$ . The induction of apoptosis by these pro-apoptotic factors occurs by interacting and opening the permeability transition pore complex (PTPC) which includes ANT and VDAC of IM and OM of mitochondria, respectively [70]. Caspase 8 from receptor mediated pathway also cleaves one of the pro-apoptotic Bcl2 family of proteins Bid in certain cell types, which is translocated in its truncated form (tBid) into OM of mitochondria. Bid provides the mechanism of linking receptor mediated pathway to the mitochondrial pathway [82]. Due to MMP there is release of Cyt C from mitochondria that forms a heptameric complex known as apoptosome in association with caspase 9 and Apaf1 (apoptotic protease activating factor-1) in the presence of binding and hydrolyzing of dATP/ATP [83]. Activated caspase 9 is released from the apoptosome complex and cleaves the downstream effector caspases such as caspase 3, 6, and 7 through its protease activity

which leads to digestion of structural proteins in the cytoplasm and degradation of chromosomal DNA, the hallmark of apoptosis [82]. MMP is also associated with release of AIF and Endo G. AIF and Endo G not only activate caspases, but also act directly on nuclei to induce peripheral chromatin condensation, and DNA fragmentation [84].

In addition to all of these factors, there is also release of Smac/DIABLO to the cytoplasm that interacts and inhibits the activity of the inhibitor of apoptotic proteins (IAPs). IAPs suppress apoptosis by binding to caspases 3, 7, and 9 [85]. By inhibiting IAPs, Smac/DIABLO enhances the process of apoptosis through caspase activation [71]. It is well accepted that Bcl2 protein controls MMP, however, susceptibility of the cell to various apoptotic triggers depends on the relevant interaction between the death promoting and death inhibiting proteins.

It is well known that apoptosis plays an important role in various disease conditions such as autoimmune diseases, neurological disorders, and human acquired immunodeficiency syndromes. Either of the pathways is important based on the condition of the cell and the type of apoptotic trigger. Since my project is on HIV-Vpr (HIV-Viral protein R), one of the proteins of HIV-AIDS; further I will discuss more in details how HIV-Vpr induces apoptosis *in vitro* specifically in monocytic cells.

### **HIV-Vpr (HIV-Viral protein R):**

Several HIV proteins including one structural protein Env, and four accessory proteins Nef, Tat, Vpu, and Vpr have been implicated in apoptosis induction [86;87]. Vpr is one of the HIV proteins packaged in great quantities into the virion nucleocapsid through specific interaction with the p6 domain of p<sup>55gag</sup> precursor protein and help in transportation of virus into the nucleus [12;13;88]. Vpr is also expressed late in the

infection suggesting the importance of this protein throughout the viral life cycle [27]. It has been suggested that Vpr induced apoptosis in CD4<sup>+</sup> T cells [34] and other cell types including neuronal [89], neutrophils and promonocytic U937 cells [90]. However, the mechanism by which HIV may cause apoptosis of monocytic cells is not clear.

HIV-1 contains in its genome three structural *gag*, *pol* and *env* genes and six accessory genes namely *tat*, *rev*, *vif*, *vpr*, *vpu* and *nef* [90]. Vpr, a 14 kDa 96 amino acid protein, is the most conserved and multifunctional regulatory protein [90-92]. The Vpr protein is characterized by three well-defined  $\alpha$ -helices: 17-33, 40-48 and 55-83 amino acid (aa) surrounded by flexible negatively charged N-terminal and basic C-terminal domains [93]. Furthermore, the amphipathic  $\alpha$ -helix (55-83 aa) overlaps with a leucine rich domain that contains a short leucine zipper-like motif [93-96]. Mapping studies performed on lymphocytes or isolated mitochondria revealed that the N-terminal 1-51 aa Vpr protein (Vpr1-51) is required for virion incorporation and nuclear localization, whereas the C-terminal domain encompassing 52-96 aa (Vpr52-96) is essential for protein stability, induction of cell cycle arrest and apoptosis [97-100]. There is evidence to suggest that Vpr induces apoptosis by directly targeting the mitochondrial permeability transition pore complex (PTPC), a polyprotein complex organized around the two most abundant proteins of the inner and outer mitochondrial membranes, causing permeabilization of the mitochondrial membranes [101;102]. The NMR structure of the Vpr domain critical for its mitochondrial effects is comprised of 11 amino acid helical 71-HFRIGCRHSRI-82 peptide, with three positively charged R residues clustered on one side of the helix. Substitution of these R residues was shown to abolish Vpr-mediated

apoptotic potential [95;102;103]. Various domains of Vpr and their functions are detailed in Fig.1.2.

There are several activities ascribed to the Vpr protein in causing HIV-AIDS. 1) It plays a key role in virus replication by causing nuclear translocation of the HIV-1 preintegration complex [88]. 2) Vpr also induces cell cycle arrest at the G2/M phase suggesting the enhancement of virus replication by increasing transcription from HIV long terminal repeats (LTRs) [104]. 3) It induces apoptosis in variety of cell types including T cells, neutrophils, macrophages, and neuronal cells following infection with Vpr-expressing HIV isolates or exposure to the extracellular Vpr protein [34;105]. 4) Vpr protein also acts as a transcriptional activator of HIV promoter [106].

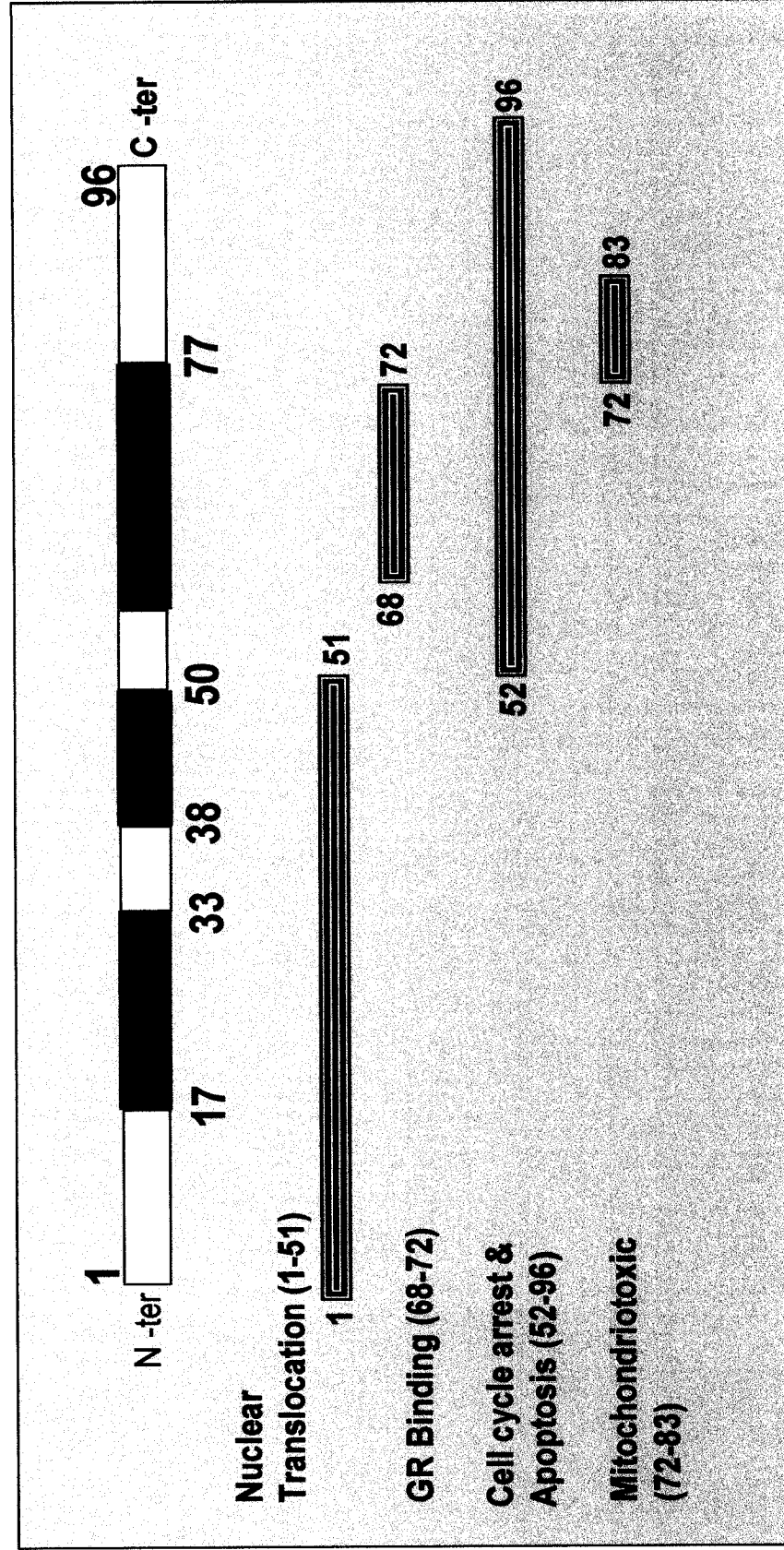
### **1) Vpr and nuclear transport of preintegration complex (PIC):**

In HIV infection, the important target for viral replication is the non replicating T cell population, and macrophages [107]. Normally, it is easy for the HIV PIC to get access into the nucleus of the dividing cell, but the entry into non-dividing cell is questionable. HIV has evolved multiple redundant karyophilic proteins to facilitate nuclear uptake of this PIC [12]. Proteins that are targeted for transport through nuclear pore complex (NPC) possess a nuclear localization signal (NLS). Although HIV-Vpr has been characterized as a nuclear protein, yet possesses no sequence homology with NLS [108]. However, it has been reported by several groups of workers that Vpr contains multiple and diffuse nuclear entry signals [109]. Furthermore, Vpr is small enough to diffuse through the NPC and is considered to contribute to the infection of monocytes/macrophages by facilitating nuclear uptake of PIC. Vpr also causes disruption in the nuclear envelope, thus facilitate the entry of PIC into the nucleus [109].

**Figure 1.2: Various domains of HIV-Vpr:**

HIV-Vpr is 96 amino acid long protein and it has various domains. As shown in the figure, N terminal domain containing 1-51 amino acid is involved in nuclear translocation, whereas C terminal 52-96 amino acid domain induces cell cycle arrest and apoptosis in various cell types. The domain containing 68-72 amino acid binds to glucocorticoid receptor (GR) and 72-83 amino acid containing domain is mitochondriotoxic [110].

## Domains of Vpr

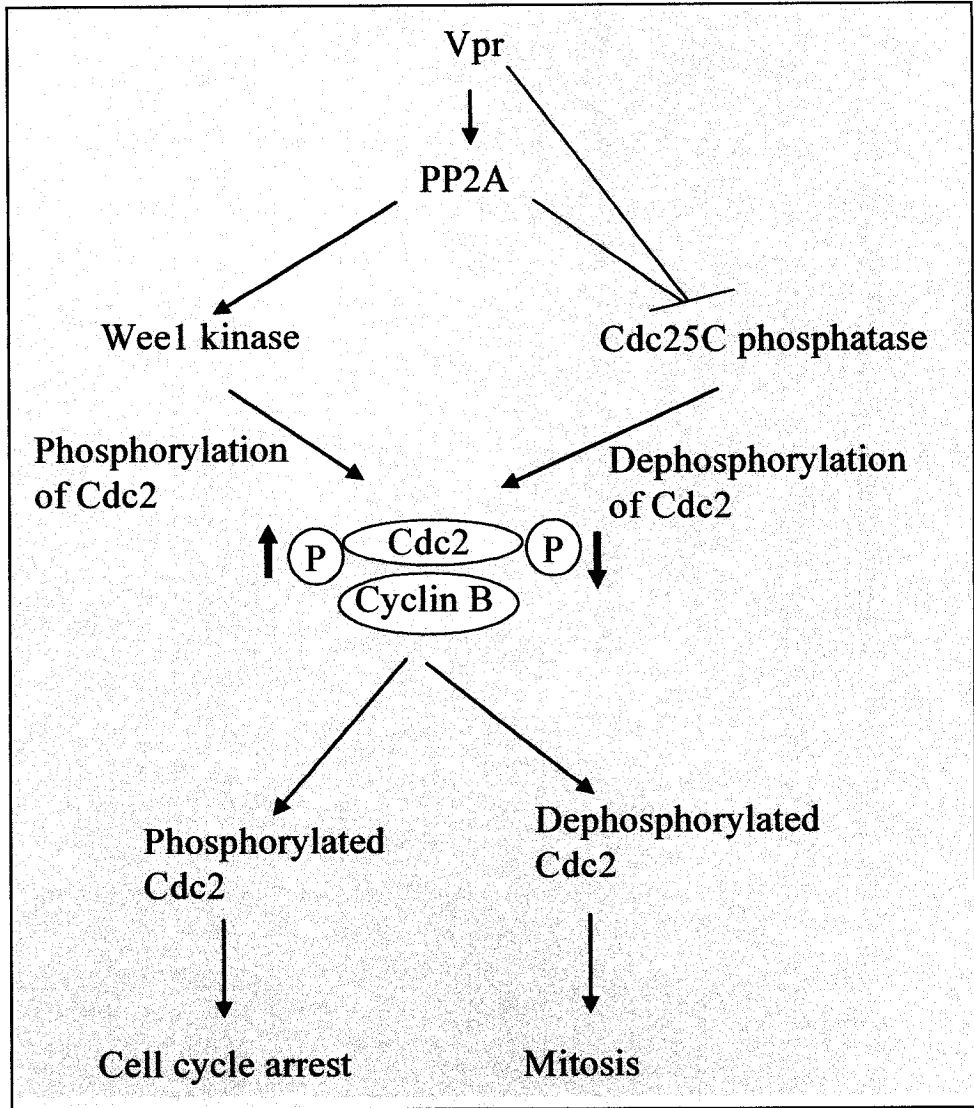


## **2) Vpr and cell cycle arrest:**

Vpr inhibits cell proliferation and causes cell cycle arrest at G2/M phase in many human cells including primary CD4<sup>+</sup> T lymphocytes and T cell lines. Transcription for HIV-LTR has been reported to increase 4-fold when cells are arrested in the G2/M phase of the cell cycle. The complex of cyclin dependent kinase 2 (Cdc2) and cyclin B1 is the key regulator for the check point between G2 and M phase [111;112]. This process is regulated mainly by Wee1 kinase and cell division cycle 25C (Cdc25C) phosphatase and detailed in the Fig. 1.3. During interphase, Wee1 kinase and Cdc2 are localized in the nucleus, whereas Cdc25C phosphatase and cyclin B1 are in the cytoplasm. Normally during that time, Cdc2 kinase is hyperphosphorylated by Wee1 kinase and transported to cytoplasm where it makes complex with cyclin B1 [104;113]. This complex is the target for Cdc25C phosphatase before it enters into the nucleus. Vpr mediated cell cycle arrest is regulated by activating protein phosphatase 2A (PP2A) which in turn activates Wee1 kinase and dephosphorylates Cdc25C phosphatase (inactive form), so that Cdc2 in a hyperphosphorylated form is attached to cyclin B1 and remains in the cytoplasm [114]. There is other evidence to suggest that Vpr may mediate cell cycle arrest by activating the ATR DNA damage response pathway. The Rad17 and Hus1 protein involved in the ATR pathway are required for cell cycle arrest by Vpr which involves the phosphorylation of Chk1 and histone 2A variant X, eventually leading to dephosphorylation of Cdc25C phosphatase and its inactivation [115]. Vpr was also shown to bind Cdc25C directly and inhibit Cdc25C phosphatase activity, perhaps blocking cyclin-B1-Cdc2 redundantly with the ATR pathway [109].

**Fig. 1.3: HIV-Vpr induces cell cycle arrest:**

Vpr mediated cell cycle arrest is regulated by activating protein phosphatase 2A (PP2A), which in turn activates Wee1 kinase and dephosphorylates Cdc25C phosphatase (inactive form). Wee1 kinase phosphorylates cyclin dependent kinase (Cdc2); and Cdc2 binds to cyclin B in its hyperphosphorylated form and remains in the cytoplasm. Cdc25C phosphatase in its active form dephosphorylates Cdc2 and helps cyclin B to enter into nucleus to participate in cell cycle. Vpr also binds to Cdc25C phosphatase directly and inhibit its activity [116;117].



### 3) Vpr and apoptosis:

Vpr induced apoptosis was first documented by Stewart *et al.* (1997) in human fibroblast, T cells, and peripheral blood lymphocytes [34]. They reported that although apoptosis occurred following G2 cell cycle arrest, maintenance of cell cycle arrest is not essential for the cells to undergo apoptosis. However, the exact mechanism of Vpr induced apoptosis is not yet clear. There are several lines of thought supporting the involvement of mitochondria as the major pathway for induction of apoptosis.

***Role of Mitochondria in Vpr induced apoptosis:*** Vpr has been shown to induce apoptosis by modifying mitochondrial activity. Macreadie *et al.* (1997) has shown mitochondrial dysfunction in constitutively Vpr expressed cells [118]. They also observed that C terminal domain of Vpr which is involved in apoptosis is involved in mitochondrial dysfunction. The intact Vpr protein (1-96 aa) as well as its C terminal (52-96 aa) peptide target the mitochondrial apoptotic pathway resulting in its destabilization. When Vpr is added to the intact cell or purified mitochondria, it causes loss of mitochondrial membrane potential ( $\Delta\psi_m$ ), leading to release of Cyt C and AIF. Mitochondrial membrane potential is normally maintained by PTPC by asymmetric distribution of ions on both sides of the inner mitochondrial membrane. The C terminal moiety of Vpr specifically interacts with the ANT or to the VDAC/ANT complex, thereby creating a composite ion channel (PTPC) resulting in loss of  $\Delta\psi_m$  and induce apoptosis [102]. Muthumani *et al.* also reported loss of  $\Delta\psi_m$  in the viral delivered (adCMV-Vpr) Vpr in Jurkat cells [119]. Critical amino acids for interaction with ANT were identified as R73, R77, and R80. Vpr induced release of Cyt C interacts with Apaf-1 and procaspase 9 to create apoptosome, the caspase activation complex that causes

activation of other effector caspases such as caspase 3, 6 and 7 and downstream effects of apoptosis [120;121].

In addition to caspase 9, caspase 8 activation has also been reported by Vpr in NT2 neuron cell and Jurkat T cells [95;122]. The findings of both reports suggest that Vpr can be oligomerized and act as a ligand for any of the cell surface death receptor. However, another report contradicts this result [121] and it needs further investigation.

Although caspases play important role in Vpr induced apoptosis, in one report, Vpr induced apoptosis in caspase independent manner. Roumier *et al.* showed that either Apaf-1<sup>-/-</sup>, caspase9<sup>-/-</sup> or AIF<sup>-/-</sup> cells failed to overcome Vpr induced apoptosis [123]. However, overexpression of Bcl2 decreased the apoptotic activity of Vpr [123]. This suggests that Vpr induces apoptosis through a mitochondrial dependent but caspase independent manner.

***Indirect role of Vpr in apoptosis:*** Vpr induced mitochondrial apoptosis is not only activated by interaction of Vpr with ANT of PTPC, but also Vpr indirectly influences other signaling molecules to be involved in this pathway. Vpr is reported to increase the expression levels of procaspase 9/caspase 9 in adCMV-Vpr infected cells [124;125]. It also suppresses the activity of NFκB transcription factor [126;127] which is involved in transcriptional modification of several survival factors such as TRAF1, TRAF2, c-IAP1, c-IAP2, and XIAP. NFκB also regulates Bcl2 family of anti-apoptotic proteins such as Bcl2, BclXL and A1 [128]. The suppressive effect of Vpr on NFκB is by interaction of Vpr with glucocorticoid receptor (GR) through Vpr interacting protein (VIP-1). Vpr mediated activation of GR leads to inhibition of NFκB by upregulation of IκB [127].

***Extracellular Vpr and apoptosis:*** The effect of extracellular Vpr by using synthetic peptide was first observed by Macreadie *et al.* (1995) [103]. They found the C terminal domain of Vpr as cytotoxic domain which causes osmotic sensitivity, cell membrane permeabilization and cell death in yeast cell and these effects were dependent on the sequence HFRIGCRHSRIG containing two H(S/F)RIG motifs [118;129].

Recently, Vpr has been detected in the sera and cerebrospinal fluid of HIV-infected subjects at levels similar to those of p24 antigen [33;97;130]. Since extracellular Vpr is detected in CSF, it is presumed that Vpr is released from macrophages and microglia infiltrated into brain during HIV infection [33]. Astrocytes are also one more source from where Vpr is released [131]. Furthermore, circulating Vpr was found to be biologically active in inducing virion production from latently infected cells, induce apoptosis and depletion of bystander cells in lymphoid tissues during HIV infection [33;97;130]. Piller *et al.* conducted a number of experiments in neurons and their findings suggested that recombinant Vpr exhibited channel forming capacity in the living cell [89]. Extracellular Vpr either in the form of recombinant protein or synthetic peptide induces apoptosis in variety of other cell types including T cells. Finally, the interaction of Vpr with ANT of mitochondria was shown by using extracellular synthetic Vpr resulting in induction of MMP, rapid dissipation of  $\Delta\psi_m$ , and release of several apoptogenic factors such as Cyt C and AIF [101;102]. It is generally accepted that extracellular Vpr enters into the cell independent of any of the cell surface receptor, most probably by endocytosis [98].

***Vpr as negative regulator of apoptosis:*** Vpr not only causes apoptosis, but also inhibits apoptosis induced by other molecules depending on the cell condition and dose

of Vpr. Several studies showed that low level of Vpr protects cells from apoptosis induced by either cyclohexamide, TNF, anti-Fas antibody, serum starvation through upregulation of Bcl2 and downregulation of Bax [26;132;133]. One group of investigator suggested that Vpr enhances the expression of survivin, one of the IAPs after inducing G2/M cell cycle arrest, resulting in the inhibition of apoptosis [134]. On the other hand, several studies showed that high level expression of Vpr results in induction of apoptosis [34;35]. Based on all these findings, it appears that during early stage of infection, when Vpr is expressed at low level, it protects infected cells from external apoptotic stimuli and HIV induced cell death contributing to the destruction of host immune system and pathogenesis of AIDS. However, at the later stage, when high level of Vpr is expressed, Vpr spontaneously induced apoptosis in the infected cells [27].

***Role of anti-apoptotic genes in Vpr induced apoptosis:*** It has been observed that the PTPC induced by Vpr is prevented by coculturing cells with recombinant Bcl2 by inhibiting ANT/Vpr interaction [101]. However, in one occasion, Bcl2 expression did not prevent the infected Jurkat cells to undergo Vpr induced apoptosis [124]. In addition to Bcl2, HAX1 (hematopoietic lineage cell specific protein 1- associated protein X-1), an anti-apoptotic factor is found to be the new mitochondrial target for Vpr [125]. The role of other pro-apoptotic proteins such as Bak and Bax in Vpr mediated apoptosis remains undetermined. IAPs are also known to inhibit apoptosis by interacting with caspases, however, their role in Vpr induced apoptosis is not known.

***Signaling pathways involved in Vpr induced apoptosis:***

The mitogen-activated protein-kinase (MAPK) family is a well characterized signaling pathway that transmit extracellular signal into the nucleus and regulate diverse

biological functions including cell proliferation, differentiation and survival/death [135]. The activation of c-Jun-N-terminal kinase (JNK) MAPK is most frequently associated with inhibition of cell growth and induction of apoptosis, whereas p38 and extracellular signal regulated kinase (ERK) MAPK are for cell survival [135;136]. Very little is known about the intracellular signaling molecules activated by Vpr and their involvement in Vpr-induced biological effects, particularly in apoptosis. Recently, the Vpr52-96 peptide was shown to activate JNK MAPK and was implicated in enhanced HIV-1 replication in chronically infected U1 promonocytic cells [137]. Also, Yoshizuka *et al.* demonstrated that Vpr-induced cell cycle arrest was associated with the down regulation of the ERK MAPK pathway in the 293 fibroblast cells [138]. The signaling pathway involved in Vpr52-96 induced-apoptosis in human monocytes is not known and will be investigated in this research project.

### **Role of LPS in apoptosis:**

LPS, a structural component of the outer membrane of Gram-negative bacteria is a potent inducer of wide variety of proinflammatory cytokines (TNF- $\alpha$ , IL-1 $\beta$ ) and prevents monocyte/macrophage apoptosis [139;140], however, in the absence of appropriate stimulation, monocytes are programmed to undergo cell death [141]. The mechanism by which LPS confers anti-apoptotic signals in monocytic cells is poorly understood. LPS may rescue monocytic cells from apoptosis directly through the activation of the CD14/TLR complex or indirectly via the induction of cytokines such as TNF- $\alpha$  in an autocrine manner [140;141], suggesting a key role for TNF- $\alpha$  in cell survival. It has also been seen that *in vitro* infection of purified monocytes with low doses of *Mycobacterium tuberculosis* markedly reduced spontaneous apoptosis of monocytes

by releasing TNF- $\alpha$  [142]. TNF- $\alpha$  is known to play an important role in inflammation, however, it also induces apoptosis when NF $\kappa$ B signal is blocked.

In general, pro- and anti-apoptotic proteins are involved in inducing apoptosis and also mediate resistance following apoptotic triggers. By now, there are two major families of proteins; Bcl2 and IAP involved in this process. Further, I will discuss more in details about these two families of proteins.

### **Bcl2 and its regulation:**

Bcl2, one of the anti-apoptotic gene was first identified at the chromosomal translocation breakpoint between chromosomes 14 and 18 (t 14;18) in non Hodgkin's follicular B cell lymphoma. It plays an important role in apoptosis by preventing release of Cyt C from the intermembrane space of mitochondria [143]. There are various studies conducted on Bcl2 to determine its anti-apoptotic activity in various cell types, however, little is known about its transcriptional regulation and post translational modification. Bcl2 is expressed in a wide variety of fetal tissues, whereas in adult, it is restricted to more proliferating and differentiating cells. It is a 26 kD protein encoding 237 amino acids and contains all four BH (BH1-4) domains [73;74]. This gene can be upregulated by IL-7 [144] and tumor suppressor p53 [145]. Bcl2 is tissue specific and it undergoes distinct type of phosphorylation catalysed by several kinases. Recent studies have shown that phosphorylation of Bcl2 at Ser 70 residue by its agonist confer its full anti-apoptotic potential, at least in murine IL3 dependent myeloid cell line [146;147]. However, the antimitotic drugs such as paclitaxel, and taxane are found to inhibit anti-apoptotic effect of Bcl2 and triggers cell death by phosphorylating Bcl2 at multiple sites including Thr69, Thr74, Ser70, and Ser87 [147-149].

The Bcl2 gene is unusually large and contains three exons, extending over 200 kb [150]. Two promoter regions have been identified in the 5' untranslated region of Bcl2 gene: P1 and P2. P1, which is present in most cell types and located 1386-1423 bp upstream of translation start site [150] and displays multiple start sites and includes several consensus binding sites for Sp1 transcription factor [151]. There is also one cAMP responsive element (CRE) site in P1 promoter of t(14;18) translocated cells as well as in normal cells which controls Bcl2 levels via the activation of a transcription factor CREB [152]. There are several NFκB binding sites in the P1 promoter of Bcl2 in B cell lymphoma cell line and in t(14;18) lymphoma cells [151;153]. P2, which is the predominant promoter in neuronal cell is located 1.3 kb downstream of P1 promoter and displays two discrete initiation sites. There is evidence to suggest that Bcl2 gene is transcriptionally regulated by NFκB and a myb family of transcription factor present in its P2 promoter region [151;154;155]. Between P1 and P2, multiple non overlapping negative regulatory elements exist in Bcl2 promoter [156].

Many of the Bcl2 family of anti-apoptotic and pro-apoptotic genes are differentially regulated in various malignancies, autoimmune diseases, and neurodegenerative disorders and some of them are used as diagnostic marker. It has also been reported that HIV induced apoptosis of T helper cells by downregulation of Bcl2 protein and simultaneous upregulation of bax [75;157]. Deregulation of Bcl2 family members has been tightly linked to tumorigenesis [158]. Anti-apoptotic Bcl2 protein is upregulated in B cell lymphoma and contributes to tumorigenesis by preventing cell death rather than by causing cell proliferation. Overexpression of Bcl2 is also associated with distinct type of tumors including prostate, colon, lungs, breast, gastric cancer, renal

cancer, neuroblastoma, non-hodgkin's lymphoma, leukemia, and skin cancer [75]. In most cases overexpression of Bcl2 is associated with resistance to chemotherapeutic and irradiation treatment.

### **IAPs:**

The prototype IAP was first discovered in the baculoviruses by Lois Miller and colleagues in 1993 [159]. So far, there are eight mammalian homologous of IAPs: XIAP, NAIP, c-IAP1 (HIAP2), c-IAP2 (HIAP1), Livin (ML-IAP, KIAP), Survivin, Ts-IAP and Apollon (Bruce) [85;160-163]. The IAP family of proteins is distinguished by the presence of one to three baculovirus inhibition repeats (BIR) domains that are positioned at the N terminal region and most of them also possess a carboxyl terminal ring finger motif [163;164] (Fig 1.4). The BIR domain is characterized by its cysteine and histidine-rich protein folding domain and forms a compact globular structure. The ring zinc finger domain is found at the carboxy terminus of most of the IAPs that functions as E3 ubiquitin ligase. The first mammalian IAP homologue to be identified was neuronal apoptosis inhibitor (NAIP) protein, which was isolated during a positional cloning effort to identify the causative gene for neurodegenerative disease spinal muscular atrophy [162]. Subsequently, c-IAP1, c-IAP2, and XIAP were identified with 3 BIR domains and a carboxy terminal zinc finger domain [160;161;165]. The IAP family of protein further continued to expand with the identification of survivin, Livin, Ts-IAP and Apollon [85;163].

When compared with other anti-apoptotic proteins, IAPs were found to protect cells against broad spectrum of apoptotic signals by inhibiting the terminal effector caspases 3, 7, and 9 [166-168] (Fig. 1.1). XIAP, c-IAP1 and c-IAP2 are shown to bind

and potently inhibit caspases. Caspase 3 and 7 are inhibited by BIR2 linker and BIR2 domain, whereas caspase 9 is inhibited by BIR3 domain [169]. In low apoptotic stress, the IAPs containing ring finger domains trigger ubiquitination of caspase 3, 7, and 9 which leads to degradation of IAP/caspase complex [170]. On the other hand, in response to lethal apoptotic stress, endogenous IAPs are saturated by interaction with Smac and/Omi which will lead to cell death by proteasome mediated degradation of IAP/Smac or IAP/Omi complexes [163;170]. In addition to caspase inhibition, XIAP, and c-IAP1 are reported to be degraded by caspases making these proteins pro-apoptotic and it happens at the late stage of apoptosis [170]. Unlike in XIAP, c-IAP1 and c-IAP2 contain a caspase recruitment domain (CARD) located between the BIR and RING finger domains [85;171]. The CARD domain may help in recruitment of c-IAP1 and c-IAP2 to the TNFR2 signaling complex. However, the function of CARD domain is not clearly known.

c-IAP2 is 8.7 kb length (70 kD) and is contained within eight coding and two non coding (5' UTR) exons [172]. The 4.5 kb c-IAP1 (68 kD) message is contained within eight coding region exons and a single 5' UTR exon [172]. The c-IAP1 and c-IAP2 genes lie in tandem at chromosome location 11q22-23 with the intrinsic distance being approximately 7 kb, a locus associated with development of leukemia and lymphoma [173]. The c-IAP1 and c-IAP2 share homology of greater than 75% at both the nucleotide (coding region) and amino acid level. It suggests that the c-IAP1 and c-IAP2 genes originate from a gene duplication event. The c-IAP1 mRNA is expressed high in adult skeletal muscle, pancreas, thymus, and testis, whereas expression of c-IAP2 is high specifically in lymphoid tissues.

**Fig. 1.4: IAPs and their domains:**

The IAP family of proteins contains one to three baculovirus inhibition repeat (BIR) domains that are positioned at the N terminal region. The BIR domain is characterized by its cysteine and histidine-rich protein folding domain and forms a compact globular structure. The ring zinc finger domain is found at the carboxy terminus of some of the IAPs that functions as E3 ubiquitin ligase. Only c-IAP1 and c-IAP2 contains CARD domain and its function is not well known [163].

**XIAP**

**TS-IAP**

**c-IAP1**

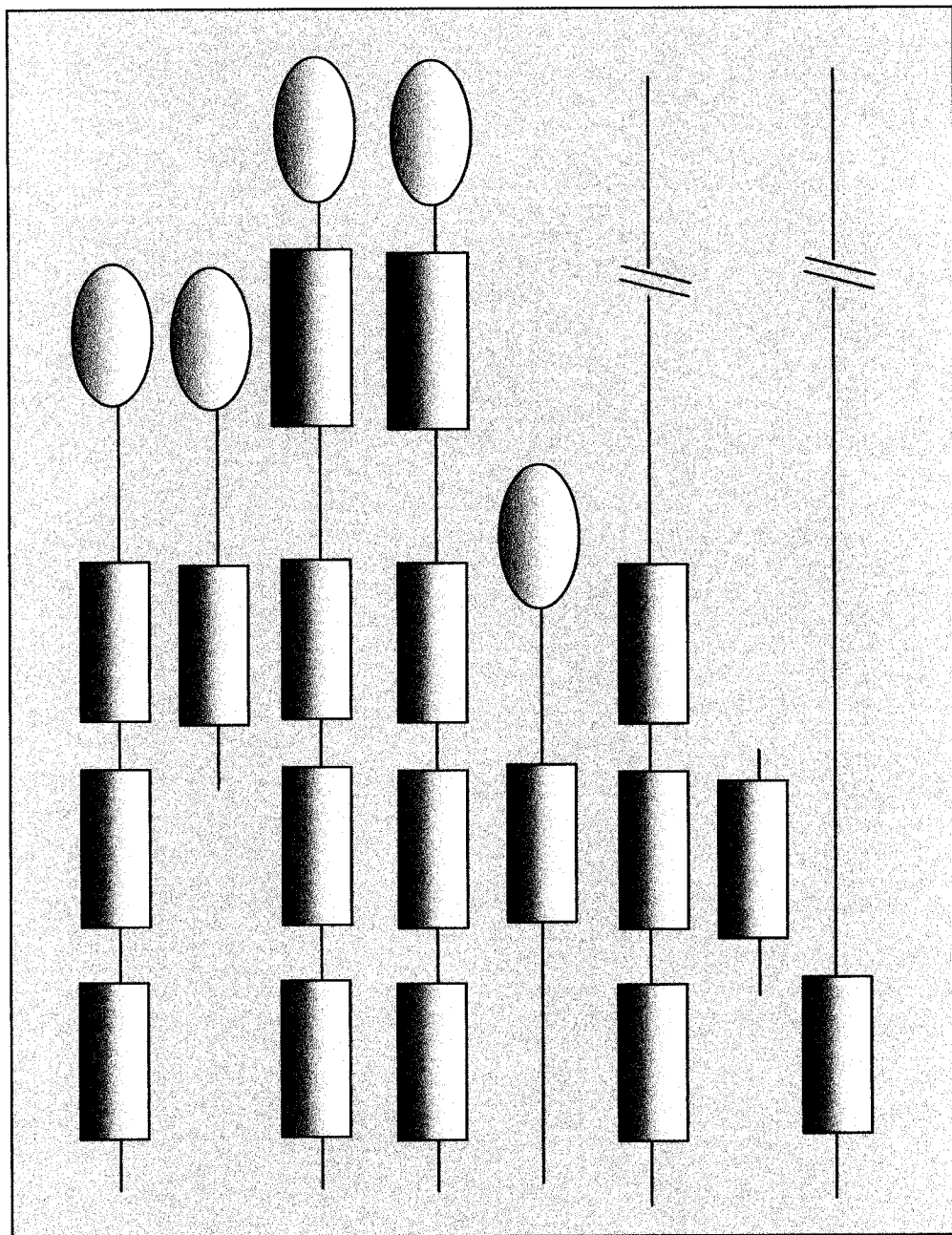
**c-IAP2**

**ML-IAP**

**NAIP**

**Survivin**

**Apollon**



■ BIR domain  
■ CARD domain  
○ RING Finger domain

### ***Role of IAPs in diseases:***

The existence of multiple IAP proteins and their expression pattern suggests specific roles in promoting cell survival during development and tissue homeostasis. In addition to that, the induction of IAPs plays a key role in the regulation of cells susceptibility to death in cancer therapeutic [170;171;174]. Among all the IAPs, XIAP (57 kD, 9.0 kb in length) is probably the best characterized IAP and is a potent inhibitor of cell death (review) [169;175]. There is also mounting biochemical and genetic data to suggest that c-IAP1 and c-IAP2 are key regulators of apoptosis within the cell and are overexpressed in many cancer cell lines [176].

Chromosomal amplification of 11q21-q23 region which encompasses both c-IAP1 and c-IAP2 has been observed in variety of malignancies including medulloblastomas, renal cell carcinoma, glioblastoma, gastric carcinomas, and non small cell lung carcinoma [85;177;178]. In esophageal squamous cell carcinoma, these genes are amplified and c-IAP1 is constantly overexpressed. There is also genetic evidence linking c-IAP2 to disease states comes from discovery that the t(11;18) (q21;q21) translocation is responsible for 50% of the mucosa associated lymphoid tissues lymphoma (MALT lymphoma) where they encode a chimeric protein containing c-IAP2 BIR domain and carboxy terminus of MALT1 [179-181]. The majority of gastric MALT lymphomas also display c-IAP2-MALT1 translocation. Overexpression of IAP proteins including c-IAP1 and c-IAP2 have been shown to suppress apoptosis in different disease model such as sciatic nerve axotomy, optic nerve axotomy, and Parkinson's disease.

### ***Regulation of IAPs by immunoregulatory molecules:***

There is evidence to suggest that LPS and TNF- $\alpha$  induce c-IAP1 and c-IAP2 in a variety of cell types and inhibit apoptosis [139;182-186]. After TNF- $\alpha$  stimulation, steady state level of c-IAP2 transcripts are markedly elevated in Jurkat T cells, whereas expression of c-IAP1 transcripts are unaffected [182]. However, XIAP, c-IAP1 and c-IAP2 are strongly upregulated in TNF- $\alpha$ /IL-1 $\beta$ /LPS stimulated human primary endothelial cells, which are resistant to variety of apoptotic death stimuli [186]. In neutrophils, c-IAP1, c-IAP2, and XIAP are expressed in various levels. However, in response to G-CSF, c-IAP2 is upregulated selectively and it is associated with G-CSF mediated antiapoptosis. There is also remarkable overexpression of c-IAP2 mRNA in chronic neutrophilic leukemia (CNL) patient and that raises the possibility of prolonged survival of neutrophils in CNL patients. Besides LPS and cytokines, other immunoregulatory molecules [187], stress [188;189] or bacterial infection also induce c-IAP2 expression. However, regulation of IAP genes by either cytokines or LPS (bacterial infection) in monocytes is not well understood. There is at least one report demonstrating the upregulation of c-IAP2 in LPS stimulated monocytes and macrophages, suggesting that LPS may protect macrophages from apoptotic cell death through induction of c-IAP2 and provide a mechanism to maintain immune function of macrophages [190].

### ***Signaling molecules involved in the regulation of IAPs:***

It is believed that activation of NF $\kappa$ B leads to upregulation of many TNF responsive genes including c-IAP2 and XIAP [186;191]. There is also strong evidence to suggest the involvement of NF $\kappa$ B transcription factor in upregulation of IAP proteins in a

number of cell types in response to LPS, TNF- $\alpha$  and IL-1 [182;186]. In addition, there are reports to suggest that stress (polyamine depletion or by X-ray induction) [188;189] and bacterial infection (*C. pneumoniae* and *H. pylori*) [192;193] induced c-IAP2 through activation of NF $\kappa$ B pathway

Recently, several reports have appeared which suggests that c-IAP2 and XIAP can act as upstream signaling molecules to regulate the activation of NF $\kappa$ B. Furthermore, two members of the IAP gene family (c-IAP1 and c-IAP2) have been shown to be involved in TNF- $\alpha$  signaling [161]. XIAP has also been shown to act as a potent activator of NF $\kappa$ B in endothelial cells. The mechanism by which XIAP target NF $\kappa$ B involves the activation of MAP3 kinase TAK1 [194]. On similar lines, selective activation of JNK in human embryonic kidney cells was found necessary for the anti-apoptotic activity of XIAP but not that of c-IAP1 and c-IAP2 [194-196].

Expression of c-IAP2 has been suggested to be regulated by multiple regulatory elements in its promoter region [182;186;191]. In addition to NF $\kappa$ B, c-IAP2 induction was recently shown to be regulated through a putative glucocorticoid response element in A549 human lung cancer cells in response to stimulation with dexamethasone [197]. In another study, the cAMP responsive element was shown to be vital for c-IAP2 induction in T84 colon cancer cells [198]. Recently, c-IAP2 expression was found to be regulated by ERK MAPK, p38 MAPK, and protein kinase C- $\delta$  (PKC- $\delta$ ) in human colon cancer cells [198;199]. In addition, phosphatidylinositol 3-kinase (PI3K) and ERK MAPK were implicated in endoplasmic reticulum (ER) stress-induced cell death, whereas the Janus Kinase2 (Jak2)-signal transducers and activators of transcription-3 (STAT-3) pathway was suggested to regulate G-CSF-stimulated c-IAP2 expression in human neutrophils

[200]. However, the molecular signaling mechanism by which c-IAP2 is induced in monocytes in response to various stimuli such as TNF- $\alpha$  and endotoxin (LPS) is not well understood.

### **Signaling pathways involved in response to cytokines:**

Signal transduction involves the transmission of biochemical information from external environment into the nucleus of cell. Cytokines are small secreted proteins which act by binding to specific receptors expressed on the target cells and then signal the cell via second messengers, most often by tyrosine kinases to alter the expression of variety of genes [201]. Cytokines may act on the cells by autocrine manner, or on the nearby cells by paracrine manner [202].

Cytokines are basically divided based on the structure of their receptors [203]. The major subset of cytokine receptor (Class I receptor) family includes receptor for most of the interleukins, colony stimulating factors, growth hormone, and prolactine. The class II cytokine receptor family includes receptors for IFNs and IL10 [204;205], whereas Class III is for TNF and related family of proteins [206]. The receptors for IL1 and related family of proteins come under class IV receptor [207]. Immunoglobulin superfamily includes receptor for SCF, M-CSF, PDGF, and VEGF [208]. Upon binding of cytokines to their respective receptors transmit the signals into the cell that is associated with protein-protein interactions and the generation of second messenger molecules (Fig. 1.5). Two major mechanisms play significant role as molecular switches in cytokine receptor signaling. One is guanine nucleotide binding proteins (G proteins) such as Ras, and Rac which oscillates between inactive (GDP bound) forms to active (GTP bound) form [209;210]. The signal is terminated when GTPase hydrolyzes and

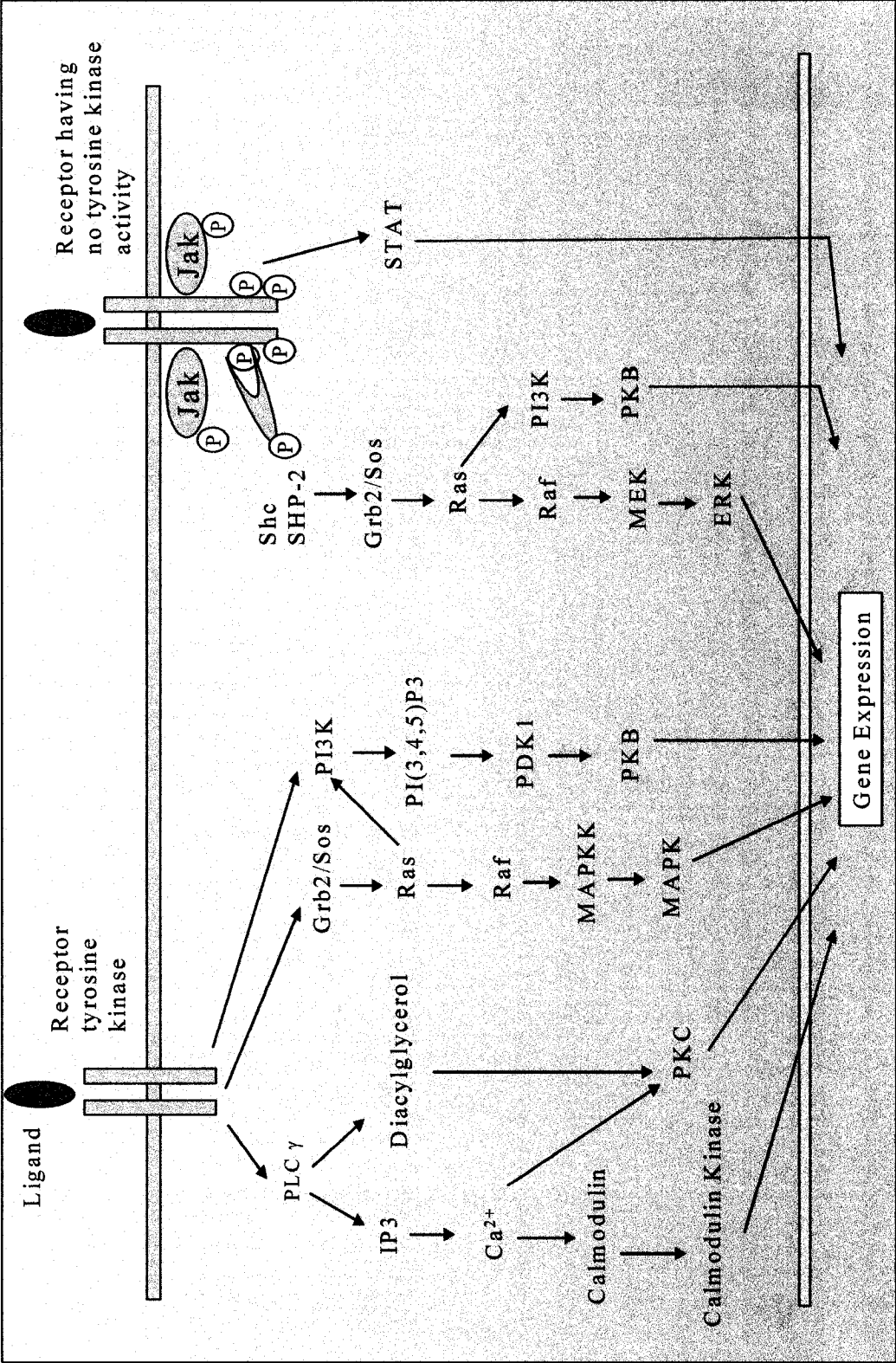
converts GTP to GDP [210]. Other mechanism is protein phosphorylation which is classified into two types: serine/threonine and tyrosine phosphorylation. Phosphorylation state of the molecule is determined by the activity of protein kinase and it also creates docking site for other signaling molecules. Type I and II receptors do not have any known enzymatic activity such as kinases or phosphatases. Therefore, cytoplasmic tyrosine kinases such as Jak associated with the cytoplasmic domain of type I and II receptors play a critical role in transmitting signals [211-213].

The immunoglobulin family of receptors has intrinsic tyrosine kinase activity. Ligand binding induces autophosphorylation of tyrosine residues of these receptors and this in turn creates docking sites for multiple signaling molecules with SH2 and PTB domains [214].

Small G protein Ras is activated by several growth factors and also by type I receptor family of cytokines [215]. In general, ligand binding to receptor induces phosphorylation of tyrosine. The phosphorylation serves as a docking site for Grb2/SOS (son of sevenless) complex which will lead to recruitment of SOS to the plasma membrane, where it can encounter Ras [216;217]. Activated Ras has several effectors of which serine/threonine kinase Raf and its downstream MEK (MAPK-ERK) cascade is activated [216;218]. It also binds directly to the p110 $\alpha$  catalytic subunit of PI3K and increase the lipid kinase activity of PI3K [216]. Ras mediated signaling is not only confined to plasma membrane but also occurs on golgi apparatus, endoplasmic reticulum and mitochondria [219;220].

**Fig. 1.5: Generalized intracellular signal transduction pathways:**

Upon binding of ligands to their respective receptors, signal is transmitted into the cell. As shown in the figure, there are two different mechanisms involved in this process, one is through the receptors having tyrosine kinase activity and the other one is without tyrosine kinase activity. Ligand binding induces autophosphorylation of tyrosine residues of these receptors and this in turn creates docking sites for multiple signaling molecules with SH2 and PTB domains. Grb2/SOS complex binds to the docking sites which will lead to recruitment of SOS to the plasma membrane, where it encounters Ras. Activated Ras has several effectors including Raf and its downstream MEK (MAPK-ERK). It also binds directly to the p110 $\alpha$  catalytic subunit of PI3K and increases the lipid kinase activity of PI3K. Phosphorylated receptor also activates phospholipase C $\gamma$  (PLC $\gamma$ ) which in turn activates the PKC pathway and the calcium signaling pathway. The receptors having no known enzymatic activity are activated by phosphorylation of Jak which is associated with the cytoplasmic domain of the receptors. As shown in the figure, the receptor then creates docking sites for various signaling molecules to transduce the signal inside the cell. Jak also activates STAT, one of the transcription factors for gene expression.



### ***MAPK pathway:***

The MAPK signaling pathway is the evolutionally well conserved signaling pathway activated by a variety of extracellular stimuli such as growth factor stimulation and plays a major role in cell differentiation, cell division and cell death and survival [221]. The signaling pathway can be schematically divided into membranous and cytoplasmic phases. The first one occurs in close proximity to the growth factor receptors and involves the activation of a small GTP binding protein (Ras) via the adapter molecule Grb2 [217]. The MAPK family is grouped into three subfamilies: ERK, p38 MAPK and JNK [222]. The MAPK cascade is a three tier system which is initiated by activation of MAPK kinase kinase (MAPKKK) [135;223]. The activated MAPKKK is a protein kinase and acts in turn on MAPK kinase (MAPKK) which follows the activation of specific MAPK [135;222]. MAPK pathway is detailed in Fig 1.7 along with the specific inhibitors mentioned in separate box.

**ERK:** The ERK pathway is activated by a number of extracellular stimuli including growth factors, LPS, and chemotherapeutic agents [223]. ERK activation is associated with cell proliferation, activation and differentiation [224]. In most cases, ERK activation protects cells from drug induced cell death, but in others it contributes to cell death. The outcome of ERK activation solely depends on the type of cell and stimuli. ERK is made up of two isoforms, ERK1 and ERK2 (commonly called as ERK1/2) [218;225]. The activation of ERK is initiated by activation of Raf (MAPKKK) followed by activation of MEK1/2 (MAPKK) which in turn activates ERK1/2 [224]. Raf is a highly conserved kinase that is activated by the G protein Ras in association with Grb2-

SOS complex [224]. ERK1/2 has been shown to activate transcription factors such as Elk-1 and STAT3 following translocation into the nucleus [226;227].

**p38 MAPK:** p38 is activated primarily by cellular stresses, endotoxin and ultraviolet exposure [228]. In some instances, activation of p38 is associated with cell death, in others as cell protection [229]. There are five different isoforms of p38 namely p38 $\alpha$  (SAPK2), p38 $\beta$ , p38 $\beta$ 2, p38 $\gamma$  (SAPK3), and p38 $\delta$  [228;230]. Expression of different isoforms of p38 is tissue specific. p38 $\alpha$  is expressed in leukocytes and bone marrow, p38 $\beta$  is expressed in heart and brain, and p38 $\gamma$  is expressed predominantly in skeletal muscle [230;231]. External stimuli initiate activation of small G protein (RAC1 and CDC42) followed by activation of MAPKKK including MEKK4, ASK1, and TGF $\beta$  activated protein kinase 1 (TAK1) [232]. These serine/threonine kinases phosphorylate and activate the MAPKK3, MKK4, and MKK6 which in turn phosphorylate p38 on Thr 180 and Tyr 182 [232]. Major substrates for p38 include MAPK activated protein kinase-2 (MAPKAP-K2) and MAPKAP-K3 [233]. p38 also phosphorylates and activates the transcription factors ATF-2 and SP1 [234].

**JNK:** JNK is preferably activated by various environmental stresses such as UV irradiation, hyperthermia, oxidative stress, protein synthesis inhibitors, inflammatory cytokines, and chemotherapeutic agents [235]. It is also induced by cytotoxic drugs and is associated with cell death. The JNK group of MAPK is encoded by three genes: *jnk1* and *jnk2* genes which are ubiquitously expressed, and the *jnk3* gene, expressed primarily in the heart, testis, and brain [235]. The immediate upstream kinases for JNK activation are two MAPKKs, MKK4 and MKK7 (SEK1) which possess dual specificity on Thr 183 and Tyr 185 [235]. Upstream of MAPKK, several MAPKKKs have been identified including

MEK kinase 1 (MEKK1), MEK kinase 4 (MEKK4), apoptosis signal regulated kinase (ASK1)/ MKKK5, and MUK/DLK/ZPK [235]. Activated JNK phosphorylates ATF-2, Elk-1 and c-jun [236;237]. Thus, JNK plays an important role in activation of the transcription factor AP-1 which is made up of either c-jun and c-fos heterocomplex or c-jun homodimer [236;237]. Activation of JNK plays an important role in T cell proliferation, differentiation and IL-2 production [235].

### ***PI3 Kinase Pathway:***

PI3 kinase plays an important role in cell survival and deregulation of this process influences numerous cellular responses which are associated with cancer phenotypes [238]. This family of enzymes is activated by growth factor receptor or by small GTPase Ras and produces 3' phosphoinositide lipids [238;239]. PI3 kinase is involved in phosphorylation of phosphatidylinositol (Ptdins) on the third carbon of the inositol ring [238;240]. The phosphorylation of Ptdins to Ptdins-3-P and Ptdins-3,4,5-P is a part of many signal cascade in a cell. The lipid products of PI3K act as second messengers by binding to and activating diverse cellular target proteins which leads to cell proliferation, differentiation, chemotaxis, survival, and trafficking [241-243]. Ptdins (3, 4) P2 and Ptdins (3, 4, 5) P3 lipids produced by PI3K are able to bind Akt recruiting it to the plasma membrane where PDK1 and PDK2 phosphorylate it to its active form [238;243]. Phosphorylated Akt targets the proteins involved in apoptosis/cell death including Bcl2 and caspase 9 and protects cell from undergoing apoptosis. The PI3 kinase is divided into 4 different classes, namely Class Ia, Ib, II, and III based on their structure and substrate specificity [238]. All of them contain one catalytic domain and one regulatory domain. Class Ia enzymes consists of any one of the catalytic unit (p110 $\alpha$ , p110 $\beta$ , and p110 $\delta$ )

complexed with any one of the regulatory subunits (p85 $\alpha$ , p85 $\beta$ , p55 $\gamma$ ) [242]. There is only one Class Ib enzyme exists and that contains p110  $\gamma$  catalytic unit and p101 regulatory subunit. Class II and III enzymes are not yet well characterized. Class Ia enzymes are activated by tyrosine kinases (e.g. growth factor receptor, antigen receptors), while the class Ib enzyme is activated by G protein coupled receptor [242].

### ***Ca<sup>2+</sup> signaling pathway:***

Ca<sup>2+</sup> is a highly versatile intracellular signal that can regulate many different cellular functions [244]. It may also synergize with other signaling pathways [245;246]. Fig.1.6 describes the calcium signaling pathway along with the specific pharmacological inhibitors highlighted in different color. One of the experimental evidence suggest the involvement of three cellular sensors of the cytosolic Ca<sup>2+</sup> levels such as calmodulin (CaM), PKC and the p21<sup>ras</sup> /PI3K/Akt pathway simultaneously links the Ca<sup>2+</sup> second messenger to NF $\kappa$ B activity [247]. PKC may integrate two types of signals, one coming from membrane receptors acting through PLC [248] and the second elicited by Ca<sup>2+</sup> for Ca<sup>2+</sup> sensitive PKCs [249]. The ras pathway acts similarly, integrating membrane receptor signals through G proteins and Ca<sup>2+</sup> signals through ras-GRF and it may activate PI3K [250;251]. Since ras activate MAPK cascade, I believe that Ca<sup>2+</sup> can activate MAPK through ras by ras GRF. CaM, a Ca<sup>2+</sup> activated protein regulates phosphatases and kinases, among which calcineurin and calmodulin kinaseII (CAMKII) have been reported to be involved in activation of NF $\kappa$ B in neuron cells [247]. Induction of NF $\kappa$ B by various stimuli has already been shown to require Ca<sup>2+</sup> for proper signal transduction [247;252;253]. Since Ca<sup>2+</sup> is upstream of all the major kinase signaling pathways, I

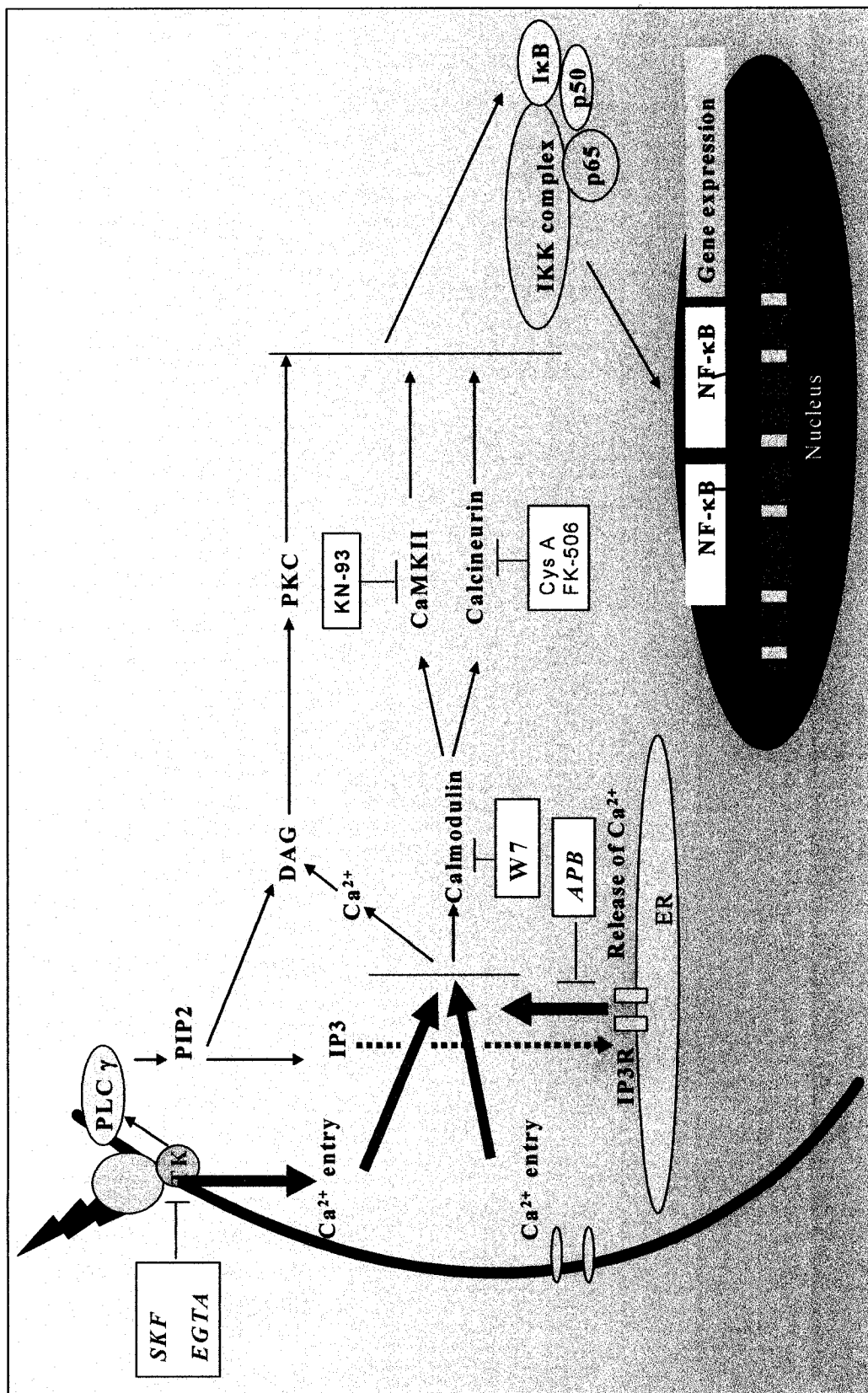
investigated the involvement of calcium signaling pathway in inducing resistance to HIV-Vpr mediated apoptosis in human monocytes.

### ***LPS Signaling Pathways:***

LPS is the principal component of the outer membrane of gram negative bacteria. It binds to the cell surface receptor CD14 present mostly on the myeloid cells including monocytes [254]. The interaction of LPS with CD14 is mediated by LPS binding protein (LBP) [255] which is present in plasma at 3-10 ng/ml, but level rises dramatically after an acute phase response. CD14 is also present in plasma in soluble form (sCD14) that helps in transducing signal mediated by LPS to the CD14 negative cells [256;257]. CD14 is expressed on the surface of myeloid cells via a glycosylphosphatidylinositol (GPI) tail, which anchors the protein to the membrane without a transmembrane segment responsible for transduction of signals into the cell [258;259]. It suggests that CD14 is not the LPS signaling receptor. The signal is mediated by toll like receptor 4 (TLR4) with leucine rich motif to the extracellular domain for interaction with the ligand such as LPS [260] (Fig. 1.7). In addition to TLR4, MD2 is associated with LPS signaling in monocytes. MD2 is also required for LPS activation of MAPK pathways [261;262]. LPS induced NF $\kappa$ B signaling is mediated by MyD88, IL-1 receptor associated kinase (IRAK), and TNF- $\alpha$  receptor associated factor (TRAF6) [263;264]. TRAF6 activates either MEKK1 or TAK1 that leads to phosphorylation of I $\kappa$ B kinase (IKKs). Normally, NF $\kappa$ B remains in the cytoplasm in association with I $\kappa$ B in a complex. The phosphorylated I $\kappa$ B kinase activates I $\kappa$ B and NF $\kappa$ B is released and translocated into the nucleus for further gene expression. Binding of LPS to TLR4 also induces PI3K activation without

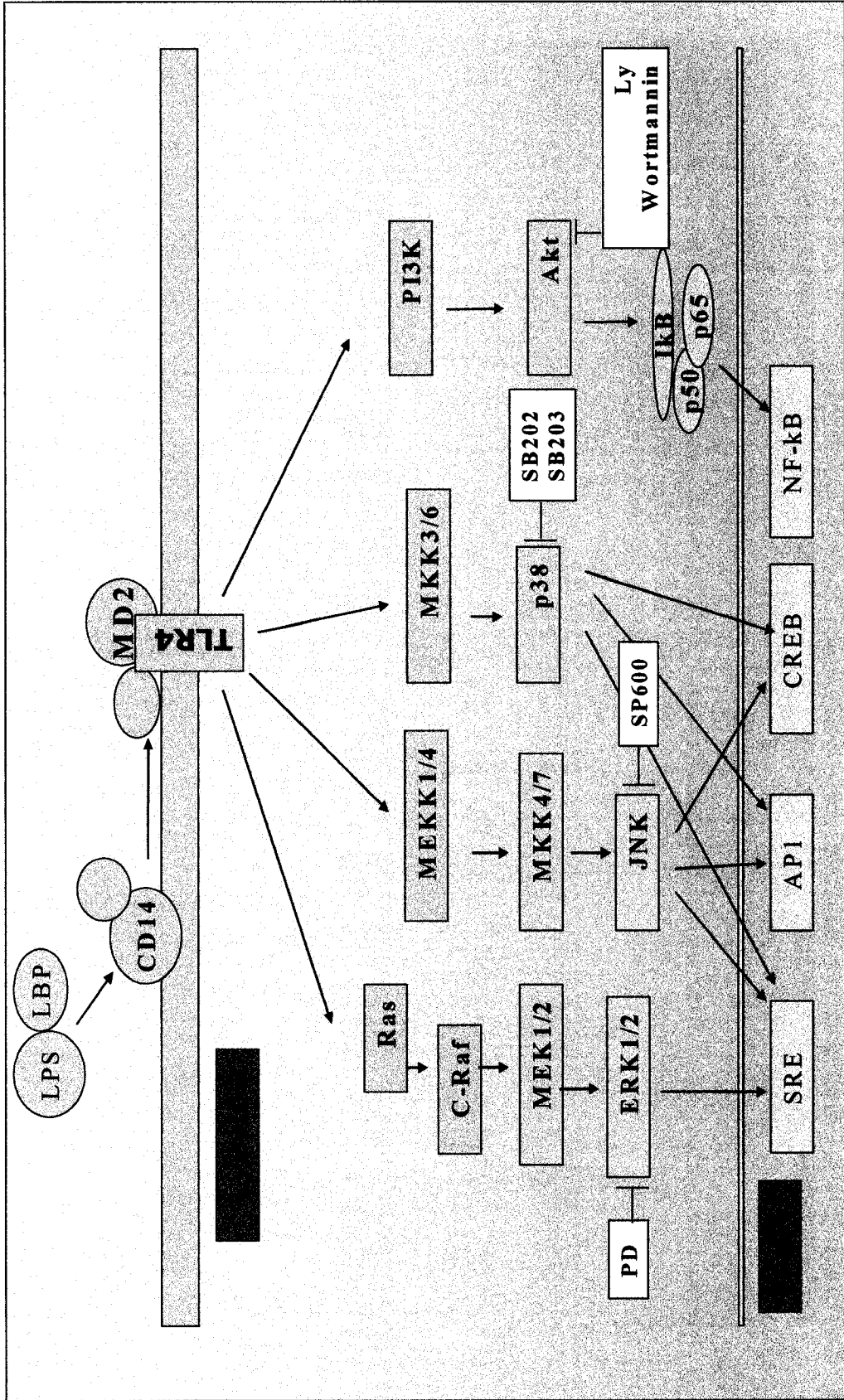
**Fig. 1.6: Calcium signaling pathway:**

Binding of ligand to respective receptor induces calcium influx either through receptor mediated entry or through voltage dependent ion channel entry from external source. There is also release of calcium from endoplasmic reticulum through binding of IP<sub>3</sub> to its receptor on endoplasmic reticulum. As shown in the figure, influx of calcium activates calmodulin followed by CAMKII and calcineurin which leads to activation of NFκB resulting in expression of various genes. Calcium also activates PKC pathway in association with diacylglycerol leading to NFκB regulated gene expression. The pharmacological inhibitors used to block the activity of specific signaling molecules are highlighted [247].



**Fig. 1.7: LPS signaling pathway:**

As shown in the figure, LPS, the principal component of the outer membrane of Gram-negative bacteria binds to LPS binding protein (LBP) which helps transport LPS to CD14. LPS then comes into contact both with TLR4 and MD-2, a small protein associated with the TLR4 ectodomain. The signal is then transmitted to various signaling molecules including MAPKs and PI3K. MAPK signaling cascades are organized hierarchically into three-tiered modules. MAPKs are phosphorylated and activated by MAPK-kinases (MAPKKs), which in turn are phosphorylated and activated by MAPKK-kinases (MAPKKKs). The MAPKKKs are in turn activated by interaction with the family of small GTPases and/or other protein kinases, connecting the MAPK module to cell surface receptors or external stimuli. The specific pharmacological inhibitors used in this study are mentioned in the yellow boxes [265].



involvement of MyD88, IRAK, and TRAF6 [265]. PI3K activates NF $\kappa$ B pathway [265], however the intermediate molecules are not so far identified.

In addition to PI3K and NF $\kappa$ B pathways, LPS also induces PKC and MAPKs signaling pathways in monocytes [266-268]. In response to LPS, tyrosine kinase in the cytoplasmic domain of receptor is phosphorylated which leads to activation of Ras-Raf-MEK1/2 followed by phosphorylation of ERK1/2 [269]. However, there is also evidence for LPS activation of ERK1/2 pathway in a c-Raf independent manner [270]. The substrates for ERK1/2 include Elk1, and SRF [271]. LPS also activates JNK pathway via activation of MEKK1/4 (MAPKKK) followed by MKK4/7 (MAPKK) [272]. The downstream signaling molecules in JNK pathway include c-Jun, ATF2 and Elk-1 transcription factors [273]. The upstream signaling molecules in LPS induced p38 signaling pathway include Cdc42, PAK, and Rac1 [263]. The MAPKKs involved in that cascade are protein kinase RNA regulated (PKR), ASK1, and TAK1 and the MAPKKs include dual specificity kinase MKK3/6 [274]. The p38 phosphorylates and activates transcription factors that include ATF2, Elk1, CHOP, and MEF2C [265].

### ***TNF Signaling Pathway:***

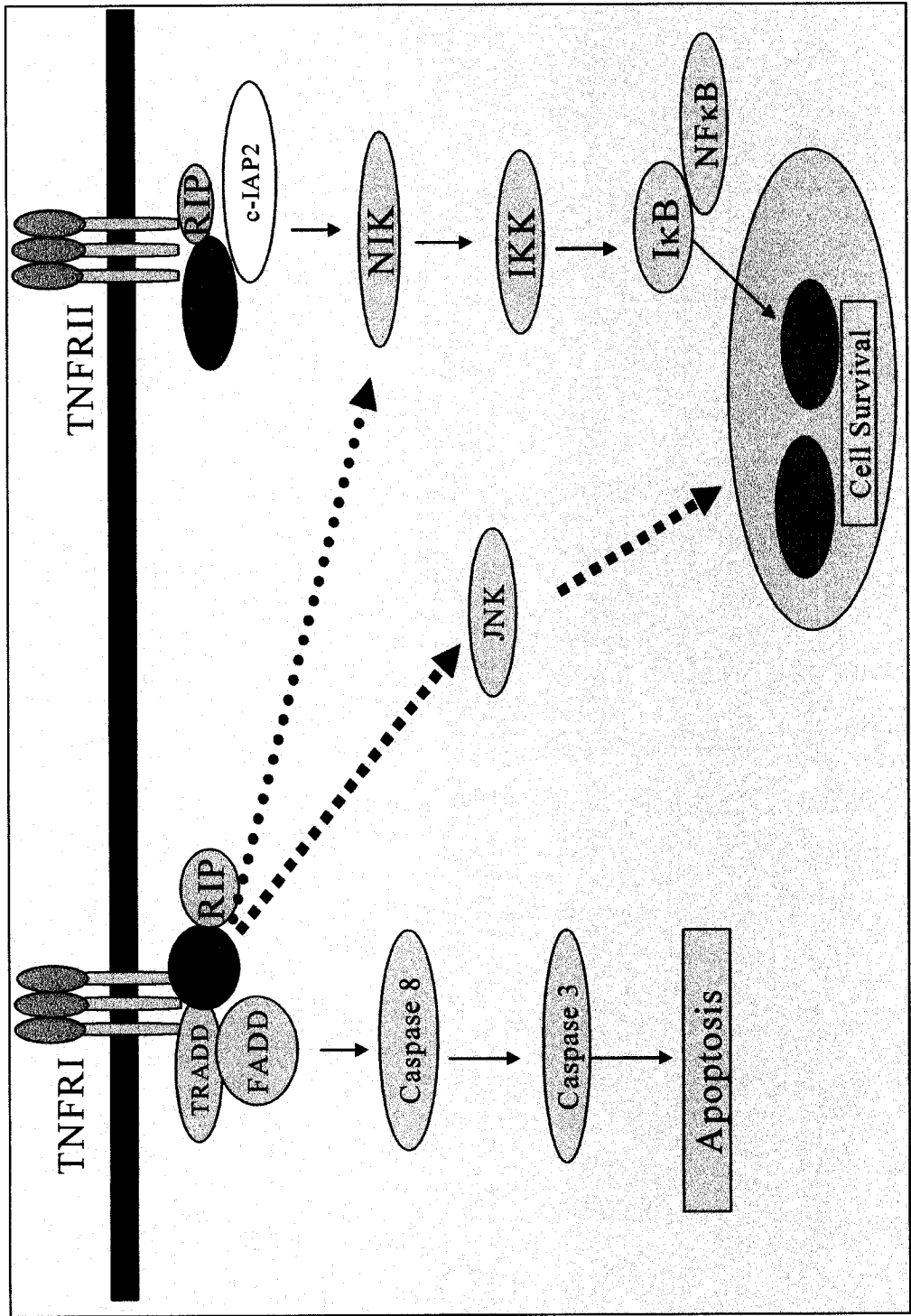
The class III cytokine receptor family mainly includes TNFR1, TNFR2, Fas, LT $\beta$ R, CD27, CD30, and CD40 [275;276]. The cytoplasmic part of the receptors in TNF receptor family has no known enzymatic activities. The activation of receptor involves trimerization of receptor following binding of trimeric ligands such as TNF- $\alpha$ , TNF- $\beta$  or Fas ligand. TNF- $\alpha$  is produced by monocytes, T and B lymphocytes [275;276]. It can also be produced by wide range of other cells. On the other hand, the main producers of

TNF- $\beta$  are only Th1 lymphocytes and some stages of B lymphocytes. TNFRI is expressed in all cell types, whereas TNFRII is quite restricted and expressed in only monocytes and lymphocytes. Both TNFRI and TNFRII are activated by TNF- $\alpha$ , and TNF- $\beta$ . In general, TNFRI and Fas induce apoptosis via caspase activation in response to their respective ligand binding in the cells where RNA or protein synthesis is blocked [277]. Fig. 1.8 describes the TNF signaling pathways in details. TNFRI and Fas possess an 80 amino acid death domain (DD) in the cytoplasmic portion of the receptor which transduces death signal inside the cell. The DD of TNFRI [277] interacts with DD of TRADD (TNFRI associated death domain), that results in recruitment of DD of FADD (Fas associated death domain) to this complex [278]. Then the death effector domain (DED) of FADD interacts with DED of caspase 8 and activates the caspase cascades to induce apoptosis. TNF not only induce cell death, but also activate NF $\kappa$ B pathway (for cell survival) by TNFRI and TNFRII receptors. Induction of NF $\kappa$ B by TNFRI involves the recruitment of TNF receptor associated factor2 (TRAF2) to TRADD, whereas TNFRII interacts directly with TRAF2 followed by recruitment of TRAF1 to that complex. TNF- $\alpha$  is shown to activate various signaling pathway including MAPKs, PI3K, PKC, and calcium signaling pathways and then from this cascade activation of AP1 and NF $\kappa$ B has been demonstrated.

I demonstrated that HIV-Vpr induces apoptosis in human monocytes by using the C-terminal domain of Vpr protein. I also showed first time that pretreatment of monocytes with LPS/TNF- $\alpha$  reversed back the process of apoptosis indicating the role of LPS/cytokines in monocyte survival in HIV infection. Further, I dissected the signaling pathways involved in HIV-Vpr induced apoptosis and determined the pro and anti-

**Fig. 1.8: TNF signaling pathway:**

Binding of TNF to TNFRI and TNFRII exerts two different kinds of signals. In TNFRI signaling, involvement of TRADD and FADD leads to activation of caspases and cells undergo apoptosis. On the contrary, when TRAF and RIP are involved, there is activation of JNK or NF $\kappa$ B pathway and cell survive. In TNFRII signaling, mostly there is involvement of TRAF and RIP which leads to NF $\kappa$ B signaling [275].



apoptotic genes involved in this process. Subsequently, I investigated the molecular mechanism involved in LPS/TNF- $\alpha$  induced resistance in Vpr mediated apoptosis along with the regulation of anti-apoptotic genes in survival of monocytic cells.

## **Rationale:**

Monocytes/macrophages are productively infected by HIV as are CD4<sup>+</sup> activated T cells, however, unlike T cells, monocytic cells survive HIV replication without major signs of HIV-induced cytopathic effects. Persistently infected monocytic cells serve as a major reservoir of HIV in lymphoid tissues at all stages of disease and represent a key challenge to eradicate HIV infection by eliminating virus reservoirs. It is believed that one of the reasons by which monocytic cells escape HIV cytopathic effects is the capacity of HIV to decrease the sensitivity of this cell type to apoptosis. This hypothesis was supported by a recent study demonstrating that nerve growth factor (NGF) produced following HIV infection can rescue monocytic cells from the cytopathic effects of HIV. Vpr, one of the accessory proteins of HIV induces apoptosis in monocytic cells. How monocytic cells develop resistance to apoptosis following HIV infection specifically by Vpr remains poorly understood. In my research work, I employed a synthetic peptide corresponding to the C-terminal 52-96 amino acid sequence of Vpr (Vpr52-96) as a model, because the apoptotic effect of Vpr has been shown to be mimicked by the C-terminal Vpr52-96 but not by the N-terminal Vpr1-51 moiety. My preliminary results suggest that Vpr52-96 peptide interestingly induced apoptosis in normal human monocytic cells as well as in the promonocytic THP-1 cells. Furthermore, this Vpr52-96-induced apoptotic effect in both cell types could be reversed by pretreatment of cells with LPS. These observations suggest that LPS or the cytokine produced endogenously by

LPS such as TNF- $\alpha$ , may be one of the critical factors responsible for protecting monocytic cells from the apoptotic effects of HIV-Vpr and consequently promoting monocytic cells to act as potent viral reservoirs. However, the molecular mechanism underlying the Vpr induced apoptosis and resistance mediated by LPS is not known and remains to be investigated.

### **Hypothesis:**

Vpr induces apoptosis through the activation of intracellular signaling pathways and by modulation of pro-or anti-apoptotic genes such as members of the Bcl2 and IAP family of genes. Furthermore, LPS or cytokines produced endogenously by LPS such as TNF- $\alpha$  protect human monocytic cells from HIV-Vpr-induced apoptosis by interfering with the intracellular signaling pathways and/ or the expression of pro-apoptotic/anti-apoptotic genes.

### **Aims and objectives:**

The main aim of this research project is to elucidate the intracellular signaling pathways involved in HIV-Vpr mediated apoptosis and the resistance induced by LPS in normal human monocytic cells and promonocytic THP-1 cell line using Vpr1-45 and Vpr52-96 peptides as models. The specific objectives of this research project are as follows:

- 1) To elucidate the signaling pathways involved in regulation of LPS mediated resistance to apoptosis in human monocytic cells.
- 2) To elucidate the signaling pathways involved in Vpr induced apoptosis and to identify the pro/anti-apoptotic genes involved in its regulation in human monocytic cells.

3) To identify the anti-apoptotic genes involved in LPS induced resistance in HIV-Vpr mediated apoptosis in human monocytic cells and to determine the intracellular signaling pathways involved in their regulation.

# **Chapter II**

## *Materials and Methods*

### **Cell line and cell culture:**

THP-1, a promonocytic cell line derived from a human acute lymphocytic leukemia patient, was obtained from the American Type Culture Collection (Manassas, VA) [279]. Cells were cultured in IMDM (Sigma-Aldrich, St-Louis, MO), supplemented with 10% FBS (Invitrogen, Grand Island, NY), 100 U/ml penicillin, 100 µg/ml gentamicin, 10 mM HEPES, and 2 mM glutamine. The cells were cultured in a T-75 cm<sup>2</sup> flask at 37° C in CO<sub>2</sub> incubator (5% CO<sub>2</sub>) until reaching confluency. Cells were washed in PBS followed by splitting into new flasks at 1 X 10<sup>6</sup> cells/ml in IMDM media. To avoid cells undergoing too many passages, cells were frozen in 10% DMSO in cryovials in liquid nitrogen storage and whenever required, cells were thawed following the standard procedure of cell culture.

### **Reagents:**

LPS derived from *Escherichia coli* 0111:B4 (Sigma-Aldrich Canada Ltd., Oakville, ON), rTNF-α (Biosource, Montreal, Quebec, Canada), and anti-TNF-αR1 Ab (R & D Systems, Minneapolis, MN) capable of neutralizing TNF-α activity were purchased. The source and dose of inhibitors used in this study are detailed in table 2.1. The MAPK inhibitors used in this study are as follows: PD98059 (2'-Amino-3'-methoxyflavone), an inhibitor of MAP/ERK kinase-1, which selectively blocks the activity of ERK MAPK and has no effect on the activity of other serine threonine protein kinases including Raf1, p38 and JNK MAPK, was also purchased [135;280]. The pyridinyl imidazole SB202190 [FHPI, 4- (4- Fluoro phenyl) -2-(4-hydroxy phenyl)- 5-(4-pyridyl)1H-imidazol], a potent inhibitor of p38 MAPK, has no significant effect on the

activity of ERK or JNK MAPK subgroups [135;281]. SP600125 (Anthra(1,9-cd)pyrazol-6(2H)-one 1,9-Pyrazoloanthrone), a specific JNK inhibitor, is a reversible ATP competitive inhibitor with more than 300 fold selectivity versus related MAPK including ERK1 and p38 [282]. Dexamethasone [(DXM; (9 $\alpha$ -fluoro-16 $\alpha$ -methylprednisolone)] and curcumin were used as JNK inhibitors as well. The PI3K inhibitors Ly294002 [2-(4-Morpholinyl)-8-phenyl-4H-1-benzopyran-4-one], a potent inhibitor that acts on the ATP binding site; and Wortmannin, a fungal metabolite that blocks the catalytic activity of PI3K without affecting the upstream signaling events were purchased from Calbiochem. The following calcium signaling inhibitors were employed: EGTA (Ethylene glycol bis(2-aminoethyl ether)-N,N,N',N'-tetraacetic acid), a calcium chelating agent; SKF-96365 hydrochloride [1-[b-[3-(4-Methoxyphenyl) propoxy] -4 -methoxyphenethyl]-1H-imidazole,HCl] specifically inhibits receptor-mediated Ca<sup>2+</sup> entry [283]; 2-APB (2-Aminoethoxydiphenylborate) inhibits inositol (1,4,5) triphosphate (IP3) induced Ca<sup>2+</sup> release from the ER [284]; W-7 hydrochloride [N-(6-Aminoethyl)-5-chloro-1-naphthalenesulfonamide, HCl] is a calmodulin antagonist; KN-93 [2-[N-(2-hydroxyethyl)]-N-(4-methoxybenzenesulfonyl)]amino-N-(4-chlorocinnamyl)-N-methyl benzylamine] is a specific cell permeable inhibitor of CAMKII; FK-506 (Tacrolimus) interacts with FK506-binding protein (FKBP), forming a FK506–FKBP complex, which binds to and blocks calcineurin; and cyclosporine A binds to cyclophilin and inhibits the Ca<sup>2+</sup> dependent phosphatases. ZVAD-fmk (Z-Val-Ala-Asp-CH<sub>2</sub>F), the broad spectrum caspase inhibitor was obtained from Calbiochem. Caffeic Acid Phenethyl Ester (CAPE) used in this study has been shown to act as a potent and specific inhibitor of NF $\kappa$ B

activation mediated by reactive oxygen species. All other chemicals used for electrophoresis and immunoblot analysis were obtained from Sigma-Aldrich.

### **Isolation of monocytes:**

Monocytes were isolated from peripheral blood mononuclear cells (PBMCs) by automacs negative selection (Miltenyi Biotech Inc. Auburn, CA). Blood was obtained for isolation of PBMCs from healthy volunteers after approval of the protocol by the ethics review committee of the Children's Hospital of Eastern Ontario, Ottawa, Canada. PBMCs were isolated by density gradient centrifugation over Ficoll-Hypaque (Pharmacia Biotech, Piscataway, NJ) as previously described [285]. Briefly, the cell layer consisting mainly of mononuclear cells was collected and washed twice in PBS containing 2% EDTA (ethylenediaminetetraacetic acid) followed by incubation with automacs FcR blocking reagent along with biotin antibody cocktail for 10 min at 4° C. Following incubation, cells were treated with anti biotin microbeads for 15 min at 4° C. Cells were then washed once and subjected to automacs negative selection separation as per the manufacturer's instructions. Cell populations thus obtained contained more than 95% CD14+ monocytes. Cells were cultured in IMDM (Sigma-Aldrich, St-Louis, MO) supplemented with 10% FBS (Invitrogen, Grand Island, NY), 100 U/ml penicillin, 100 µg/ml gentamicin, 10 mM HEPES, and 2 mM glutamine.

### **Stimulation of cells with Vpr peptides:**

Vpr C-terminal (52-96 aa) and Vpr N-terminal (1-45 aa) peptides were synthesized by Genemed Synthesis Inc, San Francisco, California, USA by automated solid-phase synthesis using 9-fluorenylmethoxycarbonyl and were purified by reverse-

**Table 2.1: Detailed description of pharmacological inhibitors, their source, and doses used in this study:**

<b>Name of the Inhibitors</b>	<b>Source</b>	<b>Used Concentration</b>	<b>Cellular Targets</b>
SB202190	Calbiochem, San Diego, CA	5-50 $\mu$ M	P38 MAPK
PD98059	Calbiochem	5-50 $\mu$ M	ERK MAPK
SP600125	Calbiochem	5-50 $\mu$ M	JNK MAPK
Dexamethasone	Sabex, Boucherville, Quebec	2-100 nM	JNK MAPK
Curcumin	Calbiochem	100-750 nM	JNK MAPK
EGTA	Calbiochem	2-10 mM	Calcium chelator
SKF96365 HCl	Calbiochem	20-100 $\mu$ M	Receptor mediated calcium entry
2-APB	Calbiochem	10-50 $\mu$ M	IP3 induced calcium release
W-7-HCl	Calbiochem	10-50 $\mu$ M	Calmodulin
KN-93	Calbiochem	5-50 $\mu$ M	CAMKII
FK 506	AG Scientific, San Diego, CA	0.5-5 $\mu$ M	Calcineurin
Cyclosporine A	Sigma-Aldrich	0.5-5 $\mu$ M	Calcineurin
Ly 294002	Calbiochem	1-20 $\mu$ M	PI3K
Wortmannin	Calbiochem	5-50 nM	PI3K
ZVAD-fmk	Calbiochem	10-50 $\mu$ M	Caspases
CAPE	Calbiochem	10-100 $\mu$ M	NF $\kappa$ B

phase HPLC (>95%) followed by analysis with electrospray mass spectrometry. The sequence of C-terminal (52-96 aa) and N-terminal end (1-45 aa) peptides are as follows: Vpr (52-96) peptide, DTWAGVEAI IRILQQLLFI HFRIGCRHSR IGVTRQRRAR NGASRS; Vpr (1-45) peptide, MEQAPEDQGP QREPYNEWTL ELLEELKSEA VRHFPRIWLH NLGQH. Because of high propensity of Vpr peptides to bind to proteins, cells ( $1 \times 10^6$  cells/ml) were treated with peptides in an isotonic buffer (13 mM HEPES, 2.4% glucose, 68 mM NaCl, 1.3 mM KCL, 4 mM  $\text{Na}_2\text{HPO}_4$ , 0.7 mM  $\text{KH}_2\text{PO}_4$ , pH 7.2) for 30 min followed by addition of cell culture medium as described [286]. Cells were also stimulated with either LPS or TNF- $\alpha$  before or after treatment of Vpr peptides wherever necessary.

### **Ca<sup>2+</sup> influx:**

THP-1 cells were washed with Ca<sup>2+</sup>-free PBS for 5 min at room temperature and resuspended in Buffer A (RPMI 1640 containing 20 mM HEPES, pH 7). The cells were washed again and resuspended in Buffer A containing 1 mM calcium binding dye Fluo3/AM (Molecular Probes, Eugene, OR) in 1 mM DMSO and 3.75% Pluronic F-127 solution (Sigma) followed by incubation in dark for 45 min in a 37°C shaking water bath. The reaction was stopped by adding equal volume of Buffer B (Buffer A containing 5% FBS, pH 7.4) followed by incubation for 15 min in a 37°C water bath. The cells were washed and resuspended in Buffer B at a final concentration of  $0.5 \times 10^6$  cells/ml and analyzed for Ca<sup>2+</sup> levels by the FACScan flow cytometer (Becton–Dickinson, Franklin Lakes, NJ) equipped with CellQuest software, Version 3.2.1fl. Cell samples were maintained at 37°C during acquisition of data. Intracellular Ca<sup>2+</sup> levels at baseline and following stimulation with LPS/TNF- $\alpha$  were measured. Ca<sup>2+</sup> ionophore A23187 (20 mM)

and 5 mM EGTA (Sigma) were used as positive and negative controls, respectively. To determine the effect of Vpr, cells were treated with different doses of Vpr peptides for 2 hr prior to load the dye.

### **Analysis of cellular apoptosis:**

***Propidium iodide (PI) staining for determination of cell cycle arrest:*** Apoptotic cells with DNA fragmentation were analyzed by flow cytometry with PI staining in permeabilized cells. Briefly, cells ( $1 \times 10^6$ /ml) were washed twice with PBS containing 1% FBS, fixed with chilled methanol for 15 min at 4°C, treated with 1 µg/ml of RNase A followed by staining with 50 µg/ml of PI (Sigma) at 4°C for 1 hr. The DNA content was analyzed by flow cytometry (FACScan, BD Bioscience, Mississauga, Canada).

***Annexin-V and PI staining for detection of apoptotic cells:*** Early stage of apoptosis is determined by annexin V which binds to phosphatidyl serine exposed on the cell surface of apoptotic cell. Following stimulation, cells were collected, washed with PBS and then stained with FITC labeled annexin-V and PI (Molecular probes, Eugene, OR) for 15 min at room temperature in the dark and analyzed by flow cytometry [287]. Annexin- positive cells were plotted as histograms.

***JC-1 staining for determination of mitochondrial membrane potential (MMP):*** JC-1 (5,5',6,6'-tetrachloro-1,1',3,3'-tetraethylbenzimidazol-carbocyanine iodide) is a lipophilic carbocyanin that exists in a monomeric form and is able to accumulate in mitochondria. In the presence of high  $\Delta\psi$ , JC-1 can reversibly form aggregates that after excitation at 488 nm emit in the orange/red channel (FL-2). The collapse in  $\Delta\psi$  provokes the decrease in the number of JC-1 aggregates, and consequent increase in JC-1

monomers (FL-1). Cells were stained with 10  $\mu\text{g/ml}$   $\Delta\psi$ -sensitive probe JC-1 (Molecular probes) in IMDM containing 10% FCS for 15 min at room temperature in dark and analyzed by flow cytometry, as described [288]. Apoptotic cells with depolarized mitochondria are present in the lower right quadrant of the panel. JC-1 monomers and aggregates were plotted as dot plot. All the histograms and dot plots were generated by using Win-MDI version 2.8 software.

### **Cell stimulation and Western blot analysis:**

Cells ( $1 \times 10^6$  cells/ml) were treated with the indicated concentration of inhibitors for 2 hr followed by stimulation with either LPS (1  $\mu\text{g/ml}$ ) or TNF- $\alpha$  (10 ng/ml) for 15-60 min for detection of kinases activation and for 24 hr to determine c-IAP2 expression by Western blot analysis as described earlier [285]. Cells ( $1 \times 10^6$ /ml) were also treated with the inhibitors for 2 hr followed by stimulation with Vpr peptide(s) for various time points for analysis of MAPKs activation, and Bcl2/c-IAP1 expression by Western blot analysis as described earlier [285]. Briefly, cell lysates were prepared by treating the cell pellets with lysis buffer for 1 hr (50 mM HEPES pH 7.5, 150 mM NaCl, 10% glycerol, 1% Triton X-100, 1.5 mM  $\text{MgCl}_2$ , 100 mM NaF, 100 mM sodium orthovanadate, and 1 mM EGTA pH 7.7), followed by centrifugation for 15 min at 20,000 x g at 4°C. The protein concentration of the supernatants was determined using the Bio-Rad protein determination assay (Bio-Rad Laboratories, Hercules, CA). Total proteins (30  $\mu\text{g}$ ) were subjected to SDS-PAGE followed by transfer onto a polyvinylidene difluoride (PVDF) membrane (Bio-Rad Laboratory, Hercules, CA). The membranes were probed with either anti-c-IAP1/c-IAP2 (RIAP-1) polyclonal antibody, anti-Bcl2, or with anti-phospho Bcl2 antibodies. To detect MAPKs, membranes were probed either with anti-phospho-JNK,

anti-phospho-ERK or with anti-phospho-p38 antibodies overnight at 4°C. Following incubation, membranes were washed with TBST and then incubated with donkey anti-rabbit polyclonal antibody conjugated to horseradish peroxidase or goat anti-mouse polyclonal antibody wherever necessary. Detailed information about the species, and source of antibodies are presented in table 2.2. To control for total protein loading, the membranes were stripped of the primary antibodies and reprobed with rabbit polyclonal antibodies specific for the total p38, ERK, or JNK MAPKs or with mouse monoclonal antibodies specific for  $\beta$ -actin. All immunoblots were visualized by enhanced chemiluminescence (Santa Cruz).

#### **Measurement of CAMKII activity:**

The CAMKII assay was performed using a CAMKII kit (Upstate Biotechnology Inc., Mississauga, Ontario, Canada) as per the manufacturer's instructions. Cells were pretreated with either inhibitors or Vpr peptides for 2 hr followed by stimulation of cells with either LPS or TNF- $\alpha$  for 30 min. Similarly cells were also transfected with DN-CAMKII or control vector before stimulation with LPS/TNF- $\alpha$ . Cell pellets were lysed and cytoplasmic extracts were collected as described previously [289]. CAMKII activity was assayed from total cellular proteins utilizing a peptide substrate (KKALRRQETVDAL) specific for CAMKII. Total proteins (200  $\mu$ g) were added to 10  $\mu$ l of CAMKII substrate, 0.4  $\mu$ M each of peptide inhibitors for PKA and PKC, and 100  $\mu$ Ci of MgCl<sub>2</sub>-[ $\gamma$ -<sup>32</sup>P] ATP in ADB II buffer (20 mM MOPS, pH 7.2, 2.5 mM  $\beta$ -glycerol phosphate, 1 mM sodium orthovanadate, 1 mM DTT, and 1 mM CaCl<sub>2</sub>). The reaction

**Table 2.2: Detailed description of antibodies and their source:**

<b>Name of the antibodies</b>	<b>Species</b>	<b>Source</b>
$\alpha$ -phospho-p38 MAPK	Rabbit	Cell Signaling, Danvers, MA
$\alpha$ -total p38-MAPK	Rabbit	Santa Cruz Biotechnology, CA
$\alpha$ -phospho-JNK MAPK	Rabbit	Cell Signaling
$\alpha$ -total JNK-MAPK	Rabbit	Santa Cruz Biotechnology
$\alpha$ -phospho-ERK MAPK	Mouse	Santa Cruz Biotechnology
$\alpha$ -total ERK-MAPK	Rabbit	Santa Cruz Biotechnology
$\alpha$ -c-IAP1	Rabbit	In house raised*
$\alpha$ -c-IAP2	Rabbit	In house raised*
$\alpha$ -phospho-Bcl2	Rabbit	Cell Signaling
$\alpha$ -total-Bcl2	Rabbit	Cell Signaling
$\alpha$ -rabbit-HRPO	Donkey	Amersham Bioscience, Montreal, Canada
$\alpha$ -mouse-HRPO	Goat	Bio Rad, CA
$\alpha$ -p50 (EMSA)	Rabbit	Santa Cruz Biotechnology
$\alpha$ -p65 (EMSA)	Rabbit	Santa Cruz Biotechnology
$\alpha$ -Sp1 (EMSA)	Rabbit	Santa Cruz Biotechnology
$\alpha$ -CREB (EMSA)	Rabbit	Santa Cruz Biotechnology

\* (Holcik *et al*, 2002)[290]

was incubated at 30°C for 10 min, and the phosphorylated substrate was separated from the residual [ $\gamma$ -<sup>32</sup>P]-ATP using p81 phosphocellulose paper. The papers were washed twice in 0.75% H<sub>3</sub>PO<sub>4</sub> and once in acetone for 2 min, and radioactivity was measured by Microbeta counter (Wallac, Turko, Finland). Blanks to correct for nonspecific binding of [ $\gamma$ -<sup>32</sup>P]-ATP and its breakdown products to the phosphocellulose paper and controls for phosphorylation of endogenous proteins in the sample were performed. CAMKII activity was expressed as cpm/ $\mu$ g of protein.

### **RNA isolation and Real time PCR for c-IAP2:**

c-IAP2 mRNA levels was measured using real time quantitative RT-PCR as per the Taqman method. Total RNA was isolated using RNeasy mini-spin columns combined with DNase I treatment (Qiagen, Mississauga, Ontario, Canada). The reverse transcribed RNA was amplified by PCR using the Taqman EZ RT-PCR kit (PE Applied Biosystems, Foster City, CA). All the RT-PCR steps were performed on an ABI Prism 7700 sequence Detector and quantified using the cycle threshold method, and normalized to GAPDH mRNA using PE-ABI supplied primers (600 nM) and probe (200 nM, JOE-labeled). The thermal cycling conditions for the RT step were: 50°C for 2 min, 60°C for 30 min, and 95°C for 5 min followed by 45 PCR cycles at 94°C for 20 sec and 60°C for 1 min per cycle.

### **Semiquantitative RT-PCR analysis for Bcl2, c-IAP1, c-IAP2, and $\beta$ actin:**

Total RNA was isolated from cells as described earlier (Qiagen, Mississauga). Total RNA (1  $\mu$ g) was reverse transcribed using Moloney murine leukemia virus reverse

transcriptase (Perkin Elmer) as described previously [285]. Equal aliquots (5  $\mu$ l) of cDNA were subsequently amplified for Bcl2, c-IAP1, c-IAP2, and  $\beta$ -actin. The oligonucleotide primer sequences used for Bcl2 (Biomol), c-IAP1, c-IAP2, and  $\beta$ -actin (Stratagene, La Jolla, CA) are described in table 2.3. The amplification conditions for Bcl2, c-IAP1, c-IAP2 and  $\beta$ -actin were as follows: denaturation at 94°C for 1 min, annealing at 58°C for 1 min, and extension at 72°C for 1 min. After 30 cycles, the amplified Bcl2, c-IAP1, c-IAP2, and  $\beta$ -actin fragments were resolved by electrophoresis on 1% agarose gels and visualized by ethidium bromide staining.

### **Plasmid construction and mutagenesis:**

The full length c-IAP2 promoter (3.5 kb) was amplified by PCR (with Pfu turbo<sup>TM</sup> enzyme) from a previously characterized bacterial artificial chromosome containing the genomic region encompassing both c-IAP1 and c-IAP2 genes (Gene Bank accession # AF070674) [172;191]. The primers used were as follows: sense-5'-GAT GGT ACC ACT AGT ACT AGA ATA ATG C-3'; and antisense 5'-GCT GAA TTC GCA TGC ACC AGC AAG GAC-3'. The underlined bases indicate restriction sites for cloning that together with the preceding bases do not correspond to sequences in the promoter. The amplified promoter fragment was cloned into pCR2.1 TOPO, sequenced and then subcloned into the pGL3B vector. Since two NF- $\kappa$ B sites (#1 and #3) are critical in induction of c-IAP2, site specific mutagenesis of these two sites was performed with the Quick Change<sup>TM</sup> multisite-directed mutagenesis kits (Stratagene, La Jolla, CA) as per the manufacturer's protocol with 5' phosphorylated primers: site # 1, 5'-CTT TTG GGT CAT GGA AAT AGC CGA GTG GGT TTG CCA G-3', site # 3, 5'-GGT TAT TAC

**Table 2.3: Sequence of primers used in PCR and oligonucleotide probes in EMSA:**

Oligonucleotides/Primers	Sequences
Bcl2 Oligonucleotides (EMSA)	
CREB sense	5'-GAA CCG TGT GAC GTT ACG CA-3'
CREB antisense	5'-TGC GTA ACG TCA CAC GGT TC-3'
NFκB sense	5'-TGC CAA GAG GGA AAC ACC AGA ATC AA-3'
NFκB antisense	5'-TTG ATT CTG GTG TTT CCC TCT TGG CA-3'
Sp1 sense	5'- CAG AGG AGG GCT CTT TCT TTC- 3'
Sp1 antisense	5'- GAA AGA AAG AGC CCT CCT CTG- 3'
c-IAP1 Oligonucleotides (EMSA)	
CREB sense	5'- GGG CGC GCT GAC GTC ATC GTG CGT- 3'
CREB antisense	5'- ACG CAC GAT GAC GTC AGC GCG CCC- 3'
NFκB sense	5'- GAG AAA GGC TAG TCC CTT TTC-3'
NFκB antisense	5'-GAA AAG GGA CTA GCC TTT CTC- 3'
c-IAP2 Oligonucleotides (EMSA)	
NFκB (site# 1) sense	5'-ATG GAA ATC CCC GA-3'
NFκB (site# 1) antisense	5'-TCG GGG ATT TCC AT-3'
NFκB (site# 3) sense	5'-GCT GGA GTT CCC CT-3'
NFκB (site# 3) antisense	5'-AGG GGA ACT CCA GC-3'
Primers for RT PCR	
Bcl2 sense	5'- TTC TTT GAG TTC GGT GGG GTC-3'
Bcl2 antisense	5'- TGC ATA TTT GTT TGG GGC AGG -3'
c-IAP1 sense	5'-AGC TGT TGT CAA CTT CAG ATA CCA CT-3'
c-IAP1 antisense	5'-TGT TTC ACC AGG TCT CTA TTA AAG CC-3'
c-IAP2 sense	5'- ACT TGA ACA GCT GCT ATC CAC ATC-3'
c-IAP2 antisense	5'-GTT GCT AGG ATT TTT CTC TGA ACT GTC-3'
β-actin sense	5'-TGA CGG GGT CAC CCA CAC TGT GCC CAT CTA-3'
β-actin antisense	5'-CTA GAA GCA TTT GCG GTG GAC GAT GGA GGG-3'

CGC TGG AGT **TAA** CCT AAG TCC TAA AAG G-3'. The mutagenized bases are indicated (underlined and bold) which created convenient EcoR1 restriction site for analysis. The primers were used together in the mutagenesis reactions to create the double mutant. Successful mutants were identified by EcoR1 digests and sequencing.

#### **Transient transfection with c-IAP2 luciferase construct and luciferase assay:**

Cells were transiently transfected with plasmids containing the c-IAP2 promoter by Lipofectamine 2000 (Invitrogen) as described previously [279;291]. Briefly, 5 µg of the test plasmid and 3 µg of pSV-β galactosidase vector (Promega, Madison, NJ) were incubated for 30 min at room temperature with 16 µl of Lipofectamine reagent in 200 µl of OPTI-MEM1 medium to allow formation of DNA-liposome complexes. These complexes were then added to the cell suspension ( $2 \times 10^6$  cells/ml) for 24 hr followed by stimulation either with LPS or TNF-α in the presence or the absence of the indicated inhibitors. Cells were also treated with Vpr peptide(s) for 2 hr following which cells were stimulated with LPS/TNF-α overnight. The cells were harvested and assayed for luciferase and β galactosidase activity by using luciferase assay and β galactosidase assay kits (both from Promega) in a Bio Orbit 1250 Luminometer (Fisher, Pittsburgh, PA) and spectrophotometer, respectively.

#### **Transient transfection with antisense c-IAP2 oligonucleotides:**

THP-1 cells were also transfected with either antisense oligonucleotides for c-IAP2 (5' GAU GTT TTG GTT CTT CUU C 3') or control oligonucleotides (5' CUU CTT CTT GGT TTT GUA G 3'). Briefly, 5 µg of the either antisense oligonucleotides or control oligonucleotides was incubated for 30 min at room temperature with 10 µl of

Lipofectamine reagent in 100  $\mu$ l of OPTI-MEM1 medium to allow formation of DNA-liposome complexes. These complexes were then added to the cell suspension ( $2 \times 10^6$  cells/ml) for 24 hr followed by stimulation either with LPS or TNF- $\alpha$  for 24 hr. Cells were collected, lysed and the expression of c-IAP2 is determined by Western blotting. Wherever it is required, cells were treated either with staurosporine or with Vpr peptides to induce apoptosis followed by detection of apoptotic cells either by PI staining or by annexin/PI staining.

### **Transient transfection with dominant negative (DN)-CAMKII:**

The dominant negative mutant for the human CAMKII  $\gamma$  isoform in pSR $\alpha$  vector (pCAMKII- $\gamma$ ) was kindly provided by Drs. Alain Lilienbaum and Alain Israel from the Institute Pasteur, Paris [292]. The control vector pSR $\alpha$  was generated from pCAMKII- $\gamma$  by digesting with EcoRI. Endotoxin-free preparations of pCAMKII- $\gamma$  and control vector were used to transfect cells. Briefly, 5  $\mu$ g of the either DN-CAMKII plasmid or control vector were incubated for 30 min at room temperature in the presence of 10  $\mu$ l of Lipofectamine reagent in 100  $\mu$ l of OPTI-MEM1 medium. Following incubation, the complexes were added to the cell suspension ( $2 \times 10^6$  cells/ml) for 24 hr followed by stimulation either with LPS or TNF- $\alpha$ . To detect CAMKII activity, CAMKII assay was conducted by using cell extracts from these transfected and stimulated cells, as described earlier. Transfected cells were also treated with either staurosporine or Vpr peptides after stimulation either with LPS/TNF- $\alpha$  followed by detection of apoptotic cell by PI or annexin/PI staining.

### **Transient transfection with stealth JNK siRNA:**

THP-1 cells were transiently transfected with stealth siRNA (Invitrogen) specific for either JNK1 or JNK2 using FuGENE 6 transfection reagent (Roche Diagnostics, Quebec, Canada) as described previously [285]. Briefly, 50 pM of either stealth JNK or control RNA were incubated for 45 min at room temperature with 3  $\mu$ l of FuGENE 6 in 100  $\mu$ l of serum free IMDM to allow formation of RNA-liposome complexes. These complexes were then added to the cell suspension ( $10^6$ /ml) for 24 hr followed by treatment with Vpr peptide(s) for either 2 or 24 hr following which cells were analyzed for JNK phosphorylation by Western blot analysis or for apoptosis, cell cycle arrest and for mitochondrial membrane potential by annexin/PI, PI, and JC-1 stain, respectively.

### **Electrophoretic mobility shift assays (EMSA):**

EMSAs were performed as per the standard technique and as described earlier [279;291]. Briefly, cells were stimulated either with LPS or TNF- $\alpha$  for 45-60 min. in the presence or the absence of the indicated inhibitors or Vpr peptides. Cells were also treated with Vpr peptide(s) for 3 hr in the presence or in the absence of indicated inhibitors. Cells were harvested in Tris-EDTA-saline buffer (pH 7.8) and centrifuged at 200Xg for 5 min. at 4°C. Subsequently, cells were lysed for 10 min at 4°C with buffer A (10 mM of HEPES, 10 mM of KCl, 1.5 mM of MgCl<sub>2</sub>, 0.5 mM of PMSF, pH 7.9) containing 0.1% Nonidet P-40. The lysates were centrifuged at 20,000 x g for 10 min at 4°C. The pellet containing the nuclei was suspended in buffer B (20 mM of HEPES, 420 mM of NaCl, 1.5 mM of MgCl<sub>2</sub>, 0.2 mM of EDTA, and 25% glycerol) at 4°C for 15 min. Both buffer A and B contained the protease inhibitors including DTT, PMSF, and

spermidine at concentrations of 0.5 mM each, as well as 0.15 mM of spermine, and 5  $\mu\text{g/ml}$  each of aprotonin, leupeptin and pepstatin. The supernatant containing the nuclear proteins was collected. Protein concentration was determined using the Bio-Rad protein determination assay kit (Bio-Rad, Hercules, CA) and frozen at  $-80^{\circ}\text{C}$  until further use. The nuclear proteins (5  $\mu\text{g}$ ) were mixed with  $^{32}\text{P}$ -labeled NF $\kappa$ B oligonucleotide probes for 20 min and the resulting complexes were separated on a 5% nondenaturing gel. The oligonucleotide probes contained sequences corresponding to the CREB, NF $\kappa$ B and Sp1 sites in the Bcl2 promoter; CREB and NF $\kappa$ B sites in the c-IAP1 promoter (Gene Bank Accession No. AF070674); and NF $\kappa$ B site # 1 and # 3 in the c-IAP2 promoter are described in table 3. To determine specificity of transcription factor binding, parallel EMSA reactions were incubated with 100-200 fold excess of unlabelled specific and non-specific oligonucleotide probes for 20 min prior to the addition of corresponding labeled probe. Supershift experiments were also performed by using rabbit anti-NF $\kappa$ B p50 and p65, anti-CREB, and anti-Sp1 polyclonal antibodies (Table 2). The gel was dried and exposed to x-ray film (Eastman Kodak).

#### **RNase protection assay (RPA):**

Cells were treated with various concentrations of Vpr peptide(s) for 0-6 hr followed by isolation of total RNA. RPA was performed by using BD Riboquant package kit (BD Bioscience) with a multi probe template set of anti- and pro-apoptotic genes of the Bcl2 family as well as GAPDH and L32 as internal controls as per the manufacturer's protocol [293]. Briefly,  $^{32}\text{P}$ -labeled riboprobes of defined length were generated using T7 RNA polymerase and 50 ng of DNA template in the presence of 150  $\mu\text{Ci}$  of  $[\alpha\text{-}^{32}\text{P}]$  UTP

(Amersham Bioscience). Template DNA was digested with RNase free DNase followed by precipitation of labeled RNA. Five  $\mu\text{g}$  of total cellular RNA was mixed with  $6.2 \times 10^5$  CPM of the  $^{32}\text{P}$ -labeled riboprobe in hybridization buffer (40 mM PIPES, 1mM EDTA, 0.4 M NaCl, and 80% formamide) and incubated for 5 min at  $90^\circ\text{C}$  followed by 12 hr at  $56^\circ\text{C}$ . The hybridized RNA duplex were then digested with RNase and proteinase K followed by extraction with phenol and precipitation by the addition of equal volumes of 4 M ammonium acetate and 2 volumes of ethanol. Labeled RNA samples were resolved on 6% urea denaturing gels, dried and visualized by autoradiography.

**Statistical analysis:** Means were compared by the two tailed Student's t test. The results are expressed as mean  $\pm$  SD.

## **Chapter III**

### *Regulation of LPS mediated resistance to apoptosis in human monocytic cells*

## **Introduction:**

Activation of macrophages by cytokines or a mild bacterial infection is shown to confer anti-apoptotic survival signal, however, in the absence of appropriate stimulation, monocytes are programmed to undergo apoptosis. Macrophage survival may thus influence inflammatory and immune responses, and susceptibility to microbial pathogens. Recently, LPS has been shown to confer survival signals in monocytic cells [190], however, the molecular mechanism by which LPS confers anti-apoptotic survival signals in monocytic cells is poorly understood.

LPS may rescue monocytic cells from apoptosis directly through the activation of the CD14/Toll like receptor complex or indirectly via the induction of cytokines such as TNF- $\alpha$  in an autocrine manner suggesting a key role for TNF- $\alpha$  in monocytic cell survival. TNF- $\alpha$  generates two opposing signals: one that triggers apoptosis and the other that inhibits apoptosis [276]. The outcome of TNF- $\alpha$ -mediated effects is determined by the balance between these two signals [275]. It has been suggested that TNF- $\alpha$ -induced cell death is mediated by the TNF-receptor-1 (TNF-RI) whereas both TNF-RI and II are required to transduce signals for anti-apoptotic activity primarily through NF $\kappa$ B activation [276]. The protective role of NF $\kappa$ B against apoptosis is believed to be mediated by the induction of anti-apoptotic genes including c-IAP2 [186;191]. It has been suggested that TNF- $\alpha$  stimulation of Jurkat T cells induced the expression of the c-IAP2 through the activation of NF $\kappa$ B and c-IAP2 exerts its anti-apoptotic activity by directly binding and inhibiting the downstream protease caspases-3, 7 and 9 [186].

Expression of c-IAP2 has been suggested to be regulated by multiple regulatory elements in its promoter region. In addition to NF $\kappa$ B, c-IAP2 induction was recently shown to be regulated through a putative glucocorticoid response element and cAMP responsive element in A549 human lung cancer cells and T84 colon cancer cells [197;294], respectively. However, the upstream signaling molecules involved in the activation of these transcription factors regulating c-IAP2 expression are not well understood. Recently, c-IAP2 expression was shown to be regulated by ERK MAPK, p38 MAPK, PI3K, JAK2-STAT3 and PKC- $\delta$  in various cell lines [198-200].

LPS was shown to induce the expression of the anti-apoptotic gene, c-IAP2, in PMA-differentiated human monocytic U-937 cells [190], however, its role in suppressing apoptosis in monocytic cells is not clear [190]. *Therefore, I hypothesize that LPS may inhibit apoptosis or enhance survival of macrophages, at least in part, through the induction of c-IAP2. However, the molecular mechanism by which LPS induce the expression of c-IAP2 is not well understood. Therefore, the present study is designed to determine the role and regulation of c-IAP2 in the development of LPS mediated resistance to apoptosis in human monocytic cell.*

Herein, I investigated the molecular mechanism by which LPS and the proinflammatory cytokine TNF- $\alpha$  induce anti-apoptotic survival signals in human monocytic cells by employing promonocytic THP-1 cells as a model system. I demonstrate for the first time that both LPS and TNF- $\alpha$  induce survival of human monocytic cells through the induction of the c-IAP2 gene. Furthermore, LPS induced c-IAP2 expression, at least in part, through the endogenous production of TNF- $\alpha$  in an autocrine manner. The molecular mechanism involved in the upregulation of c-IAP2

following stimulation of monocytic cells either with LPS or TNF- $\alpha$  is not known. I investigated the role of upstream signaling molecules including the members of the MAPK, PI3K, and the calcium signaling pathways involved in the regulation of c-IAP2 expression and consequent survival of monocytic cells. My results suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 expression in THP-1 cells and their survival are regulated selectively by CAMKII through the activation of NF $\kappa$ B.

## **Results:**

### **LPS-induced c-IAP2 expression is mediated by endogenously produced TNF- $\alpha$ in THP-1 cell:**

LPS and TNF- $\alpha$  induce variety of anti-apoptotic genes including c-IAP2 in different cell types. To determine the expression of LPS induced c-IAP2 in monocytic cell, THP-1 cells were stimulated with 1  $\mu$ g/ml of LPS for various period of time and c-IAP2 expression was determined in protein as well as in mRNA level by Western blotting (Fig. 3.1A) and real time RT-PCR (Fig. 3.1B), respectively. c-IAP2 expression was detectable as early as 2 hr and maximum induction to the extent of 20 fold was observed 24 hr following LPS stimulation compared with the unstimulated cells. Since TNF- $\alpha$  is produced in response to LPS stimulation in THP-1 cells [295], I investigated whether LPS-induced c-IAP2 expression is mediated by endogenously produced TNF- $\alpha$ . To determine the role of endogenous TNF- $\alpha$ , I employed neutralizing antibodies specific for TNFR1 (10-20  $\mu$ g/ml). This antibody is capable of neutralizing the biological activity of TNF- $\alpha$ , as described previously and recommended by the manufacturer (R & D System). The results show that anti-TNFR1 antibodies inhibited LPS-induced c-IAP2 expression in a dose dependent manner (Fig. 3.1C). Furthermore, exogenous TNF- $\alpha$  induced c-IAP2

expression in THP-1 cells as determined by both Western blot and real time PCR analysis (Fig 3.1A & B). Similar to the results obtained with LPS, c-IAP2 protein expression in response to TNF- $\alpha$  was detectable as early as 2 hr, and maximum induction to the extent of 15 fold was observed at 24 hr compared with the unstimulated cells. It may be noted that cells expressed c-IAP1 constitutively that was not inducible by either LPS or TNF- $\alpha$ .

### **c-IAP2 prevents staurosporine induced apoptosis in THP-1 cells:**

THP-1 cells are resistant to the Fas/FasL-induced apoptosis since this cell line does not express Fas on its surface [296]. Therefore, staurosporine has been used in this study to induce apoptosis in these cells [198;294]. To examine the role of c-IAP2 in LPS- and TNF- $\alpha$ -induced inhibition of apoptosis, I determined if LPS and TNF- $\alpha$  stimulation could prevent staurosporine-induced apoptosis in THP-1 cells. LPS and TNF- $\alpha$ -stimulated cells were treated with staurosporine for 4 hr followed by determination of apoptosis by PI staining. LPS/TNF- $\alpha$  alone had no effect on cell viability, whereas treatment of unstimulated THP-1 cells with staurosporine resulted in ~30% cell death. Stimulation of cells with either LPS or TNF- $\alpha$  in the presence of staurosporine resulted in significant inhibition of staurosporine-induced apoptosis from ~30% to 10% (Fig 3.1E).

To determine if c-IAP2 is involved in LPS- or TNF- $\alpha$ -induced anti-apoptotic cell survival, cells were transfected with c-IAP2 antisense (AS) or control oligonucleotides prior to stimulation with either LPS or TNF- $\alpha$  for 24 hr followed by determination of c-IAP2 expression and staurosporine-induced apoptosis. Antisense c-IAP2 oligonucleotides significantly decreased LPS- and TNF- $\alpha$ -induced expression of c-IAP2 by 4 fold as compared to the cells treated with control oligonucleotides (Fig. 3.1D). To delineate the

role of c-IAP2 in apoptosis, we induced apoptosis with staurosporine after stimulation with either LPS/TNF- $\alpha$ . Flow cytometric analysis by propidium iodide reveals that treatment of LPS- and TNF- $\alpha$ -stimulated cells with antisense c-IAP2 oligonucleotides enhanced staurosporine-induced apoptosis compared to the cells treated with control oligonucleotides (Fig 3.1E). However, antisense c-IAP2 oligonucleotides did not affect staurosporine induced apoptosis in unstimulated cells compared with the cells treated with control oligonucleotides (data not shown). It may be noted that abrogation of c-IAP2 expression by antisense oligonucleotides may not be possible because of low transfection efficiency in monocytic cells. These results suggest that stimulation with either LPS or TNF- $\alpha$  enhanced monocytic cell survival that was mediated by c-IAP2 induction.

**The MAPKs and PI3 kinase/Akt pathways are not involved in upregulation of LPS/ TNF- $\alpha$  induced c-IAP2 expression:**

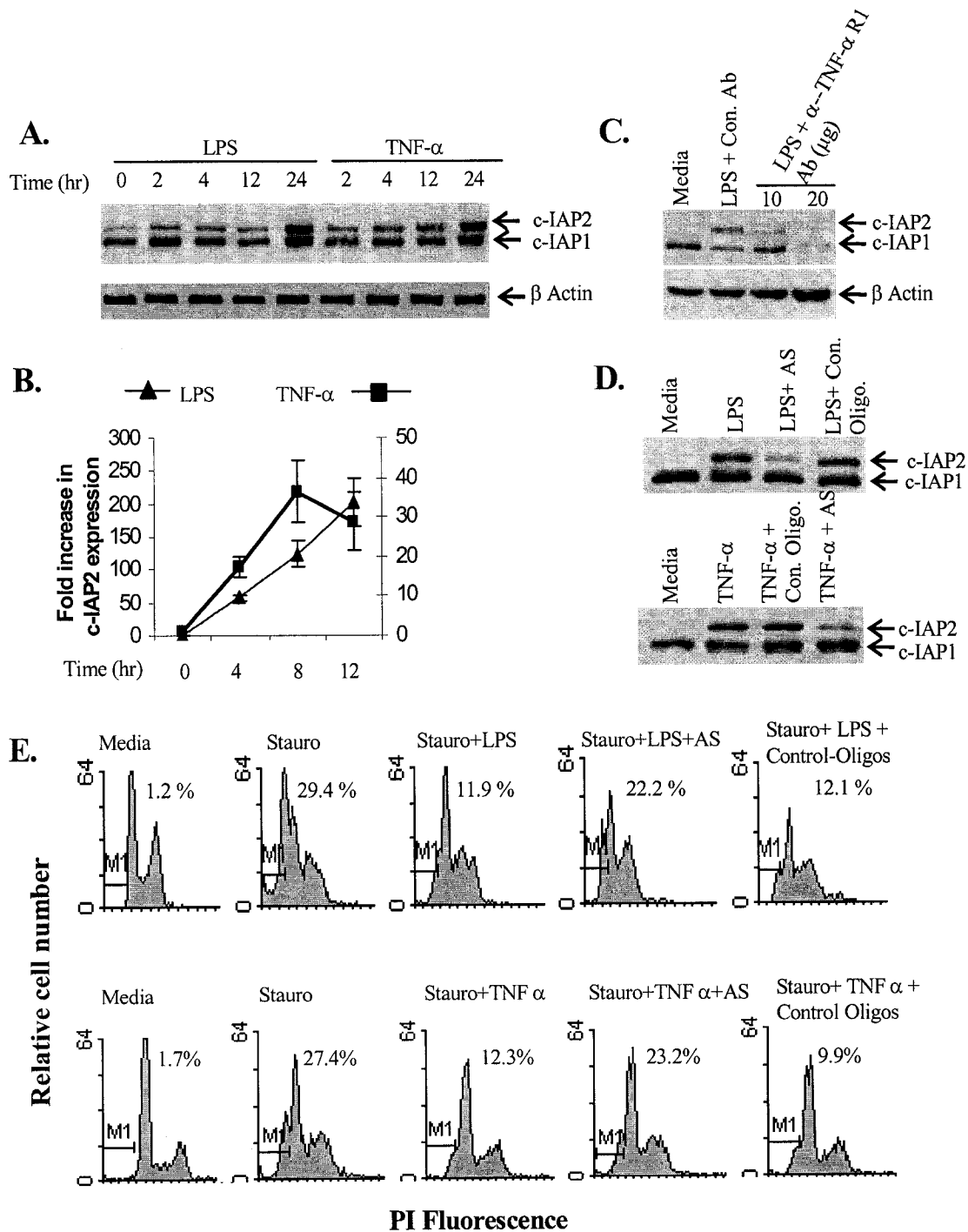
MAPK and PI3K have been shown to be involved in apoptosis in epithelial and leukemic cell systems. Recently, JNK was shown to mediate the anti-apoptotic activity of XIAP whereas p38 and ERK MAPKs were shown to regulate c-IAP2 expression in colon cancer cell lines [196;198]. In addition, PI3K and ERK MAPK have been demonstrated to be involved in endoplasmic reticulum (ER) stress-induced cell death [297]. To elucidate the signaling pathways involved in the regulation of c-IAP2 expression, I first investigated the role of MAPKs in LPS and TNF- $\alpha$ -stimulated THP-1 cells. To delineate the role of MAPKs, I first examined whether LPS and TNF- $\alpha$  stimulation induced the activation of JNK, ERK and p38 MAPKs and their activation can be inhibited by the specific inhibitors, namely, SP600125 for JNK, PD98059 for p42/44 ERK, and

**Fig. 3.1: LPS and TNF- $\alpha$ -induced inhibition of apoptosis is mediated by c-IAP2 expression in THP-1 cells.**

**A, B.** LPS and TNF- $\alpha$  induce c-IAP2 expression. Cells ( $1 \times 10^6$ /ml) were stimulated with either LPS ( $1 \mu\text{g/ml}$ ) or TNF- $\alpha$  ( $10 \text{ ng/ml}$ ) for 0-24 hr. c-IAP2 expression was determined by Western blot (**A**) and real time-RT-PCR analysis (**B**). The experiments shown are representative of three different experiments.

**C.** LPS-induced c-IAP2 expression is mediated by endogenously produced TNF- $\alpha$ . Cells ( $1 \times 10^6$ /ml) were stimulated with LPS ( $1 \mu\text{g/ml}$ ) in the presence and the absence of anti-TNF- $\alpha$ -R1 ( $10$ - $20 \mu\text{g/ml}$ ) or isotype matched control antibodies followed by determination of c-IAP2 expression by Western blot analysis. The experiments shown are representative of three different experiments.

**D, E.** LPS- and TNF- $\alpha$ -induced inhibition of apoptosis is mediated by c-IAP2 expression. Cells ( $10^6$ /ml) were transfected with either antisense (AS) c-IAP2 or control oligonucleotides followed by stimulation with LPS ( $1 \mu\text{g/ml}$ ) or TNF- $\alpha$  ( $10 \text{ ng/ml}$ ) for 24 hr followed by determination of c-IAP2 expression by Western blot analysis (**D**). Stimulated cells were also treated with staurosporine (Stauro) ( $2 \mu\text{M}$ ) for 4 hr and DNA content of cells were analyzed by PI staining (**E**). The experiments shown are representative of three different experiments.

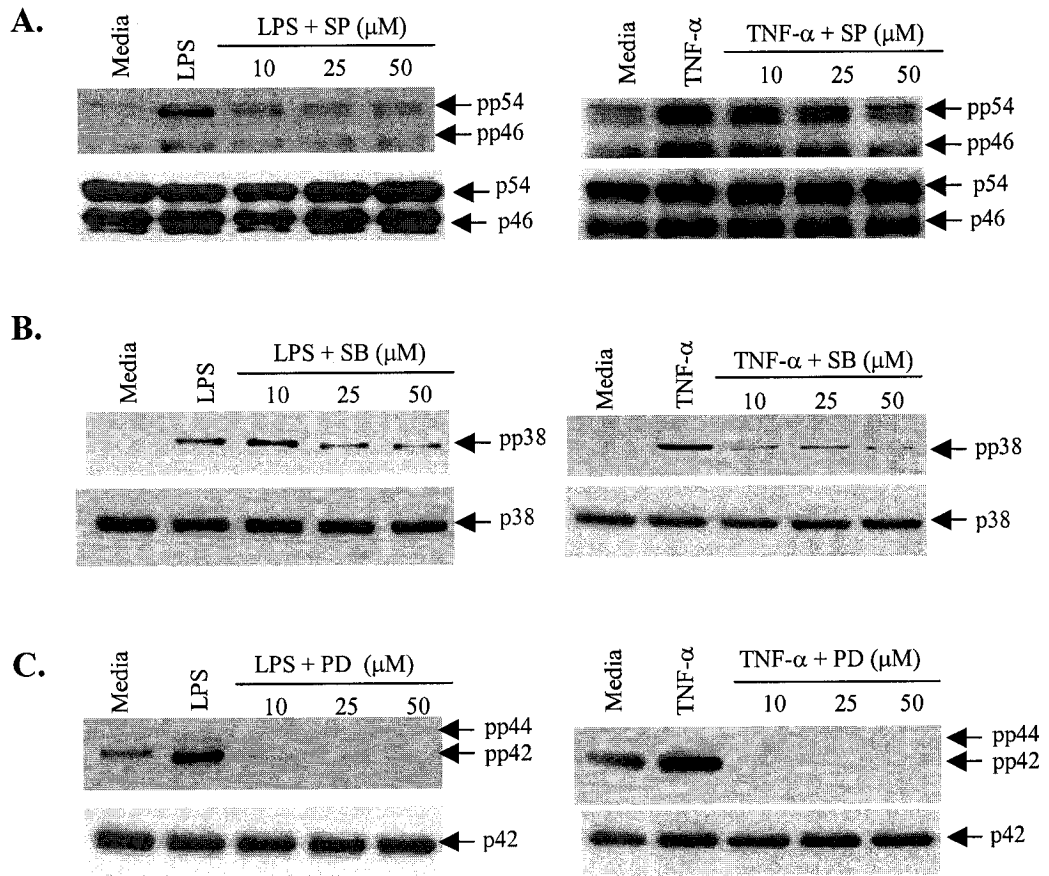


SB202190 for p38 MAPKs. Cells were stimulated with LPS or TNF- $\alpha$  for 15 min. and subjected to Western immunoblotting for phosphorylation of JNK, ERK and p38 MAPKs by using anti-phospho-JNK, anti-phospho-ERK and anti-phospho-p38 specific antibodies, respectively. The same blots were stripped and reprobed with anti-JNK, anti-p42/44 and anti-p38 Abs to ensure equal protein loading. The results show that both LPS and TNF- $\alpha$  induced the phosphorylation of JNK, p42/44 ERK and p38 MAPKs, whereas total protein of respective kinases remained same. Furthermore, LPS and TNF- $\alpha$ -induced phosphorylation of JNK, p42/44 ERK and p38 MAPKs was inhibited by their specific inhibitors in a dose dependent manner (Fig. 3.2A, B & C). To determine the role of JNK, p42/44 ERK and p38 MAPKs in LPS- and TNF- $\alpha$ -induced c-IAP2 expression, THP-1 cells were treated with SP600125, PD98059, or SB202190 for 2 hr prior to stimulation with either LPS or TNF- $\alpha$  for 24 hr. The results show that c-IAP2 expression was not inhibited by any of these inhibitors at any concentration (Fig. 3.3A, B & C). Doses higher than 50  $\mu$ M for these inhibitors were not used because of their cytotoxic effect as determined by the trypan blue exclusion test.

To determine the role of PI3K pathway, I first examined whether LPS and TNF- $\alpha$  induce phosphorylation of Akt, the downstream substrate for PI3K, and whether this phosphorylation can be inhibited by PI3K specific inhibitors, LY294002 and wortmannin. The results show that LPS and TNF- $\alpha$  induced Akt phosphorylation at 30 and 15 min post-stimulation, respectively (Fig 3.4A and B Left panel), and this phosphorylation was inhibited by both LY294002 and wortmannin in a dose dependent manner (Fig. 3.4A & B Right panel). To determine the role of PI3K in LPS- and TNF- $\alpha$ -induced c-IAP2 expression, THP-1 cells were treated with Ly294002 or wortmannin for

**Fig. 3.2: JNK, p42/44 ERK and p38 MAPKs inhibitors down regulate the expression of phospho JNK, p42/44 ERK and p38 MAPKs in LPS/TNF- $\alpha$  stimulated THP-1 cells:**

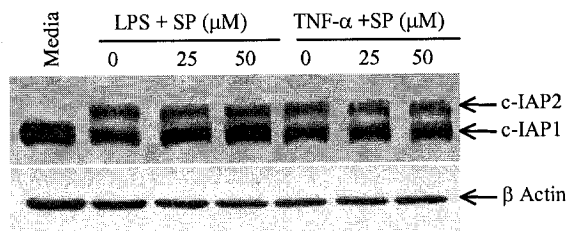
Cells ( $1.0 \times 10^6$ /ml) were pretreated with either A) SP600125, B) SB202190 or C) PD98059 at varying concentrations ranging from 0 to 50  $\mu$ M for 2 hr prior to LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) stimulation for 0-120 min. Crude protein extracts (30  $\mu$ g) were subjected to SDS-PAGE followed by Western blot analysis using either anti-phospho-JNK (indicated by arrows as pp46/54), anti-phospho-p42/44 (indicated by arrows as pp42/44) or anti-phospho-p38 (pp38) Abs. To ensure equal loading of protein, the membranes were stripped and reprobed either with anti-JNK, anti-p42/44 or anti-p38 Abs, respectively (indicated by arrows as p46/54, p42/44 and p38). The experiments shown are representative of three different experiments.



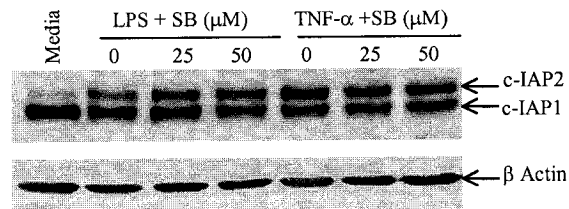
**Fig. 3.3: JNK, p42/44 ERK and p38 MAPKs inhibitors do not affect c-IAP2 expression in LPS/TNF- $\alpha$  stimulated THP-1 cells:**

THP-1 cells ( $1.0 \times 10^6$ /ml) were pretreated with either A) SP600125, B) SB202190 or C) PD98059 at varying concentrations ranging from 0 to 50  $\mu$ M for 2 h prior to LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) stimulation for 24 hr. Crude protein extracts (30  $\mu$ g) were subjected to SDS-PAGE followed by Western blot analysis. The membranes were blotted with c-IAP2 Abs. To ensure equal loading of protein, the membranes were stripped and reprobed with anti- $\beta$  actin Abs. The experiments shown are representative of three different experiments.

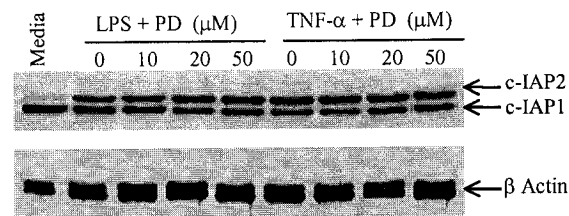
A.



B.



C.



2 hr followed by stimulation with either LPS or TNF- $\alpha$  for 24 hr. c-IAP2 expression was not inhibited by either Ly294002 or wortmannin at any concentration (Fig. 3.4C). These results suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 expression in THP-1 cells does not involve the activation of either MAPK or PI3K.

**LPS- and TNF- $\alpha$ - induced c-IAP2 expression is selectively regulated by calcium signaling pathway in monocytic cell:**

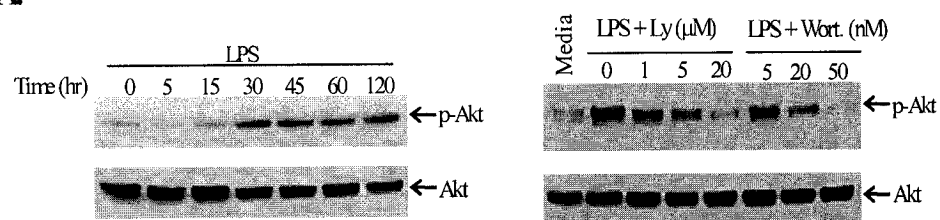
The changes in intracellular Ca<sup>2+</sup> concentrations play a major role in transcription, protein synthesis and apoptosis [244]. Calcium signaling pathway also acts at the upstream of many other major signaling pathways. To determine the role of Ca<sup>2+</sup> in LPS- and TNF- $\alpha$ -induced c-IAP2 expression, I first determined whether LPS and TNF- $\alpha$  activated calcium signaling by examining calcium influx by flow cytometry using Fluo-3 as a Ca<sup>2+</sup> binding dye. The results show that LPS and TNF- $\alpha$  both induced calcium influx at 12 and 8 min poststimulation, respectively. To delineate the role of calcium in the regulation of LPS induced c-IAP2 expression, EGTA (2-10 mM), one of the calcium chelator was used. The results revealed that EGTA inhibited influx of calcium to the basal level (Fig 3.5A). To determine the role of Ca<sup>2+</sup> in the regulation of c-IAP2 expression, I analyzed c-IAP2 expression in THP-1 cells treated with EGTA (2.5-10 mM) for 2 hr prior to stimulation with either LPS or TNF- $\alpha$  for 24 hr. LPS- as well as TNF- $\alpha$ -induced c-IAP2 expression was inhibited by EGTA in a dose dependent manner (Fig. 3.5B). EGTA at concentrations of 10 mM decreased the expression of c-IAP2 to undetectable levels following LPS stimulation and by 6 fold following TNF- $\alpha$  stimulation suggesting the involvement of Ca<sup>2+</sup> signaling pathway in LPS- and TNF- $\alpha$ -induced expression of c-IAP2.

**Fig. 3.4: PI3K inhibitors do not inhibit the expression of c-IAP2 expression in LPS/TNF- $\alpha$  stimulated THP-1 cells:**

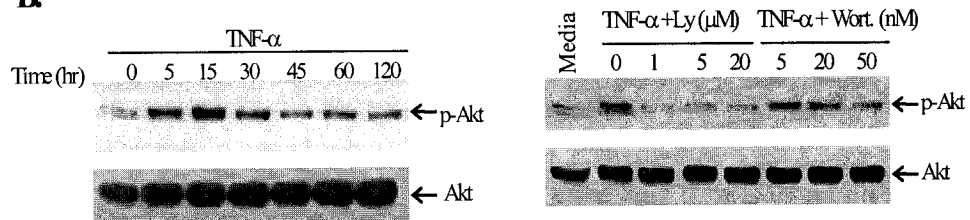
**A & B. Left panel:** THP-1 cells ( $1.0 \times 10^6$ /ml) were stimulated with either LPS or TNF- $\alpha$  for a period of 0-120 minutes and cell extracts were subjected to Western blot analysis using anti-phospho-Akt Abs. To normalize equal loading of protein, the membranes were stripped and reprobed with anti-Akt Abs. **Right panel:** THP-1 cells ( $1.0 \times 10^6$ /ml) were pretreated with either Ly294002 (1-20  $\mu$ M) or wortmannin (5-50 nM) for 2 hr prior to LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) stimulation for 15-30 min. Crude protein extracts (30  $\mu$ g) were subjected to SDS-PAGE followed by Western blot analysis using anti-phospho-Akt Abs. To normalize equal loading of protein, the membranes were stripped and reprobed with anti-Akt Abs.

**C.** THP-1 cells ( $1.0 \times 10^6$ /ml) were pretreated with either Ly29420 (1-20  $\mu$ M) or wortmannin (5-50 nM) for 2 hr prior to LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) stimulation for 24 h. Crude protein extracts (30  $\mu$ g) were subjected to SDS-PAGE followed by Western blot analysis. The membranes were blotted with c-IAP2 Abs. To ensure equal loading of protein, the membranes were stripped and reprobed with anti- $\beta$  actin Abs. The experiments shown in A, B, and C are representative of three different experiments.

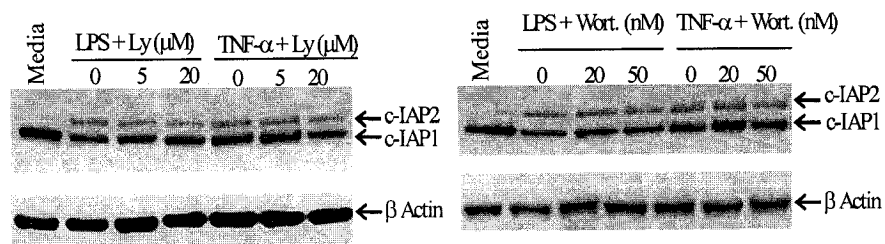
**A.**



**B.**



**C.**



Increase in cytoplasmic  $\text{Ca}^{2+}$  concentration occurs via diverse stimuli which activate voltage ligand-gated  $\text{Ca}^{2+}$  channels in the surface membrane or by release of  $\text{Ca}^{2+}$  contained in intracellular stores, mainly in endoplasmic reticulum (ER), and followed by extracellular  $\text{Ca}^{2+}$  entry [244;298]. To check the possibility that  $\text{Ca}^{2+}$  release from intracellular store could regulate c-IAP2 expression, I used one of the inositol 1,4,5-triphosphate receptor ( $\text{IP}_3\text{R}$ ) inhibitor, 2-APB that inhibits the release of  $\text{Ca}^{2+}$  from ER [284]. Our results show that 2-APB even at high concentration (100  $\mu\text{M}$ ) did not inhibit either LPS- or TNF- $\alpha$ -induced c-IAP2 expression (Fig. 3.5C). In the next series of experiments, I investigated the role of receptor-mediated entry of extracellular  $\text{Ca}^{2+}$  following LPS or TNF- $\alpha$  stimulation by employing SKF-96365, a specific inhibitor for receptor-mediated  $\text{Ca}^{2+}$  entry [283]. Cells were pretreated with SKF-96365 for 2 hr prior to stimulation with either LPS or TNF- $\alpha$ . SKF-96365 treatment significantly reduced both LPS- and TNF- $\alpha$ -induced c-IAP2 expressions in a dose dependent manner (Fig. 3.5D). SKF-96365 and 2-APB were biologically active as both of these agents inhibited TNF- $\alpha$ -induced CD44 expression (data not shown). Taken together, these results suggest that receptor-mediated  $\text{Ca}^{2+}$  entry rather than the  $\text{Ca}^{2+}$  release from the ER may be involved in LPS- and TNF- $\alpha$ -induced c-IAP2 expression.

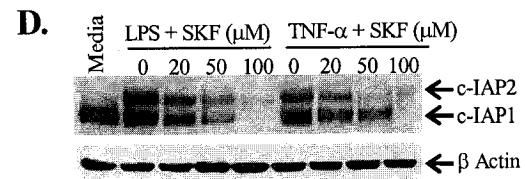
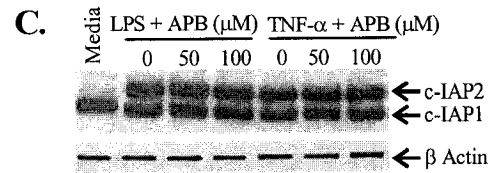
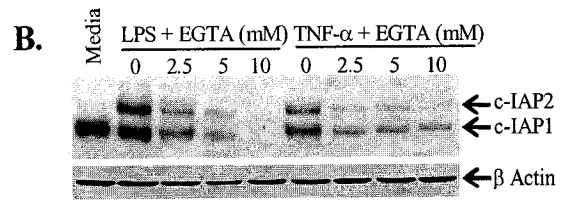
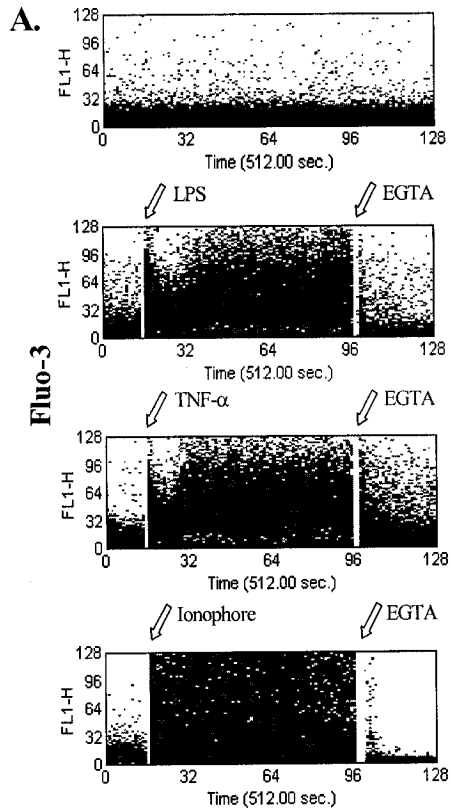
### **CaM and CAMKII regulate LPS- and TNF- $\alpha$ -mediated c-IAP2 expression:**

CaM, a 17 kDa protein that serves as a major  $\text{Ca}^{2+}$  receptor present in cytoplasmic and nuclear compartments, regulates several downstream targets such as protein kinases and protein phosphatases [299]. To understand the role of CaM, I examined whether its

**Fig. 3.5: Involvement of receptor-mediated Ca<sup>2+</sup> entry rather than the Ca<sup>2+</sup> release from endoplasmic reticulum in LPS- and TNF- $\alpha$ -induced c-IAP2 expression in THP-1 cells:**

**A.** Stimulation of THP-1 cells with either LPS or TNF- $\alpha$  induces Ca<sup>2+</sup> influx. THP-1 cells ( $0.5 \times 10^6$ /ml) loaded with Fluo3/AM were stimulated with either LPS or TNF- $\alpha$  and the resulting Ca<sup>2+</sup> influx was measured by flow cytometric analysis. **Top panel:** Baseline Ca<sup>2+</sup> levels in unstimulated cells. **2<sup>nd</sup> panel:** Stimulation with LPS followed by the addition of EGTA. **3<sup>rd</sup> panel:** Stimulation with TNF- $\alpha$  followed by the addition of EGTA; **Bottom panel:** Stimulation with the Ca<sup>2+</sup> ionophore A23187 followed by the addition of EGTA.

**B,C, & D.** Cells ( $1 \times 10^6$ /ml) were pretreated with either **(B)** EGTA, **(C)** 2-APB, or **(D)** SKF-96365 for 2 hr prior to stimulation with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for 24 h followed by analysis of c-IAP2 expression by Western blot analysis. To ensure equal loading of protein, the membranes were stripped and reprobed with anti- $\beta$ -actin antibodies. The experiments shown in A, B, C, and D are representative of three different experiments.



specific inhibitor are able to downregulate c-IAP2 expression in response to stimulation with LPS and TNF- $\alpha$ . The results show that W-7-Hydrochloride, a specific CaM antagonist [247], inhibited LPS- and TNF- $\alpha$ -induced c-IAP2 expression in a dose dependent manner (Fig. 3.6A Left panel). To further gain insight into the role of CaM pathway, I examined the involvement of CAMKII which is activated subsequently to the binding of Ca<sup>2+</sup> to CaM by employing its specific inhibitor KN-93 [247;299]. To determine the role of CAMKII in c-IAP2 induction, cells were treated with KN-93 for 2 hr followed by stimulation with either LPS or TNF- $\alpha$  for 24 hr. KN-93 inhibited both LPS- and TNF- $\alpha$ -induced c-IAP2 expressions by 7- and 11- fold respectively and in a dose dependent manner (Fig. 3.6A Middle & Right panel). I also demonstrated that stimulation of cells with either LPS or TNF- $\alpha$  for 30 min induced CAMKII activity. To determine the biological activity of KN-93 and W-7, cells were treated with these inhibitors at varying concentrations for 2 hr followed by stimulation with LPS or TNF- $\alpha$  for 30 min. The results show that both W-7 and KN-93 inhibited LPS- and TNF- $\alpha$ -induced CAMKII activity in a dose dependent manner (Fig. 3.6B).

To confirm the involvement of CAMKII in LPS and TNF- $\alpha$ -induced c-IAP2 expression, cells were transfected with a DN CAMKII plasmid or a control vector. c-IAP2 expression was significantly inhibited by 4 fold in cells transfected with the DN CAMKII plasmid following LPS as well as TNF- $\alpha$  stimulation compared to the cells transfected with the control vector (Fig 3.6C). In addition, LPS- and TNF- $\alpha$ -induced CAMKII activity was inhibited by transfecting cells with DN CAMKII plasmid. Following transfection with the DN CAMKII plasmid, CAMKII activity was observed as  $3 \pm 1.0$  and  $2.8 \pm 1.0$  pM following stimulation with either LPS or TNF- $\alpha$ , respectively

compared to the activity of  $6.5 \pm 1.0$  pM in LPS- and  $5.5 \pm 1.0$  pM in TNF- $\alpha$ -stimulated cells transfected with the control vector.

Calcineurin is also activated by the binding of  $\text{Ca}^{2+}$  to CaM, which dissociates the two components and allows the catalytic site of calcineurin to become accessible [247;300]. To determine the role of calcineurin, cells were treated with cyclosporine A (Cyclo) or FK-506, the inhibitors of calcineurin, prior to stimulation with either LPS or TNF- $\alpha$ . Neither cyclosporine A nor FK-506 inhibited LPS- or TNF- $\alpha$ -induced c-IAP2 expression at any concentration (Fig. 3.6D). The biological activity of cyclosporine A and FK506 was determined by analysis of NFAT4 expression in Jurkat T cells, as described [301;302]. PMA and ionomycin are potent activators of calcineurin and cause dephosphorylation of NFAT proteins. Cyclo and FK506 are potent inhibitors of calcineurin phosphatase activity and restore PMA- and ionomycin induced NFAT dephosphorylation and thus, NFAT mediated gene induction. My results show that NFAT4 phosphorylation was significantly reduced after stimulation of Jurkat T cells with PMA and ionomycin. Pretreatment of cells with either Cyclo or FK506 prior to stimulation with PMA and ionomycin restored NFAT4 phosphorylation (Fig. 3.6E). These results suggest that calcineurin is not involved in c-IAP2 induction, however, LPS and TNF- $\alpha$ -induced c-IAP2 expression is regulated by calmodulin through the activation of CAMKII. It should be noted that none of these inhibitors were found to be apoptotic at the concentrations used as determined by PI staining (data not shown). Based on all these findings, it is concluded that c-IAP2 expression is regulated by activation of CAMKII through influx of calcium via CaM.

**Fig. 3.6: CaM and CAMKII regulate LPS- and TNF- $\alpha$ -induced c-IAP2 expression:**

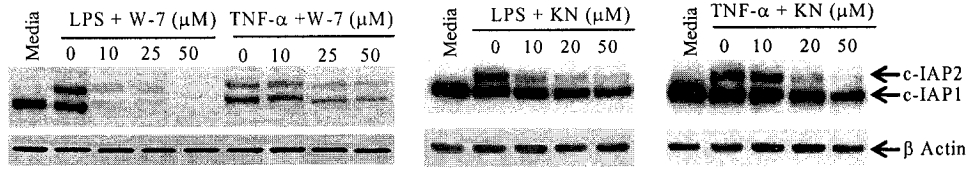
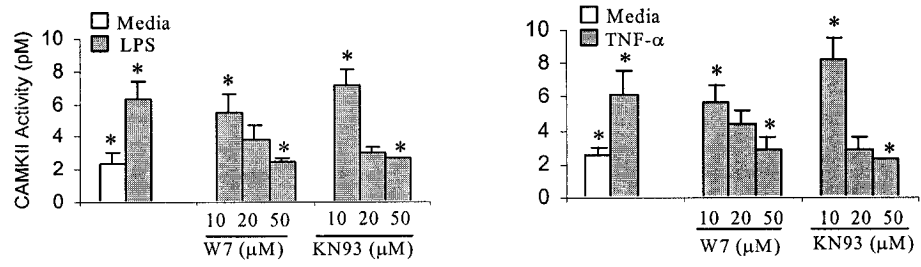
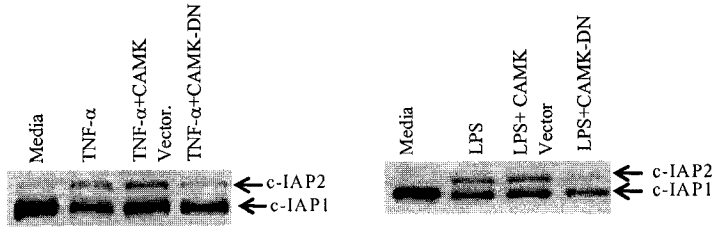
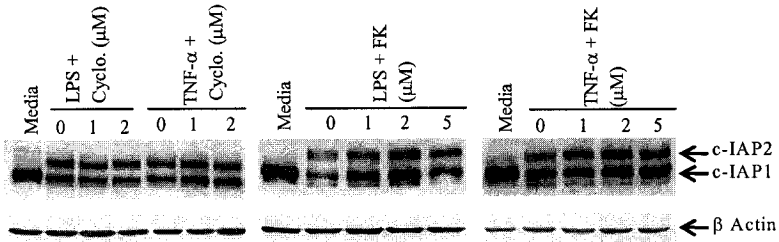
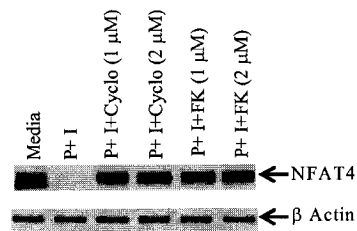
**A.** LPS- and TNF- $\alpha$ -induced c-IAP2 expression is mediated by CaM and CAMKII. THP-1 cells ( $1 \times 10^6$ /ml) were treated with either W-7 or KN-93 for 2 h prior to stimulation with either LPS ( $1 \mu\text{g/ml}$ ) or TNF- $\alpha$  ( $10 \text{ ng/ml}$ ) for 24 h followed by determination of c-IAP2 expression by Western blot analysis.

**B.** LPS- and TNF- $\alpha$ -induced CAMKII activity is inhibited by W-7 and KN-93. THP-1 cells were pretreated with inhibitors for 2 h followed by stimulation of cells with either LPS or TNF- $\alpha$  for 30 min. CAMKII activity was assayed from total cell proteins utilizing a peptide substrate (KKALRRQETVDAL) specific for CAMKII. The results shown represent the mean  $\pm$  S.D. of three independent experiments (\*  $p < 0.01$ ).

**C.** Cells were transfected with either DN CAMKII or control vector and cultured for 24 h, followed by stimulation with either LPS ( $1 \mu\text{g/ml}$ ) or TNF- $\alpha$  ( $10 \text{ ng/ml}$ ) for another 24 h. c-IAP2 expression was determined by Western blot analysis.

**D.** Cyclo and FK506 do not induce LPS- or TNF- $\alpha$ -mediated c-IAP2 expression. THP-1 cells ( $1 \times 10^6$ /ml) were treated with various concentrations of either Cyclo or FK506 for 2 h prior to stimulation with either LPS ( $1 \mu\text{g/ml}$ ) or TNF- $\alpha$  ( $10 \text{ ng/ml}$ ) for 24 h followed by determination of c-IAP2 expression by Western blot analysis.

**E.** Jurkat T cells ( $1 \times 10^6$ /ml) were treated with either Cyclo or FK506 for 2 h prior to stimulation with PMA (*P*) and ionomycin (*I*) for 5 min followed by determination of expression of NFAT4 by employing anti-NFAT4 antibodies by Western blot analysis. To ensure equal loading of protein, the membranes were stripped and re probed with anti- $\beta$ -actin antibodies. All of the experiments shown above are representative of three different experiments.

**A****B****C****D****E**

### **Involvement of the NFκB binding sites within the c-IAP2 promoter in the regulation of LPS- and TNF-α-induced c-IAP2 expression:**

c-IAP2 gene transcription has been shown to be regulated by the activation of NFκB transcription factor. NFκB is a heterodimer of rel proteins consisting of a DNA binding subunit (p50) and a transactivation domain (relA/p65) [303;304]. NFκB is normally present in the cytoplasm in association with IκB. IκB is degraded by phosphorylation by NFκB inducing kinase (NIK) and allow the NFκB to enter into the nucleus for further transcription [303]. To understand the role of NFκB in LPS- and TNF-α-induced c-IAP2 expression, THP-1 cells were transfected with c-IAP2 promoter (+121 to -606 bp) linked to the luciferase reporter construct (pc-IAP2Pr-GL3B) followed by stimulation with either LPS or TNF-α. The results show that in response to LPS as well as TNF-α, significant six to ten fold increase in luciferase activity was observed at 24 hr following stimulation compared to the unstimulated cells (Fig 3.8A). A computer aided analysis of the c-IAP2 promoter sequence between +1 and -606 bp revealed the existence of 3 NFκB consensus sequences (Fig. 3.7). However, sites 1 and 3 have been shown to be important for c-IAP2 gene transcription. Therefore, NFκB sites 1 and 3 were mutated by site directed mutagenesis followed by cloning into the pGL3B vector. THP-1 cells transfected with the c-IAP2 promoter construct containing the NFκB mutant sites and linked to the luciferase reporter vector (pc-IAP2Pr-mNFκB-GL3B) were stimulated with either LPS or TNF-α. The results show that luciferase activity was significantly decreased in cells transfected with pc-IAP2Pr-mNFκB-GL3B compared to cells transfected with the wild type pc-IAP2Pr-GL3B (Fig. 3.8B). To further confirm the role of NFκB, cells were cotransfected with either IκB super repressor plasmid or the IκB

control vector along with the wild type pc-IAP2Pr-GL3B following which the cells were stimulated with either LPS or TNF- $\alpha$ . Results show that LPS or TNF- $\alpha$  stimulation of cells cotransfected with I $\kappa$ B super repressor and pc-IAP2Pr-GL3B plasmids resulted in a significantly decreased luciferase activity compared to the cells cotransfected with control I $\kappa$ B vector and the wild type pc-IAP2Pr-GL3B (Fig. 3.8B). The role of NF $\kappa$ B was also confirmed by treating THP-1 cells transfected with the wild type pc-IAP2Pr-GL3B with CAPE, the broad spectrum NF $\kappa$ B inhibitor for 2 hr prior to stimulation with either LPS or TNF- $\alpha$  followed by detection of c-IAP2 expression by luciferase reporter assay. The results show that treatment of cells with CAPE inhibited LPS- and TNF- $\alpha$ -induced c-IAP2 expression in a dose dependent manner as determined by luciferase activity (Fig. 3.8C). Treatment of THP-1 cells with CAPE prior to stimulation with either LPS or TNF- $\alpha$  also resulted in downregulation of c-IAP2 expression as determined by Western blot analysis. CAPE at a concentration of 100  $\mu$ M decreased the expression of c-IAP2 to undetectable levels following LPS stimulation and by 5 fold following TNF- $\alpha$  stimulation (Fig. 3.8D). Taken together, these results suggest that NF $\kappa$ B activation plays a key role in LPS- and TNF- $\alpha$ -induced c-IAP2 expression in THP-1 cells.

### **CaM and CAMKII regulate c-IAP2 expression in LPS- and TNF- $\alpha$ -stimulated THP-1 cells through the activation of NF $\kappa$ B:**

It has been previously demonstrated that CAMKII acts as a mediator of IKK activation specifically in response to T cell receptor/CD3 and phorbol ester stimulation [305;306]. The above results suggest that LPS and TNF- $\alpha$ -induced c-IAP2 expression is regulated by CAMKII through the activation of CaM and Ca<sup>2+</sup> influx. To gain further insights into signaling pathways involved in c-IAP2 expression, we investigated whether

**Fig. 3.7: Nucleotide sequence of the first exon and 5' flanking promoter region of c-IAP2 gene (GeneBank accession No. AF070674). NFκB binding sites are boxed. Mutation is underlined and in bold type.**

-606 at ctttaaaatg gtaaaaataa actgcaaagg agaactgcat gattttttc acataccct  
-544 acatttcctt tcaccttta ctttcttgat cagaacaaaa agtaaaaata aatagaaata  
-484 tttcaciaag tttcgatttt tttttttta aatgctggac ttctgcagct atagtagaag  
-424 attgaaaaac ctaacctttt tacgtgtaaa gtgtatggcg gatggagggt ggagaacagg  
-364 gcatattgac ctttccagg caggctaagc aatgatcgtc ctctctatat gggttgttat  
-304 caagatttcc tctgaccac gagcaatgaa gcaaagtct ttcagtaaat gccgcgaaga  
NFkB site# 1  
-244 tatgccacgg ttaagagtca tgcttttggg tcatggaaat c<sup>A</sup>c<sup>G</sup>ccgagtgg gtttgccagg  
NFkB site# 3  
-184 ccaactgatta agaggaagtg tgtgtgggta ttaccgctgg agttc<sup>A</sup>c<sup>A</sup>ctta agtcctaaaa  
-124 ggaaagcacc agtgcacatg caaaccactg ggaggagtgc ggaacgcctg gtacagatag  
-64 ggggtgggat ttgggtgacg cattt<sup>A</sup>aaaag acagcgtgag actcgcgccc tccggcacgg  
-4 aaaa ggccaggcga caggtgtcgc ttgaaaagac tgggcttgtc cttgctgggt catgcgtcgt  
+61 cggcctctgg gcagcaggtt taaaaggag gaaaacgact tcttctagat ttttttca  
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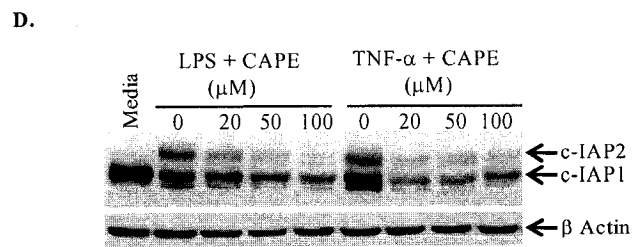
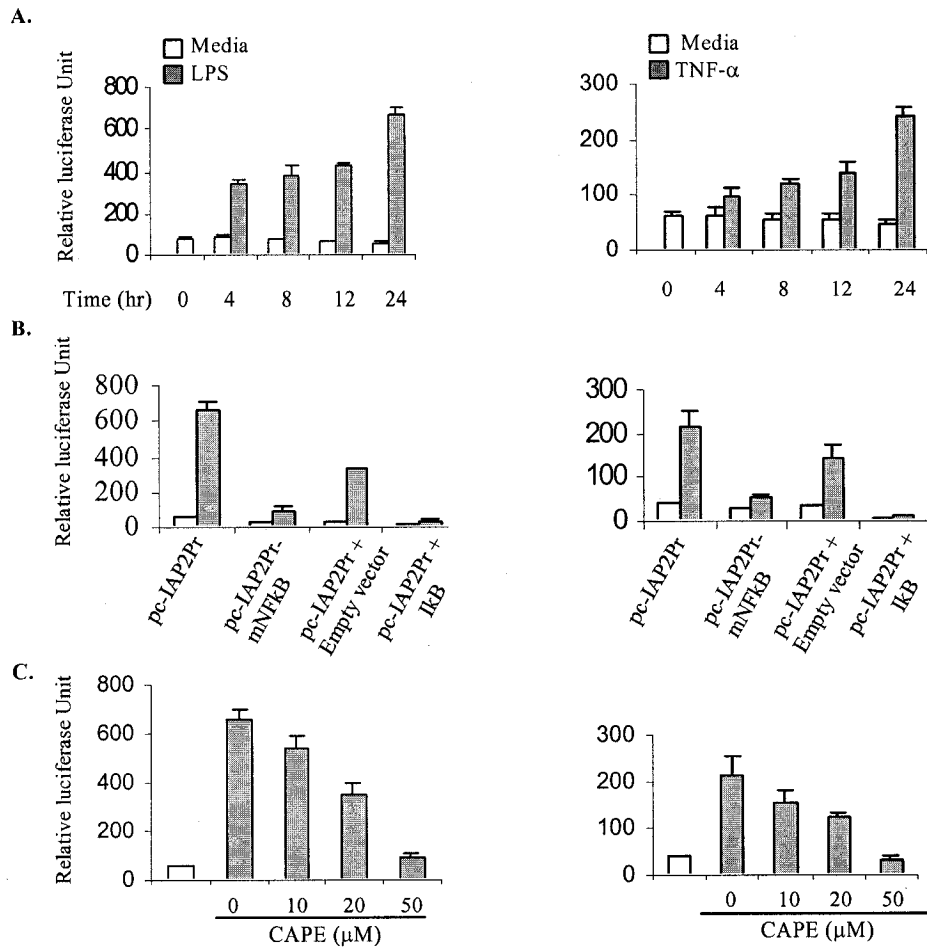
**Fig. 3.8: Involvement of the NFκB binding sites within the c-IAP2 promoter in the regulation of LPS and TNF-α-induced c-IAP2 expression.**

**A.** Kinetics of c-IAP2 promoter activity following LPS and TNF-α stimulation. THP-1 cells ( $10^6$ /ml) were transiently cotransfected with 5 μg of pc-IAP2pr-GL3B and 3 μg of β-galactosidase plasmid. After 24 h, cells were stimulated with either 1 μg/ml LPS or 10 ng/ml TNF-α for 0–24 h, followed by determination of luciferase and β-galactosidase activities. Luciferase activity was normalized for β-galactosidase activity to give relative luciferase units (RLU).

**B.** NFκB regulates c-IAP2 promoter activity. Cells ( $10^6$ /ml) were cotransfected with 5 μg of either WT pc-IAP2pr or NFκB mutant pc-IAP2pr-mNFκB, and 3 μg of β-galactosidase plasmid. Cells were also transfected with either the IκB superrepressor gene in pcDNA3 or vector alone. After 24 h, cells were stimulated with either LPS (1 μg/ml) or TNF-α (10 ng/ml), followed by determination of luciferase activity.

**C.** Cells ( $10^6$ /ml) cotransfected with 5 μg of pc-IAP2pr and 3 μg of β-galactosidase plasmid were pretreated with varying doses of CAPE (10–50 μM) for 2 h followed by stimulation with either 1 μg/ml of LPS or 10 ng/ml of TNF-α for 24 h. Cell lysates were analyzed for luciferase activity (relative luciferase units) as described for *A*. All of the results shown above are a mean ± S.D. of three experiments performed in triplicate.

**D.** Cells ( $10^6$ /ml) were pretreated with various concentrations of CAPE (20–100 μM) for 2 h prior to stimulation with either LPS (1 μg/ml) or TNF-α (10 ng/ml) for 24 h followed by determination of c-IAP2 expression by Western blot analysis. The experiment shown is representative of three different experiments.



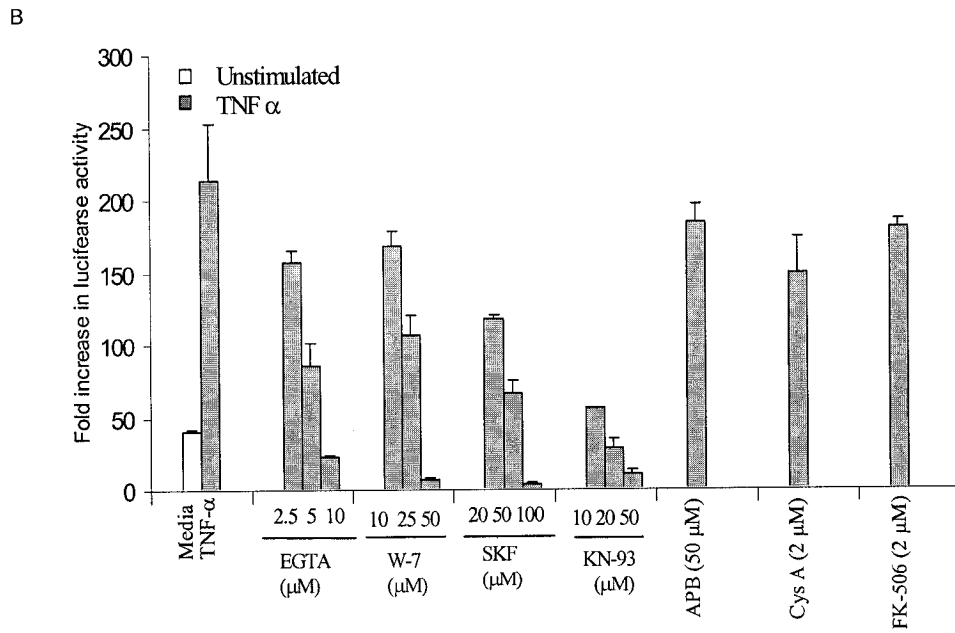
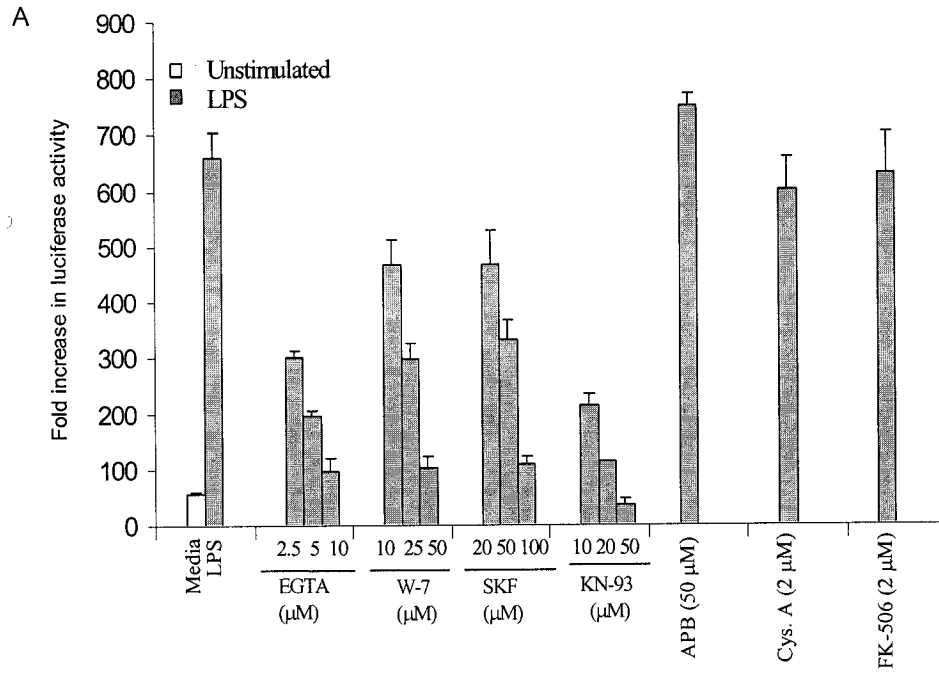
CAMKII and CaM regulate LPS- and TNF- $\alpha$ -induced c-IAP2 expression through the activation of NF $\kappa$ B. To address this issue, I examined the effect of pharmacological inhibitors of CaM and CAMKII as well as of other inhibitors of calcium signaling pathway such as EGTA, APB, SKF-96365, W-7, KN-93, FK506, and Cyclo on the luciferase activity of cells transfected with the wild type pc-IAP2Pr-GL3B following stimulation with either LPS or TNF- $\alpha$ . THP-1 cells transfected with the full length pc-IAP2Pr-GL3B plasmid were treated for 2 hr with the above mentioned inhibitors of calcium signaling pathway prior to stimulation with either LPS or TNF- $\alpha$  for 24 hr followed by measurement of luciferase activity. As expected, pretreatment of cells with either EGTA or SKF-96365 reduced the LPS- or TNF- $\alpha$ -induced luciferase activity in a dose dependent manner (Fig. 3.9A, & B)). Similar to the results observed above, the involvement of CaM and CAMKII in the regulation of c-IAP2 was confirmed as CaM antagonist W-7 and CAMKII inhibitor KN-93 significantly reduced the luciferase activity in cells in a dose dependent manner (Fig 3.9A, & B). In contrast, pretreatment of cells with high concentrations of either 2-APB, FK506 or Cyclo under similar experimental conditions did not have any effect on luciferase activity as compared with LPS/TNF- $\alpha$  stimulated cells (Fig. 3.9A, & B). These results further suggest that CaM and CAMKII regulate LPS- and TNF- $\alpha$ -induced c-IAP2 transcription through the activation of NF $\kappa$ B.

**CaM and CAMKII regulate binding of transcription factor NF $\kappa$ B to NF $\kappa$ B binding sites of c-IAP2 promoter in LPS- and TNF- $\alpha$ -stimulated THP-1 cells:**

To further confirm the role of calcium signaling pathway and in particular the role of CaM and CAMKII in the regulation of c-IAP2 gene transcription through NF $\kappa$ B activation, I investigated whether LPS and TNF- $\alpha$ -stimulation of THP-1 cells induced the

**Fig. 3.9: CaM and CAMKII regulate c-IAP2 expression in LPS- and TNF- $\alpha$ -stimulated THP-1 cells through NF $\kappa$ B activation.**

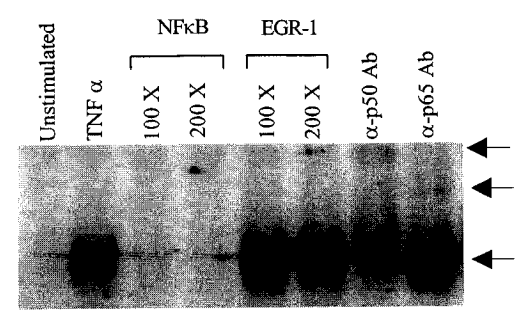
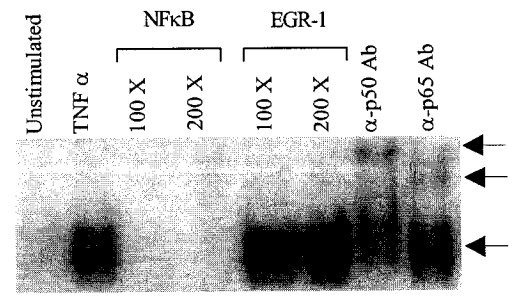
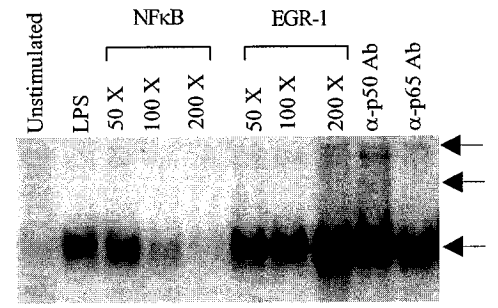
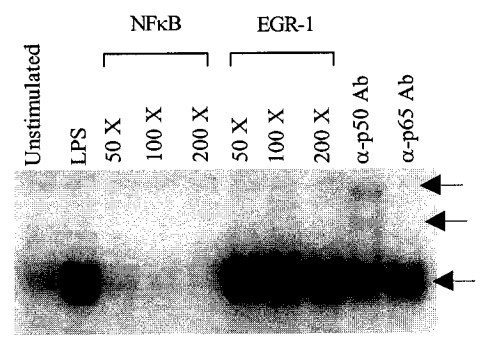
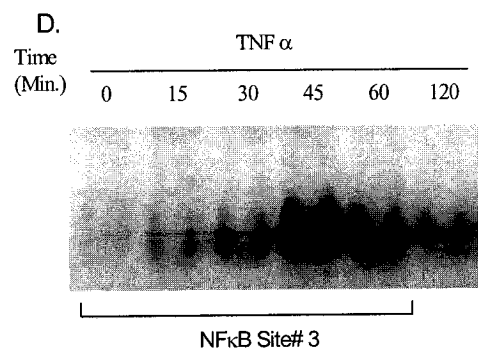
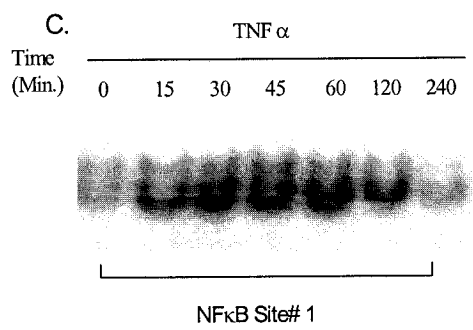
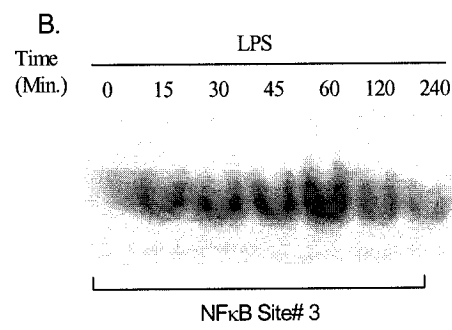
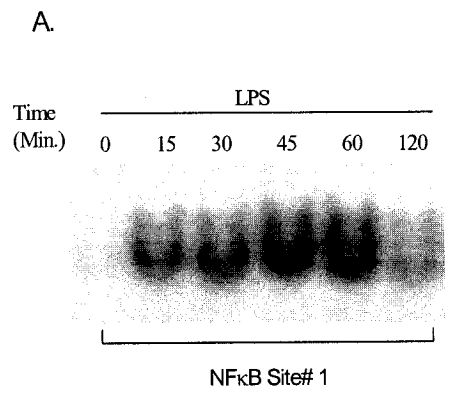
Cells ( $10^6$ /ml) were cotransfected with 5  $\mu$ g of wild type pc-IAP2pr and 3  $\mu$ g of  $\beta$ -galactosidase plasmid. After 24 h, the transfected cells were pretreated with varying concentrations of either EGTA, W-7, SKF-96365, KN-93, APB, Cyclosporin A or FK-506 for 2 h followed by stimulation with 1  $\mu$ g/ml LPS or 10 ng/ml TNF- $\alpha$  for 24 h. Cell lysates were assessed for luciferase activities (relative luciferase units; RLU) as described above in the legend of 3.7. The results shown are a mean  $\pm$  S.D. of three experiments performed in triplicate.



binding of NF $\kappa$ B to its binding sites 1 and 3 present in the c-IAP2 promoter. THP-1 cells were stimulated with LPS or TNF- $\alpha$  over a period of time ranging from 0-240 min. The nuclear extracts thus harvested from cells stimulated with either LPS or TNF- $\alpha$  for 0-4 hr were analyzed by electrophoretic mobility shift assay for binding of NF $\kappa$ B to NF $\kappa$ B oligonucleotide probes corresponding to their sites in the c-IAP2 promoter. The results show a significant binding of NF $\kappa$ B to site # 1 and # 3 in 45-60 min following stimulation of cells with either LPS or TNF- $\alpha$  (Fig. 3.10, left panels). The specificity of NF $\kappa$ B binding was demonstrated by cold competition experiments employing specific and non-specific oligonucleotides and by super shift analysis with anti NF $\kappa$ B p50 and p65 antibodies (Fig. 3.10, right panels). To determine whether binding of NF $\kappa$ B to the NF $\kappa$ B binding sites # 1 and # 3 in the c-IAP2 promoter was regulated by the pharmacological inhibitors of the calcium signaling pathway, THP-1 cells were treated with pharmacological inhibitors of CaM and CAMKII as well as of other inhibitors of calcium signaling pathway such as EGTA, APB, SKF-96365, FK506, and Cyclo for 2 hr before stimulation with either LPS or TNF- $\alpha$  for 60 and 45 min, respectively, followed by analysis of NF $\kappa$ B binding to its corresponding oligonucleotide probes. The results suggest that both EGTA and SKF-96365 inhibited binding of NF $\kappa$ B to NF $\kappa$ B oligonucleotide probes corresponding to both NF $\kappa$ B sites #1 and # 3, in LPS and TNF- $\alpha$  stimulated THP-1 cells (Fig. 3.11A, & B). The involvement of CaM and CAMKII in c-IAP2 transcription was similarly demonstrated by showing that pretreatment of cells with either W-7 or KN-93 inhibited the binding of NF $\kappa$ B to its sites on c-IAP2 promoter in both LPS and TNF- $\alpha$ -stimulated THP-1 cells (Fig. 3.11A, B, & C). Taken together, the

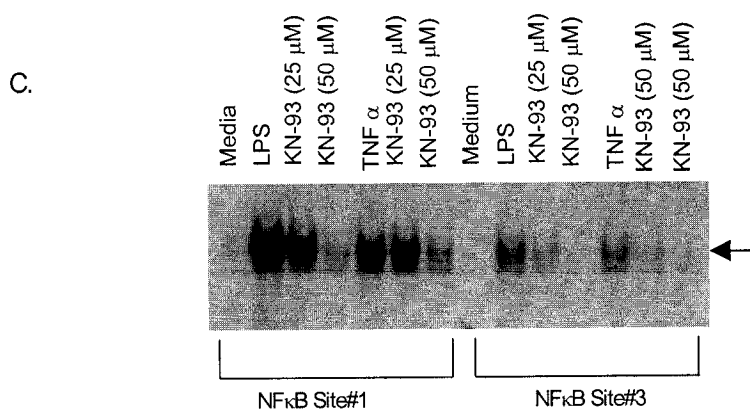
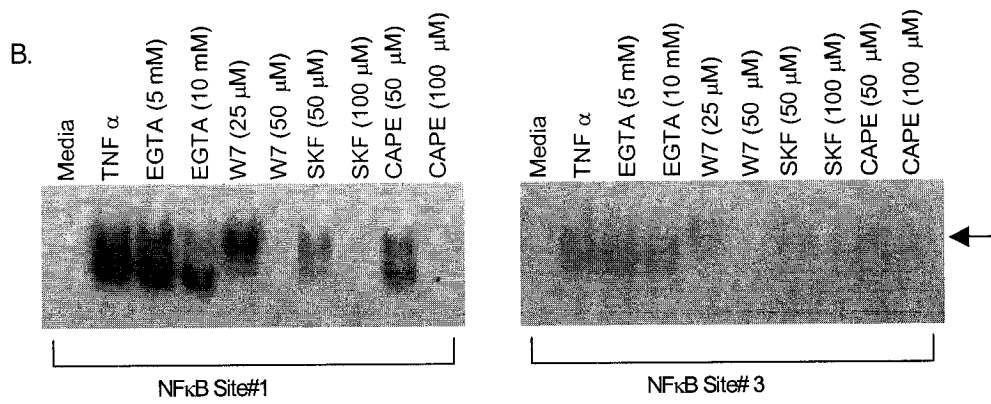
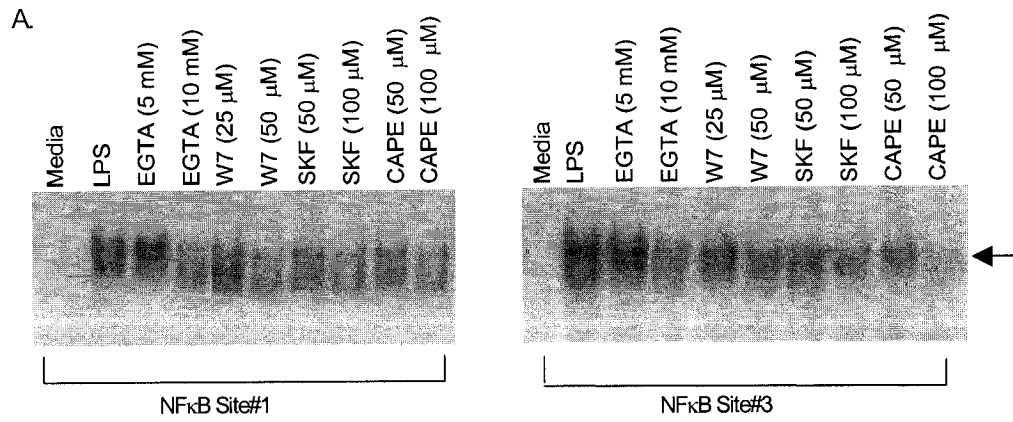
**Fig. 3.10: A, B, C, & D. NFκB transcription factor binds to the site 1 and 3 of NFκB on the c-IAP2 promoter in LPS- and TNF-α-stimulated cells.**

Cells were stimulated with either LPS (1 μg/ml) or TNF-α (10 ng/ml) for 0-240 min for time course and cells were also stimulated with LPS for 60 min and TNF-α for 45 min for rest of the experiments. Nuclear proteins (5 μg) were incubated with <sup>32</sup>P-labeled oligonucleotide probes corresponding to NFκB site 1 and 3 sequences derived from the c-IAP2 promoter. The specificity of NFκB binding was determined by incubating nuclear proteins with unlabeled NFκB or nonspecific Egr-1 oligonucleotides. The supershift analysis was performed by treating the nuclear proteins with oligonucleotide probes in the presence or the absence of anti-p50 or anti-p65 NFκB antibodies. The supershifted bands are indicated by arrows. The results shown are representative of three different experiments.



**Fig 3.11: A, B, & C. CaM and CAMKII regulate binding of NFκB to its binding sites on the c-IAP2 promoter in LPS- and TNF-α-stimulated cells.**

THP-1 cells were pretreated with either EGTA, W-7, SKF-96365, CAPE, or KN-93, for 2 h followed by stimulation with 1 μg/ml LPS or 10 ng/ml TNF-α for 60 and 45 min, respectively. Nuclear proteins (5 μg) were analyzed for NFκB binding by <sup>32</sup>P-labeled oligonucleotide probes corresponding to site 1 and 3 sequences. The results shown are representative of three different experiments.



results suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 gene transcription may be selectively regulated by CaM and CAMKII through the activation of NF $\kappa$ B.

### **CaM and CAMKII regulate LPS- and TNF- $\alpha$ -mediated inhibition of apoptosis in THP-1 cells:**

In view of the above results suggesting the involvement of CaM and CAMKII in c-IAP2 expression, I determined whether CaM and CAMKII also regulated LPS- and TNF- $\alpha$ -mediated inhibition of apoptosis in THP-1 cells. Cells were treated with various inhibitors of the calcium signaling pathway for 2 hr before stimulation with either LPS or TNF- $\alpha$  followed by analysis of staurosporine-induced apoptosis by PI staining. As expected, stimulation with either LPS or TNF- $\alpha$  inhibited staurosporine-induced apoptosis in a dose dependent manner. Significantly, prior treatment of cells with EGTA, SKF-96365, W-7, and KN-93 reversed the LPS- and TNF- $\alpha$ -mediated inhibition of staurosporine induced apoptosis, whereas inhibitors of MAPK, PI3K, and calcineurin did not have any effect (Fig. 3.12A).

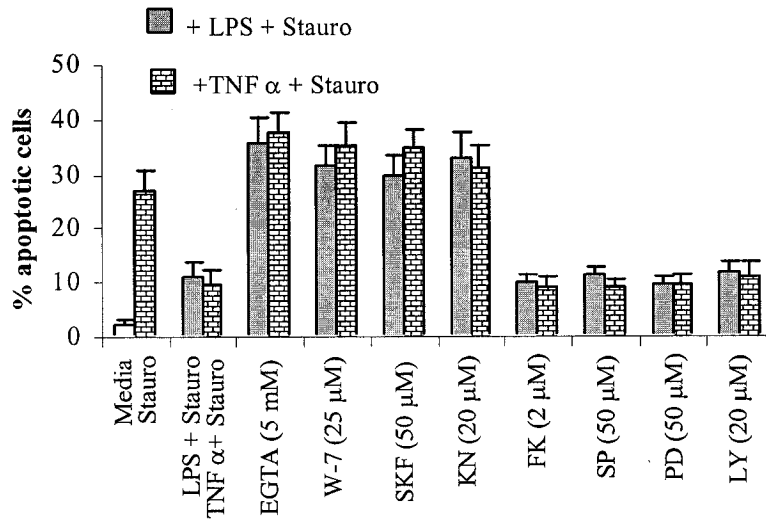
To further confirm the involvement of CAMKII in LPS- and TNF- $\alpha$ -mediated inhibition of apoptosis, THP-1 cells were transfected with a DN CAMKII mutant construct. After 24 hr, transfected cells were stimulated with either LPS or TNF- $\alpha$  followed by analysis of staurosporine-induced apoptosis. Stimulation with either LPS or TNF- $\alpha$  of cells transfected with control vector inhibited staurosporine-induced apoptosis. In contrast, transfection of cells with DN CAMKII mutant construct reversed the LPS- and TNF- $\alpha$ -mediated inhibition of staurosporine-induced apoptosis (Fig 3.12B).

**Fig. 3.12: A. CaM and CAMKII regulate LPS- and TNF- $\alpha$ -mediated inhibition of apoptosis in THP-1 cells.**

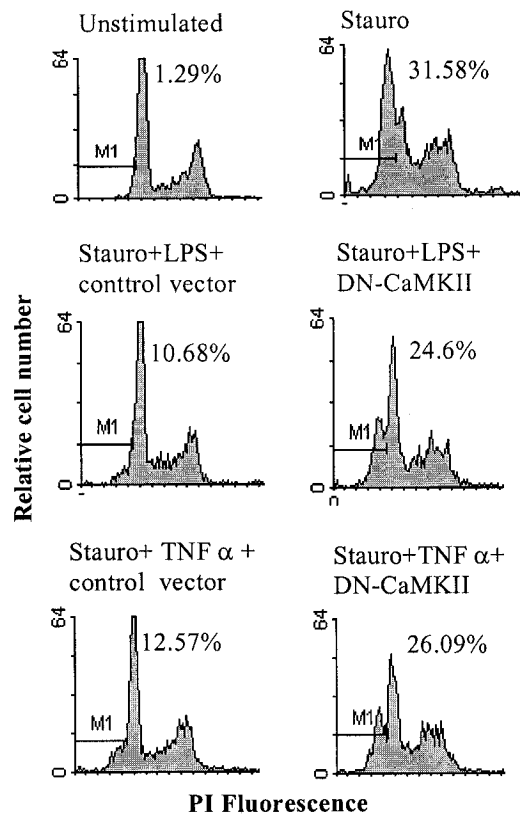
**A.** Cells ( $1 \times 10^6$ /ml) were pretreated with indicated doses of either EGTA, W-7, SKF-96365, KN-93, FK506, SP600125, PD98059, or LY294002 for 2 h prior to stimulation with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml). After 24 h, cells were treated with staurosporine (2  $\mu$ M) for 4 h followed by analysis of apoptotic cells by PI staining and flow cytometry. The results shown are mean  $\pm$  S.D. of three different experiments.

**B.** DN CAMKII reverses LPS- and TNF- $\alpha$ -mediated inhibition of staurosporine-induced apoptosis in THP-1 cells. Cells ( $1 \times 10^6$ /ml) were transfected with either 5  $\mu$ g of DN-CAMKII plasmid or control vector and cultured for 24 h followed by stimulation with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for another 24 h. Stimulated cells were treated with staurosporine (Stauro)(2  $\mu$ M) for 4 h, following which DNA content of cells was analyzed by PI staining. The values shown in the histograms indicate percentage of apoptotic cells. The experiment shown is representative of three different experiments.

A.



B.



Overall, my findings suggest that c-IAP2 is induced by LPS through the endogenous production of TNF- $\alpha$  and it is regulated selectively by CAMKII through activation of NF $\kappa$ B. c-IAP2 also plays a key role in monocytic cell survival.

## **Discussion:**

Monocytes/macrophages play a central role in orchestrating the immune response to infection and tumors. In the absence of appropriate stimulus, monocytes are programmed to undergo a sequence of events leading to apoptosis. Modulation of monocyte apoptosis by either endotoxin or pro-inflammatory cytokines may be closely associated with the outcome of inflammation. Both LPS and TNF- $\alpha$  have been shown to induce the expression of various anti-apoptotic proteins including members of the Bcl2 and IAP families in various cell types such as Jurkat T cells, primary endothelial cells and human monocytic cells [182;189-191;197;294]. However, the molecular mechanism by which LPS and TNF- $\alpha$  induce anti-apoptotic activity in monocytic cells remains unknown. I have demonstrated that LPS- and TNF- $\alpha$ -induced c-IAP2 expression and its associated anti-apoptotic survival signals in THP-1 cells are regulated selectively by CaM/CAMKII through NF $\kappa$ B activation.

It is well known that cytokines produced during inflammation affect monocyte survival. LPS, a component of bacterial endotoxin and a potent inducer of proinflammatory cytokine TNF- $\alpha$ , has been shown to prevent apoptosis. TNF- $\alpha$  has also been shown to prevent apoptosis in *Mycobacterium tuberculosis* infected monocytes. I have investigated the role of IAP family of anti-apoptotic genes in LPS-/TNF- $\alpha$ -induced resistance to apoptosis. My results revealed that c-IAP1 is constitutively expressed in THP-1 cells, whereas, the level of expression of c-IAP2 is very low, even sometimes non-detectable. It is interesting to observe that c-IAP1 and c-IAP2 are differentially induced following stimulation with LPS and TNF- $\alpha$  in THP-1 cells suggesting a cell type

specific role for these molecules. Specific inhibition of c-IAP2 by antisense oligonucleotides reversed LPS- and TNF- $\alpha$ -mediated protection from staurosporine-induced apoptosis suggesting a key role for c-IAP2 in this anti-apoptotic effect. Furthermore, LPS-induced c-IAP2 expression was regulated by the endogenous production of TNF- $\alpha$ . The IAP family of proteins has been shown to suppress apoptosis induced by a variety of stimuli including TNF- $\alpha$ , Fas, and growth factor withdrawal by inhibiting activation of procaspase-9, and active caspase-3 and caspase-7 [164;170]. In addition, c-IAP2 appears to be a part of the signaling complex recruited to the cytoplasmic domain of TNFR by binding to the TRAF-1/TRAF-2 heterocomplexes and functions to suppress caspase-8 activation [161;164;168]. These observations suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 may inhibit apoptosis by acting on caspases in THP-1 cells.

LPS exerts its effects following its association with the plasma-LPS-binding protein and the binding of this complex with the CD14/TLR-4 complex. Therefore, regulation of LPS-induced c-IAP2 expression in monocytic cells may involve a combination of signals delivered by the interaction of LPS with the CD14/TLR complex as well as by the interaction of endogenously produced TNF- $\alpha$  with its cognate receptors TNFR1 and TNFR2. Although TNF-induced cell death is mediated primarily by TNFR1, both TNF receptors can transduce signals leading to the activation of transcription factors including NF $\kappa$ B that help cells to survive. It is believed that NF $\kappa$ B activation leads to the upregulation of many TNF responsive genes such as c-IAP2. The molecular signaling pathways particularly the upstream signaling molecules involved in upregulation of c-

IAP2 in monocytic cells in response to stimulation with either LPS or TNF- $\alpha$  are not known.

Apoptosis has been shown to be regulated by a number of upstream protein kinases activation including MAPK and PI3K in epithelial and leukemic cells [168;196;297;297;307;308]. Recently, JNK was shown to mediate the anti-apoptotic activity of XIAP [196], whereas p38 and ERK MAPKs were shown to regulate c-IAP2 expression in colon cancer cell lines [198]. I first investigated the role of MAPK and PI3K in LPS- and TNF- $\alpha$ -induced c-IAP2 expression. Although both LPS- and TNF- $\alpha$ -induced the activation of p38, ERK, and JNK MAPK, and PI3K in this study, none of these kinases were involved in LPS- or TNF- $\alpha$ -induced c-IAP2 expression or anti-apoptotic activity in monocytic cells. Specific MAPKs and PI3K inhibitors, even when used at very high concentrations failed to inhibit either LPS- or TNF- $\alpha$ -induced c-IAP2 expression.

Because of the lack of involvement of these major signaling pathways, I investigated the role of upstream Ca<sup>2+</sup> signaling proteins, which are important intracellular messengers in many biological processes including apoptosis [244;298]. Influx of Ca<sup>2+</sup> through ligand and voltage gated calcium channels in the plasma membrane together with Ca<sup>2+</sup> release from ER stores, results in complex calcium signaling cascades [244;298]. Several mechanisms may control Ca<sup>2+</sup> entry in response to external stimuli including membrane depolarization, activation of intracellular messengers, and depletion of intracellular calcium storage [299]. The release of Ca<sup>2+</sup> from internal stores (ER) is controlled by Ca<sup>2+</sup> itself or by an expanding group of messengers. For example, the inositol 1,3,4 triphosphate (IP3), produced in response to a

signal from the membrane lipid phosphatidyl inositol, triggers  $\text{Ca}^{2+}$  release from the ER after binding to the IP3 receptor [299].

Calcium signaling has been shown to play a key role in LPS- and TNF- $\alpha$ -induced regulation of several genes [309-315]. Both LPS and TNF- $\alpha$  have been shown to induce calcium flux by several laboratories [309-311;316-319]. Furthermore, lipid A component of LPS has been suggested to markedly enhance free intracellular calcium [316]. There is also evidence to suggest that the sources of increased cytosolic calcium are extracellular calcium as well as stored calcium from the endoplasmic reticulum [320]. To determine the role of  $\text{Ca}^{2+}$  signaling pathway, we first employed EGTA, the  $\text{Ca}^{2+}$  chelator, which is known to block the binding of  $\text{Ca}^{2+}$  to any other molecules. EGTA inhibited the expression of c-IAP2 to its basal level in a dose dependent manner in both LPS- and TNF- $\alpha$ -stimulated cells. I further examined the source of  $\text{Ca}^{2+}$  (extracellular/intracellular or both) involved in regulation of c-IAP2. To understand the role of extracellular  $\text{Ca}^{2+}$ , I employed SKF-96365, a  $\text{Ca}^{2+}$  channel blocker that prevents the entry of extracellular  $\text{Ca}^{2+}$  from the plasma membrane into the cytosol. SKF-96365 inhibited the induction of c-IAP2 in both LPS and TNF- $\alpha$  stimulated THP-1 cells. It is known that entry of extracellular  $\text{Ca}^{2+}$  is activated itself or by release of  $\text{Ca}^{2+}$  from intracellular stores (ER). To check the involvement of intracellular  $\text{Ca}^{2+}$  release, I used 2-APB, one of the IP3 receptor blockers on ER. I demonstrated that blocking of intracellular release of  $\text{Ca}^{2+}$  did not alter the c-IAP2 induction. The results of this study suggest that LPS- and TNF- $\alpha$ -mediated c-IAP2 expression and anti-apoptotic activity required extracellular influx of  $\text{Ca}^{2+}$  into the cytosol. However, calcium influx observed after LPS or TNF- $\alpha$  stimulation was observed several minutes after stimulation compared to some highly potent agents

such as ionomycin in which calcium influx is observed within seconds. Although LPS has been found to increase ( $\text{Ca}^{2+}$ ) ion, and that the lipid A component has been specifically found to trigger calcium flux [316;321], the precise mechanism by which LPS and TNF- $\alpha$  impact calcium signaling is still not understood.

Calmodulin, a key signaling protein responsible for integrating the  $\text{Ca}^{2+}$  signal with transcription factor activation, is known to regulate cell cycle and related cytoskeletal functions and ion channel activity [299;322;323]. CaM is highly conserved among different species with 148 aa residues and a M.W. of 17 kD. Following binding to  $\text{Ca}^{2+}$ , CaM undergoes a conformational change that renders it active and able to recognize and bind target proteins with high affinity. To determine the role of CaM, I employed CaM antagonist, W-7, which inhibited c-IAP2 expression in both LPS- and TNF- $\alpha$ -stimulated THP-1 cells [299;323]. Amongst the possible downstream targets of CaM are calcineurin and CAMKII [324-326]. Since one of the targets of CaM is calcineurin, I further used two pharmacological inhibitors, Cyclo and FK-506 to demonstrate whether CaM regulates c-IAP2 expression via calcineurin activation. Neither inhibitor affected c-IAP2 expression suggesting that calcineurin is not involved in c-IAP2 regulation in both LPS- and TNF- $\alpha$ -stimulated THP-1 cells.

Another kinase known to be activated by CaM is CAMKII.  $\text{Ca}^{2+}$ /CAMKII was found to have relatively broad substrate specificities with respect to endogenous protein substrate in nervous system. CAMKII from rat brain is a large multimeric enzyme composed of two related subunits with  $9\alpha$  (50 kDa) and  $3\beta$  (60 kDa), respectively. Like other kinases, it undergoes an autophosphorylation that seems to be an intramolecular process. The autophosphorylation of  $\text{Ca}^{2+}$ /CAMKII on a threonine residue contained in a

phosphopeptide common to  $\alpha$  and  $\beta$  subunits converts it into a  $\text{Ca}^{2+}$ /CaM independent enzyme [191]. To determine the role of CAMKII, I used KN-93, a selective inhibitor of CAMKII. KN-93 selectively and directly binds to CaM binding site of CAMKII or its vicinity and prevents the association of CaM with CAMKII. My results show that KN-93 significantly inhibited c-IAP2 expression in a dose dependent manner. Furthermore, I confirmed the involvement of CAMKII by using DN CAMKII construct in c-IAP2 expression suggesting that CAMKII acts as a key link for CaM activation and c-IAP2 expression. I also demonstrated that LPS and TNF- $\alpha$  induced CAMKII plays an important role in mediating protection to staurosporine induced apoptosis. Taken together, my results clearly suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 expression and its associated anti-apoptotic activity are regulated distinctly by calmodulin/CAMKII.

NF $\kappa$ B plays an important role in cell development, cell survival and oncogenesis and mediates its function through homodimer or heterodimers formed by NF $\kappa$ B/Rel family members (RelA/p65, RelB, C-Rel, NF $\kappa$ B1/p50 and NF $\kappa$ B2/p52) [303]. The activity of NF $\kappa$ B is strictly regulated by one of the I $\kappa$ B-inhibiting proteins such as I $\kappa$ B $\alpha$  or I $\kappa$ B $\beta$ , which form a complex with NF $\kappa$ B and keeps NF $\kappa$ B sequestered in cytoplasm. Upon activation, I $\kappa$ B becomes phosphorylated, ubiquitinated and subsequently degraded by proteasome, enabling nuclear translocation of NF $\kappa$ B and participation in transactivation of a variety of genes [303;304]. Inhibition of NF $\kappa$ B, one of the upstream signaling pathways during TNF- $\alpha$  stimulation, has been shown to induce apoptosis in a variety of cell types originally resistant to TNF- $\alpha$ - induced apoptosis.

Intracellular mobilization of  $\text{Ca}^{2+}$  triggered by various stimuli is known to act as a key second messenger necessary for the induction of NF $\kappa$ B activity [247;324;326].

Furthermore, the protective role of NF $\kappa$ B against apoptosis is believed to be mediated by the induction of various anti-apoptotic genes including IAPs. NF $\kappa$ B has been shown to regulate c-IAP2 gene transcription in Jurkat T cells in response to stimulation with TNF- $\alpha$ . In this study, I demonstrate for the first time that LPS- and TNF- $\alpha$ -induced c-IAP2 expression is regulated by NF $\kappa$ B. It has been shown that two NF $\kappa$ B elements are required for promoter activity and they function cooperatively in mediating TNF- $\alpha$ -induced c-IAP2 promoter activity [191]. The involvement of both NF $\kappa$ B binding sites in the upregulation of LPS- and TNF- $\alpha$ -induced c-IAP2 expression was demonstrated by analysis of c-IAP2 promoter activity and gel shift assays. The involvement of NF $\kappa$ B was confirmed by employing its specific physiological inhibitor, CAPE, and by co-transfection of cells with I $\kappa$ B superrepressor and c-IAP2 promoter constructs.

Having shown the role of calcium and NF $\kappa$ B in LPS- and TNF- $\alpha$ -induced c-IAP2 expression, I examined whether LPS- and TNF- $\alpha$ -induced c-IAP2 expression is regulated by NF $\kappa$ B through intracellular calcium mobilization and subsequent activation of calmodulin/calmodulin kinase signaling pathway. My results clearly show that prevention of receptor-mediated Ca<sup>2+</sup> entry by specific inhibitor SKF 96365 inhibited LPS- and TNF- $\alpha$ -induced c-IAP2 expression, NF $\kappa$ B activity in the c-IAP2 promoter and the binding of NF $\kappa$ B transcription factor to its binding sites on the c-IAP2 promoter. In contrast, blocking of Ca<sup>2+</sup> release from ER failed to have any effect on the NF $\kappa$ B activity or NF $\kappa$ B binding to its promoter. This identified a calcium triggered signaling cascade which may stimulate p50/p65 NF $\kappa$ B transactivating potential eventually leading to c-IAP2 gene transcription. I therefore investigated if calmodulin and calmodulin kinase

could establish a link between receptor-mediated intracellular mobilization of  $\text{Ca}^{2+}$  on one hand and p50/p65 NF $\kappa$ B on the other. Surprisingly, I found that CaM and the CAMKII, one of the pathways linking calcium signal to downstream transcription factors, regulated c-IAP2 expression through the activation of NF $\kappa$ B. W-7 and KN-93, the CaM and CAMKII inhibitors, respectively, inhibited LPS- and TNF- $\alpha$ -induced c-IAP2 expression, NF $\kappa$ B activity in the c-IAP2 promoter and the binding of NF $\kappa$ B transcription factor to its binding sites on the c-IAP2 promoter. In contrast, calcineurin, the other pathway linking calcium with the downstream transcription factor, did not influence NF $\kappa$ B activity in the c-IAP2 promoter. Intracellular mobilization of calcium triggered by various stimuli is known to induce NF $\kappa$ B activity in different cell types suggesting that  $\text{Ca}^{2+}$  acts as a key second messenger necessary for the induction of NF $\kappa$ B activity. CAMKII has also been previously demonstrated to act as a mediator of IKK activation specifically in response to T cell receptor/CD3 and phorbol ester stimulation [305;306]. A recent report has also demonstrated that CAMKII transactivates p65 subunit of NF $\kappa$ B. In conclusion, in the present work, I show that intracellular mobilization of  $\text{Ca}^{2+}$  selectively activates CaM/CAMKII kinase pathway to induce NF $\kappa$ B phosphorylation and eventually c-IAP2 expression.

At present, the role of c-IAP1 in LPS- and TNF- $\alpha$ -mediated anti-apoptotic effect is not clear. Both c-IAP1 and c-IAP2 have been suggested to contribute towards apoptotic resistance of different cancers [199]. The genes encoding c-IAP1 and c-IAP2 share 75% homology at the level of nucleotide and amino acid sequence and are thought to have arisen from a gene duplication event [172]. The molecular mechanism involved in the regulation of c-IAP1 expression is not clear at present. Herein, I show that c-IAP1 is

expressed constitutively, and is not induced by either LPS or TNF- $\alpha$ . Furthermore, constitutive expression of c-IAP1 may be regulated selectively by the calcium pathway as its expression levels were down-regulated by EGTA, SKF, and W-7. However, c-IAP1 does not seem to be regulated by the CAMKII pathway as its inhibitor KN-93 inhibited LPS/TNF- $\alpha$ -induced expression of c-IAP2 alone. Since expression levels of c-IAP1 are not affected by antisense c-IAP2 oligonucleotides, LPS- and TNF- $\alpha$ -induced anti-apoptotic activity may not be regulated by c-IAP1. It is likely that c-IAP1 may have a role in spontaneous survival of THP-1 cells. Furthermore, the role of other inhibitory proteins including Bcl2 and other members of the IAP family in LPS- and TNF- $\alpha$ -induced anti-apoptotic activity can not be ruled out and needs further investigation.

In summary, this is the first study that demonstrates the involvement of c-IAP2 in LPS and TNF- $\alpha$ -induced anti-apoptotic survival of human monocytic cells. My results clearly suggest that LPS- and TNF- $\alpha$ -induced c-IAP2 expression and its associated anti-apoptotic activity are regulated distinctly by CaM/CAMKII through the activation of NF $\kappa$ B pathway. Since c-IAP2 is one of the important anti-apoptotic genes in cell apoptosis and recruited to TNFR signaling complex, understanding the regulation of this gene and characterization of signal transduction pathways may help in providing insight into general TNF signaling in regulation of NF $\kappa$ B, one of the prosurvival transcription factors in various cell types. In addition to that, modulation of signaling molecules involved in c-IAP2 upregulation may be helpful in controlling infection with pathogenic organisms and inflammatory responses.

## Chapter IV

*Molecular mechanism involved in induction  
of resistance by LPS to Vpr-mediated  
apoptosis in monocytes*

## **Introduction:**

It is well known that cells of the myelomonocytic lineage play a crucial role in HIV pathogenesis and disease progression [3;327;328]. Monocytic cells which play a central role in both innate and acquired immunity are productively infected by HIV as are CD4<sup>+</sup> activated T cells, however, unlike CD4<sup>+</sup> T cells, monocytic cells survive HIV replication without major signs of HIV-induced cytopathic effects [8]. Persistently infected monocytic cells serve as a major reservoir of HIV in lymphoid tissues at all stages of disease [329-331] and represent a key challenge to eradicate HIV infection by eliminating virus reservoirs in spite of use of antiretroviral therapy [332-336]. It is believed that one of the reasons by which monocytic cells escape HIV cytopathic effects is the capacity of HIV to decrease the sensitivity of this cell type to apoptosis. This hypothesis was supported by a couple of studies demonstrating that cytokines such as nerve growth factor [39] and IL-13 can rescue monocytic cells from the cytopathic effects of HIV [40]. However, there is evidence to suggest that monocytic cells or monocyte derived macrophages from HIV infected patients and monocytic cell line U937 infected *in vitro* with HIV exhibit enhanced propensity to apoptosis [41-43].

The first part of my research work was to investigate the molecular mechanisms involved in resistance to apoptosis in human monocytic cells. I demonstrated that monocytic cells exhibit resistance to staurosporine induced apoptosis by upregulating anti-apoptotic c-IAP2 gene [11]. However, staurosporine is not considered as a physiological trigger to cause apoptosis. In an attempt to understand protection against apoptosis in response to physiological stimuli, I employed Vpr, the accessory protein of HIV-1, which is believed to interfere with cell proliferation and causes growth arrest in

the G2/M phase of the cell cycle and apoptosis in several cell types including CD4+ T cells and neuronal cells [35;117;120;337;338]. More specifically, I employed a synthetic peptide corresponding to the C-terminal 52-96 amino acid sequence of Vpr (Vpr52-96). The apoptotic effect of Vpr has been shown to be mimicked by the C-terminal Vpr52-96 but not by the N-terminal Vpr1-51 moiety [101;102]. My preliminary results suggest that this Vpr52-96 peptide interestingly induced apoptosis in normal human monocytic cells as well as in the promonocytic THP-1 cells. Furthermore, Vpr-induced apoptotic effect in both cell types could be reversed by pretreatment of cells with LPS. Based on these observations, I hypothesize that TNF- $\alpha$ , the cytokine known to be produced in abundance in HIV infection may be one of the critical factors responsible for protecting monocytic cells from the apoptotic effects of Vpr and consequently promoting monocytic cells to act as potent viral reservoirs [339-341]. However, the mechanism responsible for the resistance developed by the monocytes to undergo apoptosis in HIV infection is not known. *Therefore, in the second part of my research work I studied the intracellular signaling pathways responsible for inducing apoptosis in response to Vpr52-96 peptide as a model. In addition, I also studied the signaling molecules and/or the anti-apoptotic/pro-apoptotic genes responsible for inducing LPS mediated protective anti-apoptotic signals in monocytic cells.*

First of all, I investigated the signaling pathways in particular the role of MAPKs, and the transcription factors involved in the regulation of genes mediating Vpr52-96 induced apoptosis in primary human monocytes and human promonocytic THP-1 cells. My results suggest that Vpr1-45 and Vpr52-96 peptides induced phosphorylation of all the three p38, ERK and JNK MAPKs, however, Vpr52-96 induced apoptosis was regulated

selectively through JNK activation. Furthermore, Vpr induced apoptosis was mediated by downregulation of anti-apoptotic genes Bcl2 and c-IAP1 through activation of upstream JNK MAPKs.

Further, I demonstrated for the first time that LPS-/TNF- $\alpha$ -induced resistance to Vpr52-96 mediated apoptosis. I also investigated the involvement of c-IAP2 and its regulation by calcium signaling pathway in this process. Pretreatment of cells with Vpr52-96 peptide inhibited LPS-/TNF- $\alpha$ -induced calcium influx, activation of CAMKII, and c-IAP2 induction as determined by Western blot and luciferase assays. Furthermore, Vpr peptide inhibited the binding of NF $\kappa$ B to its binding site on the c-IAP2 promoter as determined by gel shift analysis. Taken together, my results suggest that c-IAP2 gene plays a critical role in LPS- and TNF- $\alpha$ -induced resistance to HIV-Vpr-mediated apoptosis in human monocytic cells.

## **Objective # 1**

### **Signaling pathways involved in Vpr-induced apoptosis.**

#### **Results:**

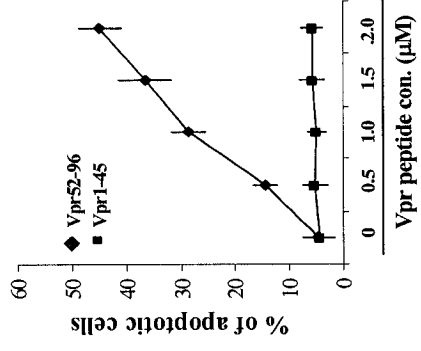
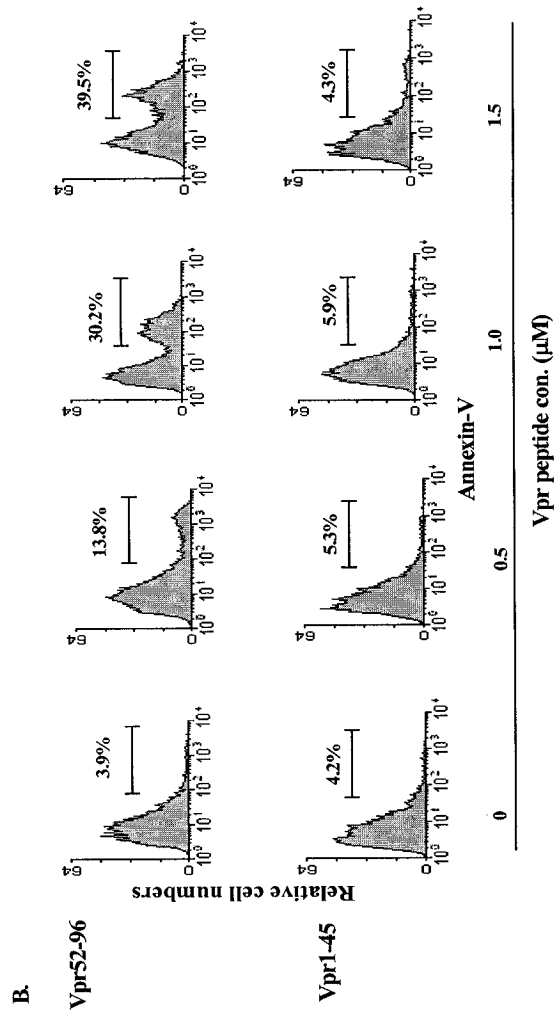
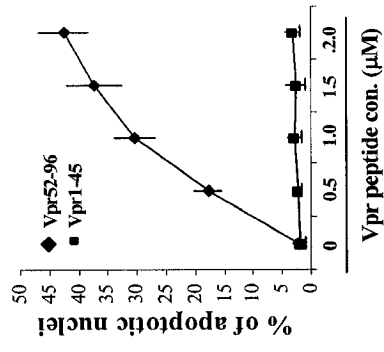
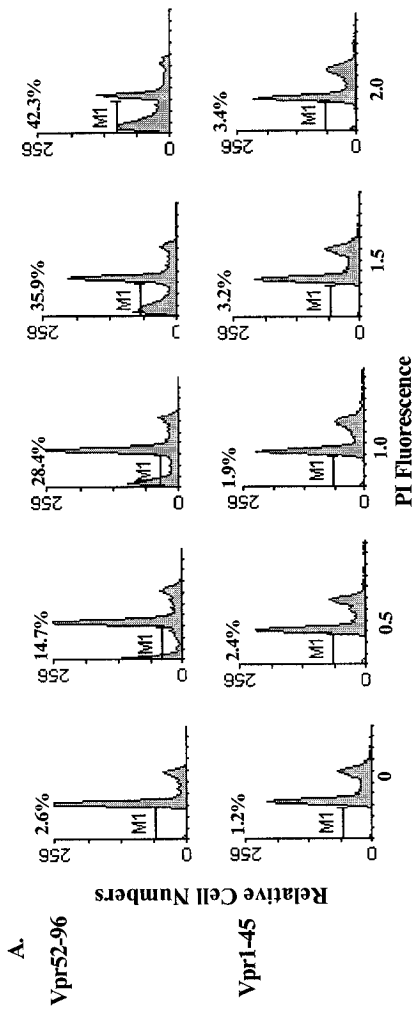
#### **Vpr52-96 peptide induces apoptosis in THP-1 cells:**

C-terminal region of Vpr containing highly conserved amino acid sequences was shown to cause cell cycle arrest and apoptosis in T cells [102;123;286]. To determine if monocytic cells transduced with Vpr peptides undergo a similar cell cycle arrest, THP-1 cells were treated with various concentrations of Vpr52-96 or Vpr1-45 peptides for 24 hr followed by cell cycle analysis and apoptosis as determined by PI and annexin-V staining and flow cytometry. As shown in Fig. 4-1.1A, & B, Vpr52-96 in contrast to Vpr1-45 peptide induced apoptosis in a dose dependent manner, with approximately 40% cells showing apoptosis at a concentration of 2  $\mu$ M. These results suggested that Vpr52-96 peptide selectively arrested cells at G2/M phase of the cell cycle. To further confirm, stimulated cells were also analysed by annexin/PI staining. Annexin detects the phosphatidyl serine positive cells, which is exposed to cell surface in apoptotic cell in the very early stage of apoptosis. Similar kind of results were obtained in annexin/PI staining with 45% of apoptosis detected in Vpr52-96 treated cells as compared to 7% in Vpr1-45 treated cells (Fig. 4-1.1B).

In the apoptotic signal transduction pathway, mitochondria play a key role by releasing caspase-activating apoptotic factors such as cytochrome C released during mitochondrial membrane potential loss [342]. To elucidate further the mechanism

**Fig. 4-1.1: Vpr52-96-induced apoptosis in THP-1 cells:**

Cells ( $0.5 \times 10^6$ /ml) were stimulated with various concentrations of Vpr52-96 or Vpr1-45 peptide for 24 h followed by staining with intracellular PI for DNA content (**A**) and annexin-V/PI for measurement of apoptosis (**B**). The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.



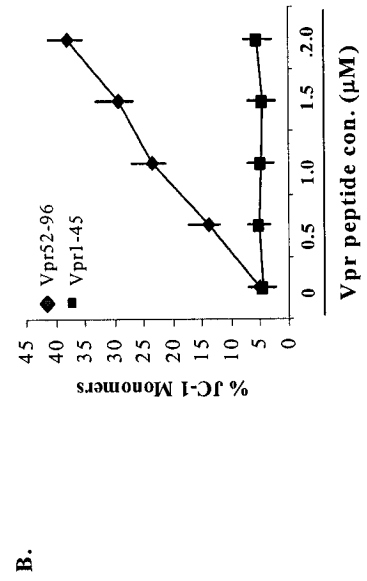
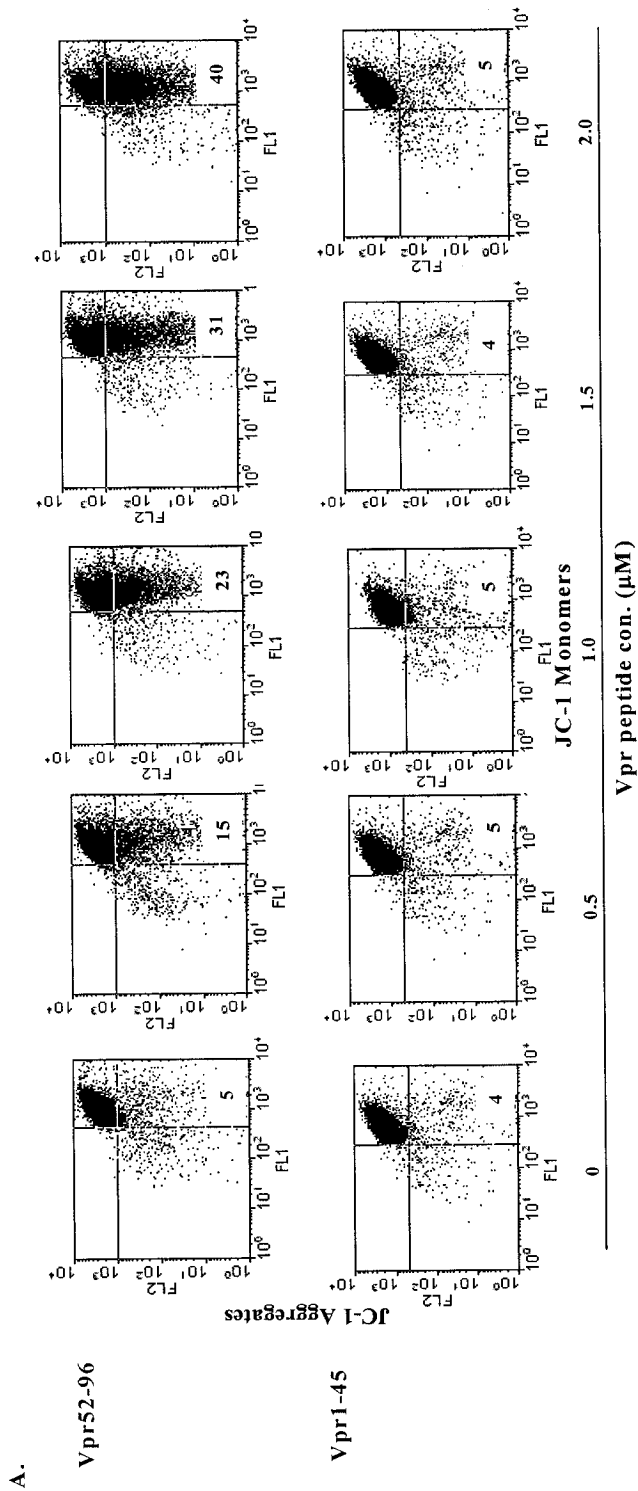
underlying Vpr-induced apoptosis with respect to the loss of mitochondrial membrane potential, Vpr52-96 and Vpr1-45 peptides treated cells were stained with JC-1 and analyzed by flow cytometry. JC-1 is a lipophilic cation agent that can form an orderly arrangement in an electric field generating aggregates revealed as orange red fluorescent color around normally functioning mitochondria in healthy cells in contrast to the exaggerated monomeric green form in the apoptotic cells. The results show that Vpr52-96, in contrast to Vpr1-45 peptide, induced loss of mitochondrial membrane potential in a dose dependent manner, with approximately 40% cells showing monomeric green color at a concentration of 2  $\mu$ M (Fig 4-1.2A, & B). These results suggest a distinct involvement of mitochondria in Vpr52-96-induced apoptosis.

#### **Vpr52-96 peptide-induced apoptosis is caspase-dependent:**

Cytochrome-C release from mitochondria results in sequential procaspase activation and ultimately apoptosis [342]. To determine the involvement of caspase in Vpr52-96-induced apoptosis, the effect of broad spectrum caspase inhibitor ZVAD-fmk was examined. Our results showed that pretreatment of cells with ZVAD-fmk resulted in a significant reduction of apoptosis in a dose dependent manner as determined by PI and annexin/PI staining (Fig. 4-1.3A, & B). In contrast, ZVAD-fmk pretreatment did not affect Vpr52-96-mediated loss of mitochondrial membrane potential in THP-1 cells (Fig. 4-1.3C). Since the effect of caspase inhibitors is limited to block nuclear fragmentation and not the mitochondrial damage, the results suggest that loss of mitochondrial potential is regulated independently of ZVAD-fmk inhibitable caspases in monocytic cells as observed in T cells [343].

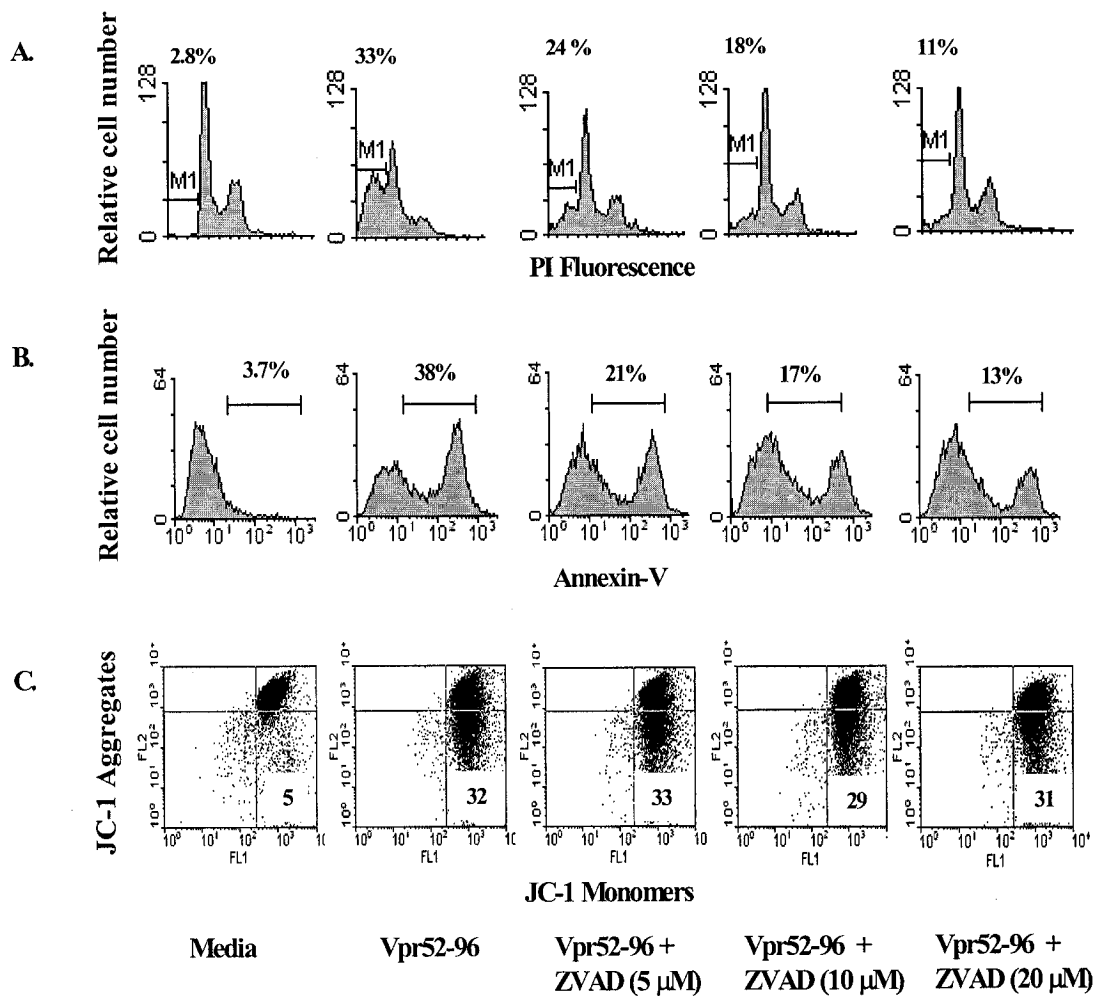
**Fig. 4-1.2: Vpr52-96-induced apoptosis is mediated by the mitochondrial pathway:**

Cells ( $0.5 \times 10^6/\text{ml}$ ) were stimulated with various concentrations of Vpr52-96 or Vpr1-45 peptide for 24 h followed by staining with JC-1 for mitochondrial membrane potential. The values shown in the lower right quarter in **C** indicate percentage of apoptotic cells. The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.



**Fig. 4-1.3: Vpr52-96-induced apoptosis is caspase-dependent:**

THP-1 cells ( $0.5 \times 10^6/\text{ml}$ ) were treated with  $1.5 \mu\text{M}$  of Vpr 52-96 peptide in the presence or the absence of various concentrations of ZVAD-fmk for 24 h followed by staining with intracellular PI (**A**), annexin/PI (**B**) or JC-1 (**C**). The values shown in the lower right quarter in **C** indicate percentage of apoptotic cells. The results shown are a representative of three different experiments.



### **Vpr52-96 peptide activated JNK selectively induces apoptosis in THP-1 cells:**

Because MAPKs play a key role in cell proliferation and apoptosis [135], I investigated the role of MAPK pathway in Vpr-induced apoptosis. To understand the MAPKs pathway involved in Vpr52-96-induced apoptosis, I first investigated if Vpr peptides activated either of the p38, ERK, or JNK MAPKs in THP-1 cells. Cells were treated with either 1.5  $\mu$ M of Vpr52-96 or Vpr1-45 peptide for various times and subjected to Western immunoblotting for p38, ERKs and JNK MAPKs activation by using anti-phospho-p38, anti-phospho-p42/44 ERK and anti-phospho-JNK specific antibodies, respectively. The same blots were stripped and reprobed with anti-p38, anti-p42/44 and anti-JNK antibodies to ensure equal protein loading. The results show that treatment of cells with Vpr52-96 peptide resulted in strong activation of ERK and JNK MAPKs. Activation of both MAPKs became apparent at about 1 hr following treatment and was sustained over the next 4 hr (Fig.4-1.4A, & C). In contrast, p38 MAPK was phosphorylated as early as 10 min after incubation with Vpr52-96 peptide and the phosphorylation was sustained for 4 hr (Fig. 4-1.4B). Similarly, treatment of cells with Vpr1-45 peptide induced phosphorylation of p38, p42/44 ERK and JNK MAPKs in a similar manner (Fig. 4-1.4A, B, & C). Prior treatment of cells with specific inhibitors of MAPK family member such as PD98059 (ERK), SB202190 (p38), SP600125 (JNK) or DXM (JNK) [282] inhibited Vpr52-96- and Vpr1-45 peptides-induced phosphorylation of ERK, p38 and JNK MAPKs, respectively (Fig. 4-1.4A, B, & C).

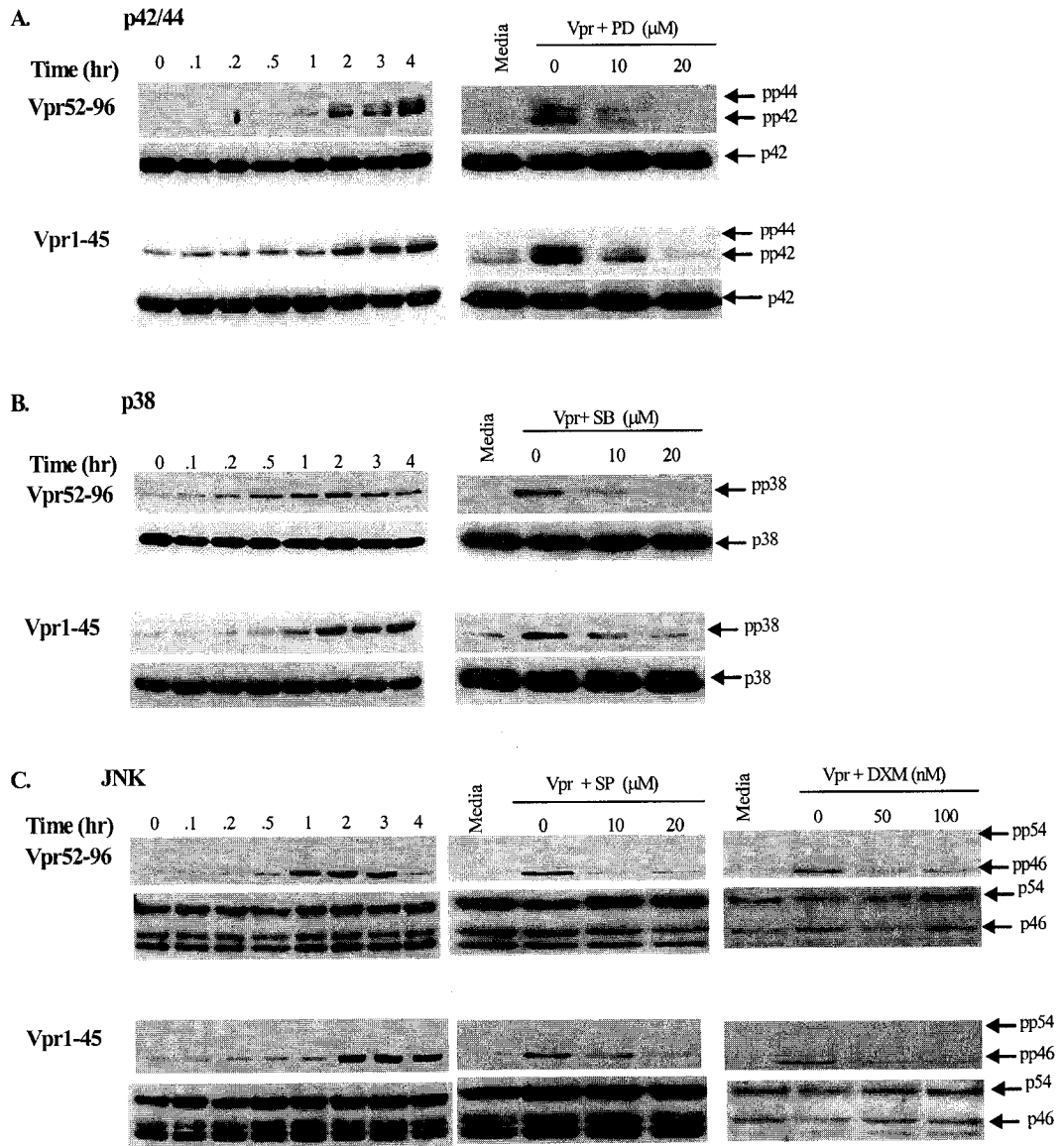
To determine the possible involvement of MAPKs in the regulation of Vpr52-96 peptide-induced apoptosis, cells were treated with inhibitors specific for p38, ERK and

**Fig. 4-1.4: Vpr52-96 and Vpr1-45 peptides activate p38, p42/44 ERK and JNK MAP kinases:**

**Left panel (A, B and C).**

**Left panel (A, B and C).** THP-1 cells ( $1.0 \times 10^6$ /ml) were treated with 1.5  $\mu$ M of either Vpr52-96 or Vpr1-45 peptides for 0-240 min and cell extracts were subjected to Western blot analysis using anti-phospho-p42/44 (indicated by arrows as pp42/44), anti-phospho-p38 (pp38) or anti-phospho-JNK (pp46/54) antibodies. To normalize protein loading, the membranes were stripped and reprobed either with anti-p42/44, anti-p38 or anti-JNK antibodies, respectively.

**Right panel (A, B and C).** Cells ( $1.0 \times 10^6$ /ml) were pretreated with indicated concentrations of either (A) PD98059, (B) SB202190, (C) SP600125 or DXM for 2 hr prior to stimulation with 1.5  $\mu$ M of Vpr52-96 or Vpr1-45 peptides. Total proteins (30  $\mu$ g) were subjected to SDS-PAGE followed by Western blot analysis using either anti-phospho-p42/44 (pp42/44), anti-phospho-p38 (pp38) or anti-phospho-JNK antibodies (pp46/54). To ensure equal protein loading, the membranes were stripped and reprobed either with anti-p42/44, anti-p38 or anti-JNK antibodies, respectively. The results shown are representative of three different experiments.



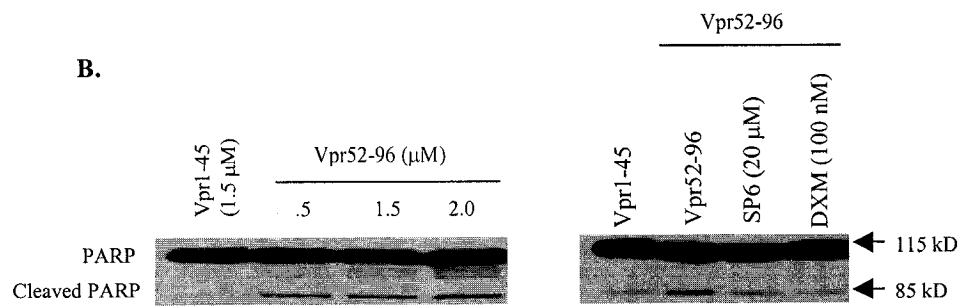
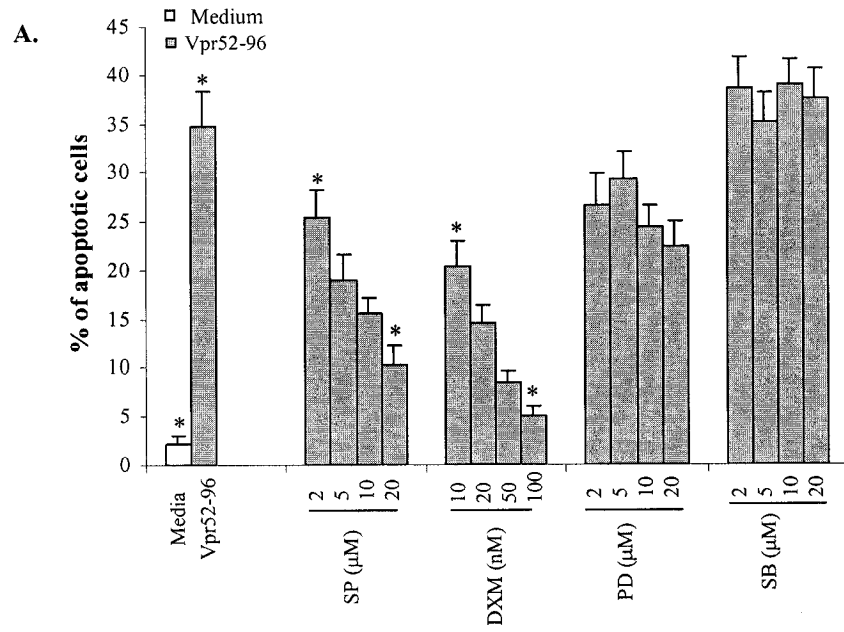
JNK MAPKs for 2 hr followed by stimulation with 1.5  $\mu$ M of either Vpr52-96 or Vpr1-45 peptides for 24 hr following which cells were analyzed for apoptosis. In the absence of Vpr52-96 peptide, pretreatment with any inhibitor at the concentration used did not affect cell growth as determined by PI staining over the course of experiment (data not shown). As observed earlier, Vpr52-96 peptide treatment significantly enhanced apoptotic cell population as determined by PI staining. Interestingly, pretreatment of cells with SP600125 and DXM significantly reversed the Vpr52-96-induced apoptosis in a dose dependent manner (Fig. 4-1.5A). Similar results were obtained by another broad spectrum JNK inhibitor, curcumin (data not shown). In contrast, neither SB202190 nor PD98059 affected Vpr52-96-induced apoptosis significantly even when used at the highest concentration (Fig. 4-1.5A). Similar observations were made when cells were analyzed by staining with either annexin V/PI or JC-1 (data not shown).

Poly (ADP-ribose) polymerase (PARP), a 118 kD nuclear enzyme, recognizes DNA strand breaks and is implicated in DNA repair and apoptosis [344]. On activation, PARP gets cleaved into two fragments of 89 kD and 24 kD which occurs early in apoptotic response as a result of the activity of caspase 3. PARP cleavage has been used as a marker of apoptosis [344]. Therefore, it was interesting to determine whether Vpr52-96 peptide-induced JNK phosphorylation and associated apoptosis involves PARP activation and cleavage. The results show that treatment of THP-1 cells with Vpr52-96 induced cleavage of PARP suggestive of apoptosis. Furthermore, pretreatment of cells with JNK inhibitor SP600125 and DXM inhibited PARP cleavage indicative of reversion of apoptotic process (Fig. 4-1.5B).

**Fig. 4-1.5: Vpr52-96-activated JNK selectively induced apoptosis in THP-1 cells:**

**A.** Cells ( $0.5 \times 10^6$ /ml) were pretreated with indicated concentrations of either SP600125, DXM, PD98059, or SB202190 for 2 h prior to stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide for 24 h followed by intracellular PI staining and analyzed by flow cytometry. The results shown are mean  $\pm$  SD of three different experiments (\* $p < 0.001$ ).

**B.** Cells ( $1 \times 10^6$ /ml) were pretreated with indicated concentrations of SP600125 or DXM for 2 h prior to stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide for 12 h. Cell lysates were subjected to SDS-PAGE and Western blot analysis for PARP expression by using anti-PARP antibodies. The results shown are a representative of three different experiments.

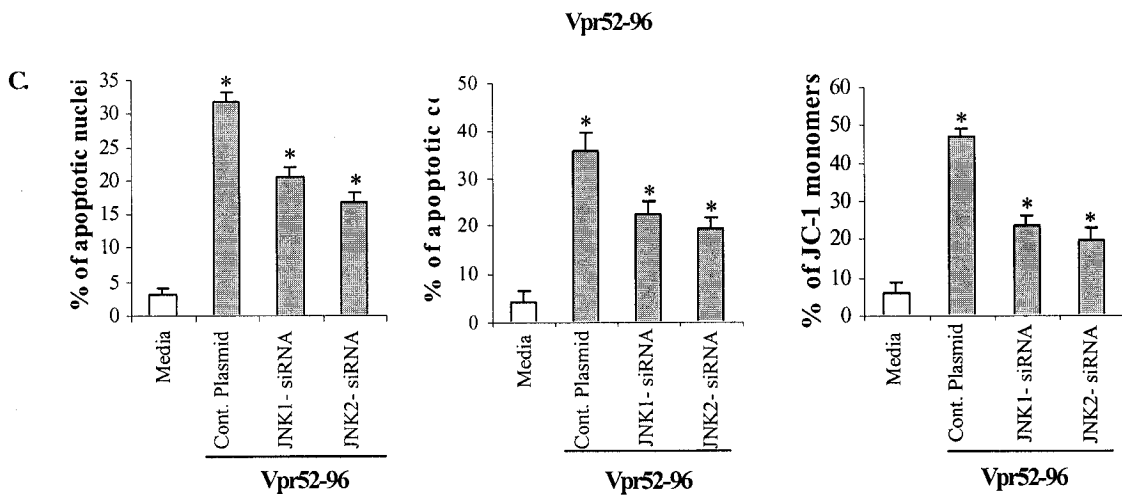
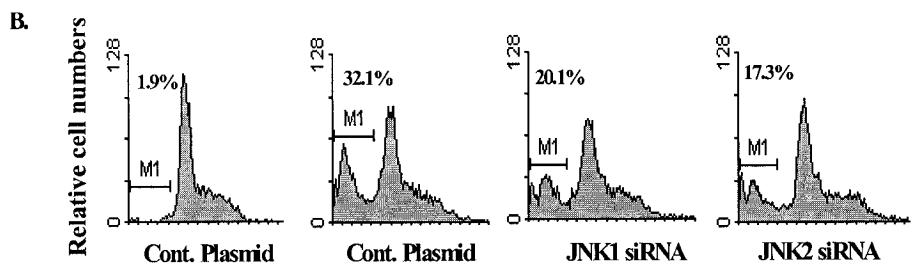
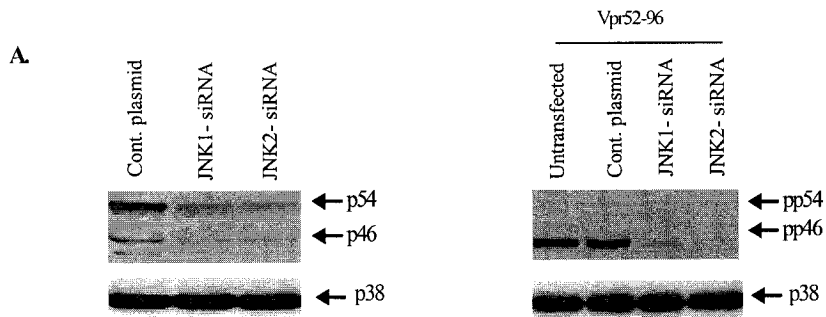


To confirm that Vpr52-96 peptide induced apoptosis involves JNK MAPK activation, I used stealth siRNA specific for JNK1 and JNK2 to knockdown endogenous and Vpr52-96 induced JNK activation and determined its effect on apoptosis. THP-1 cells were transfected either with siRNA for JNK1, JNK2 or control siRNA followed by treatment with Vpr peptides for another 2 hr. Transfection of cells either with siJNK1 or siJNK2 RNAs significantly inhibited endogenous expression of JNK1 and JNK2, respectively (Fig. 4-1.6A, left panel). Vpr52-96 peptide stimulation of cells transfected with either siRNAs specific for JNK-1 or JNK-2 failed to induce phosphorylation of JNK-1 and JNK-2, respectively (Fig 4-1.6A, right panel) compared to cells transfected with control siRNA. Cell cycle analysis of Vpr52-96 peptide treated cells transfected with either JNK-1 or JNK-2 siRNA revealed a significant decrease in apoptotic cell population from 32% to 17% as determined by PI staining and flow cytometry (Fig. 4-1.6B). Similar results were obtained when cells were analyzed for apoptosis by staining with annexin/PI or JC-1. Percentage of annexin-V positive apoptotic cells drops down from ~40 to ~20% in JNK1/JNK2 stealth RNA treated cells. Similarly, JC-1 monomers also declined from ~50 to ~25% in the siRNA treated cells (Fig. 4-1.6C). Overall, the results suggest that Vpr52-96 peptide induced apoptosis through the selective activation of JNK. In contrast, Vpr1-45 peptide treatment although induced JNK activation yet it did not affect apoptosis.

**Fig. 4-1.6: JNK specific siRNAs reverse Vpr52-96-induced apoptosis in THP-1 cells:**

**A.** JNK specific siRNA reduced endogenous and Vpr52-96-stimulated phospho-JNK: Cells ( $1 \times 10^6$ /ml) were transfected with either JNK1, JNK2 or control stealth siRNA for 24 h (**left panel**) followed by stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide for 2 h (right panel). Cell lysates were analyzed by Western blot analysis using anti-JNK (**left panel**) or anti-phospho JNK antibodies (**right panel**). To ensure equal protein loading, the membranes were reprobated with total anti-p38 antibodies. The results shown are a representative of three different experiments.

**B & C.** JNK specific siRNAs reversed Vpr52-96-induced apoptosis: THP-1 cells ( $1 \times 10^6$  /ml) were transfected with either JNK1, JNK2 or control stealth siRNA for 24 h followed by stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide for 24 h and staining with intracellular PI (**B and left panel of C**), annexin/PI (**middle panel, C**) or JC-1 (**right panel, C**). The results shown in C represent a mean  $\pm$  SD of three independent experiments (\* $p < 0.01$ ).



### **Vpr52-96 peptide-induced apoptosis is mediated via down regulation of anti-apoptotic Bcl2 and c-IAP1 genes:**

Vpr52-96 peptide may cause apoptosis either by upregulating the expression of pro-apoptotic genes or by down regulating the anti-apoptotic genes. This was investigated by determining the effect of Vpr52-96 peptide on the expression of pro-apoptotic and anti-apoptotic genes by RNase protection assay by employing the Riboquant kit (BD Biosciences). This kit contained probes for the Bcl2 family of pro- and anti-apoptotic genes (BclW, BclX, BikB, Bad, Bax, Bak, and Bcl2 in addition to that of Mcl1). THP-1 cells were treated with either Vpr52-96 or Vpr1-45 peptides for 1-6 hr followed by analysis of gene expression by RNase protection assay. Results suggest that Vpr52-96 peptide significantly inhibited selectively the expression of Bcl2 gene. Decreased expression of Bcl2 mRNA was detected at 3 hr following treatment of cells with Vpr52-96 peptide and the level of mRNA expression was decreased significantly by 6 hr of treatment as compared to the cells treated with the Vpr1-45 peptide (Fig. 4-1.7A). Surprisingly, there was no significant change in the level of apoptotic genes (Bak and Bax) and anti-apoptotic genes (BclXL, and Mcl1). The densitometric analysis of all the bands were performed by using Image J software and normalized with house keeping genes such as L32 and GAPDH (Fig. 4-1.7B). The effect of Vpr52-96 peptides on the expression of Bcl2 was further confirmed by RT-PCR and Western blot analysis (Fig 4-1.7C & E).

I also investigated the effect of Vpr peptides on the expression of another IAP family of anti-apoptotic genes by RT-PCR analysis. Treatment of cells with the Vpr52-96 and not the Vpr1-45 peptide significantly reduced the expression of c-IAP1 gene. Neither

of these peptides significantly affected the expression of c-IAP2 genes in THP-1 cells as determined by RT-PCR (data not shown) and Western blot analysis (Fig. 4-1.7D & E).

**Vpr52-96 peptide-induced apoptosis is mediated by down regulation of anti-apoptotic Bcl2 and c-IAP1 genes through JNK MAPK activation:**

Because Vpr52-96 peptide induced JNK activation, and blockage of JNK phosphorylation by JNK inhibitors inhibited Vpr52-96- induced apoptosis, it was interesting to determine if Vpr-induced apoptosis is regulated by Bcl2 and c-IAP1 through the activation of JNK MAPKs. Further to assess the involvement of JNK MAPK in regulation of Bcl2 mediated Vpr52-96 peptide-induced apoptosis, I performed RT-PCR. THP-1 cells were treated with Vpr52-96 peptide in the presence or absence of JNK MAPK inhibitors. Vpr52-96 peptide significantly reduced the expression of Bcl2 in THP-1 cells as compared to Vpr1-45 peptide treated cells. JNK MAPK inhibitors SP600125 and dexamethasone restored the expression of Bcl2 as well as c-IAP1 as determined by RT-PCR and Western blot analysis (Fig 4-1.7C, D, & E). Pretreatment of cells with the p38 inhibitor SB202190 did not affect Vpr52-96 peptide induced expression of either Bcl2 or c-IAP1 (Fig 4-1.7C, D, & E).

Since Bcl2 is post-translationally modified by phosphorylation, it is believed that expression of Bcl2 alone is not enough to exert its anti-apoptotic effects [345]. IL-3 and erythropoietin have been shown to induce their anti-apoptotic effects through phosphorylation of Bcl2 at S70 [148]. In contrast, Bcl2 phosphorylation at T69, S70 and S87 has been proposed to inactivate Bcl2-mediated anti-apoptotic effects. Therefore, I determined if Vpr52-96 peptide modulated Bcl2 phosphorylation at S70 and whether

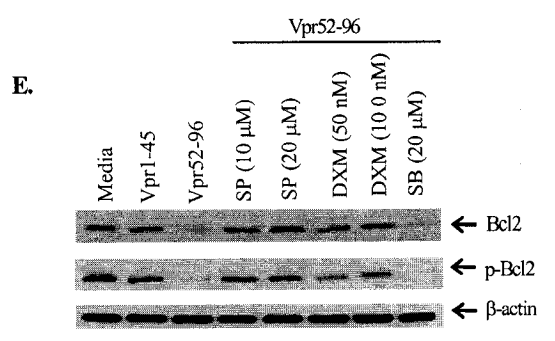
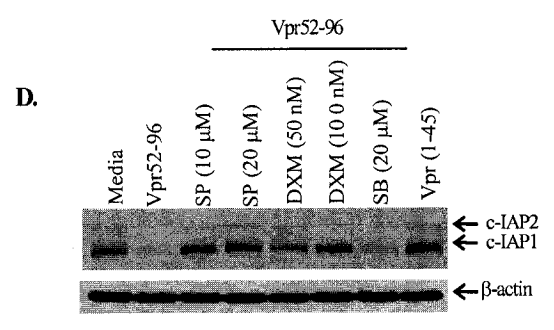
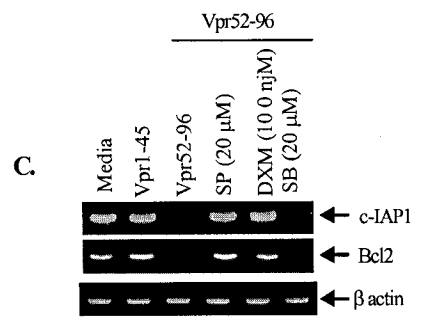
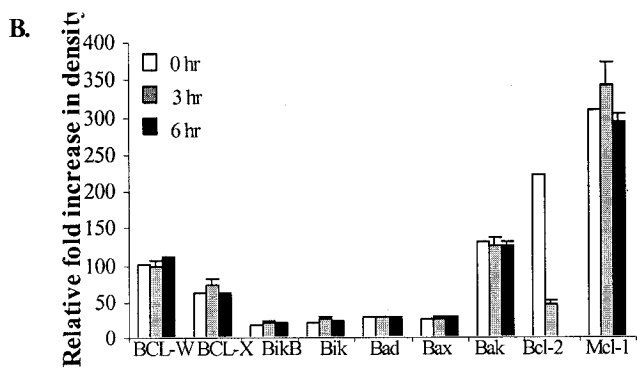
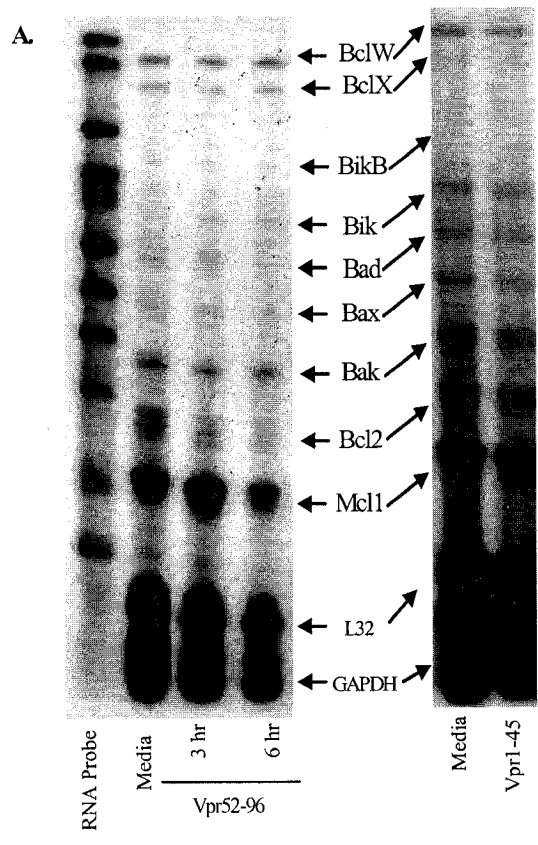
**Fig. 4-1.7: Vpr52-96-activated JNK induces down regulation of anti-apoptotic Bcl2 and c-IAP1 genes:**

**A.** Vpr52-96 peptide inhibited Bcl2 expression as determined by RPA: THP-1 cells ( $5 \times 10^6$ /ml) were stimulated with 1.5  $\mu$ M of Vpr52-96 or Vpr1-45 peptides for 0-6 h. RNA was extracted as described in materials and methods. RPA was performed by using BD Riboquant package kit with a multi-probe template set of anti- and pro-apoptotic genes of the Bcl2 family, and GAPDH and L32 as internal controls. The results shown are a representative of three different experiments.

**B.** Densitometric analysis of Bcl2 genes following Vpr52-96 treatment from the results shown in 6A.

**C.** Vpr52-96 peptide induced down regulation of anti-apoptotic Bcl2 and c-IAP1 genes through JNK activation: Cells ( $5 \times 10^6$ /ml) were stimulated with 1.5  $\mu$ M of Vpr52-96 peptides for 3 hr in the presence or the absence of JNK (SP600125 and DXM) or p38 inhibitors (SB202190) followed by RNA extraction and semiquantitative RT-PCR analysis for Bcl2 and c-IAP1 expression.

**D & E.** Cells ( $1 \times 10^6$ /ml) were pretreated with either JNK (SP600125 and DXM) or p38 inhibitors (SB202190) for 2 hr followed by stimulation with 1.5  $\mu$ M of Vpr52-96 peptides for 24 hr. Cell lysates were subjected to Western blot analysis for expression of c-IAP1 (**D**), and Bcl2 and phospho-Bcl2 (**E**) using anti RIAP1, anti-Bcl2, and anti-phospho-Bcl2 antibodies, respectively. To ensure equal protein loading, the membranes were reprobbed with anti- $\beta$ -actin antibodies. The results shown are representative of three different experiments.



JNK inhibitors reversed Bcl2 phosphorylation at S70 corresponding to its enhancing effects on cell survival. THP-1 cells exhibited high basal level of Bcl2 phosphorylation at the serine 70 residues, and their treatment with Vpr52-96 peptide abrogated S70 phosphorylation. Furthermore, pretreatment with JNK inhibitors SP600125 and DXM restored the Vpr52-96-mediated down regulation of S70 phosphorylation (Fig 4-1.7E). As observed above with total Bcl2 expression, treatment of cells with the p38 inhibitor SB202190 did not affect the Vpr52-96-mediated down regulation of Bcl2 phosphorylation. The results suggest the involvement of S70 phosphorylation of Bcl2 in Vpr52-96-mediated apoptosis and cell survival of THP-1 cells following inhibition of JNK activation.

**Vpr52-96 peptide-activated-JNK MAPK inhibits Bcl2 transcription by down regulating the binding of NFκB, Sp1 and CREB transcription factors to their respective binding site in the Bcl2 promoter in THP-1 cells:**

Vpr52-96 peptide-induced apoptosis may be regulated by Bcl2 and/or c-IAP1 at the level of transcription through JNK activation. Bcl2 gene is regulated by multiple transcription factors namely NFκB, CREB and Sp-1 [151;346]. It is likely that Vpr52-96 peptide activated JNK MAPK may down regulate Bcl2 transcription by inhibiting the activities of either NFκB, CREB and/or Sp-1. Therefore, I investigated whether Vpr52-96 peptide-activated transcription factors NFκB, CREB and Sp-1 to their binding sites present in the Bcl2 promoter by gel shift assay. Nuclear extracts harvested from Vpr52-96 treated and untreated THP-1 cells were analyzed for binding of all these three transcription factors to the oligonucleotide probes corresponding to their binding sites in the Bcl2 promoter. In the untreated THP-1 cells, significant constitutional binding of NFκB, CREB and Sp-1 to their respective oligonucleotide probes was observed (Fig. 4-

1.8A, B & C, left panels). The specificity of these transcription factors binding was demonstrated by competition with specific and non specific oligonucleotides and supershift analysis with respective rabbit polyclonal antibodies (Fig 4-1.8A, B, & C, left and middle panels). Interestingly, treatment of THP-1 cells with the Vpr52-96 resulted in the inhibition of binding of NFκB, CREB and Sp-1 to their respective oligonucleotide probes (Fig 4-1.8A, B, & C, right panels). To determine if Vpr52-96 peptide activated JNK MAPK caused the inhibition of NFκB, CREB and Sp-1 binding, cells were pretreated with JNK inhibitors SP600125, DXM, or SB202190 for 2 hr followed by stimulation with either Vpr52-96 or Vpr1-45 peptides. Surprisingly, SP600125 and DXM pretreatment restored the binding of all the three transcription factors namely NFκB, Sp-1 and CREB to their respective probes whereas SB202190 pretreatment did not have any effect on their binding (Fig 4-1.8A, B, & C, right panels).

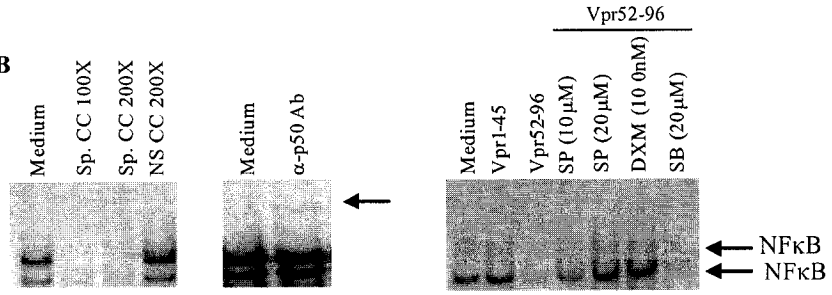
**Vpr52-96 peptide-activated-JNK MAPK inhibits c-IAP1 transcription by down regulating the binding of NFκB and CREB transcription factors to their respective binding site in the c-IAP1 promoter in THP-1 cells:**

Since the above results also suggest that Vpr52-96 peptide induced apoptosis may be attributed to the inhibition of another anti-apoptotic gene, c-IAP1, I investigated whether Vpr-induced apoptosis is also regulated by c-IAP1 at the level of transcription through JNK activation. c-IAP1 transcription has been shown to be regulated by NFκB and CREB-1 [199;347]. Experiments conducted on similar lines suggest that untreated THP-1 cells exhibited constitutional binding of NFκB and CREB transcription factors to their oligonucleotide probes with sequences corresponding to their binding site in the

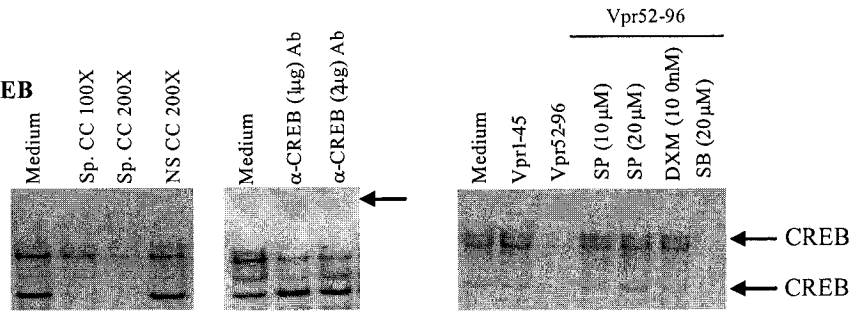
**Fig. 4-1.8: Vpr52-96-activated JNK inhibits Bcl2 transcription by down regulating the binding of NFκB, CREB or Sp1 transcription factors:**

Cells ( $5 \times 10^6$ /ml) were treated with 1.5  $\mu$ M of Vpr52-96 or Vpr1-45 peptides for 2 h in the presence or the absence of JNK (SP600125 and DXM) or p38 inhibitors (SB202190). Nuclear proteins (5  $\mu$ g) were incubated with  $^{32}$ P-labelled oligonucleotide probes corresponding to NFκB (A), CREB (B) or Sp1 (C) sequences derived from the Bcl2 promoter. The specificity of NFκB, CREB and Sp1 binding was determined by incubating nuclear proteins with unlabelled NFκB, CREB and Sp1 or non-specific oligonucleotides. The supershift analysis was performed by treating the nuclear proteins with oligonucleotide probes in the presence or the absence of anti-p50, anti-p65 NFκB, anti-CREB or anti-Sp1 antibodies. The results shown are representative of three different experiments.

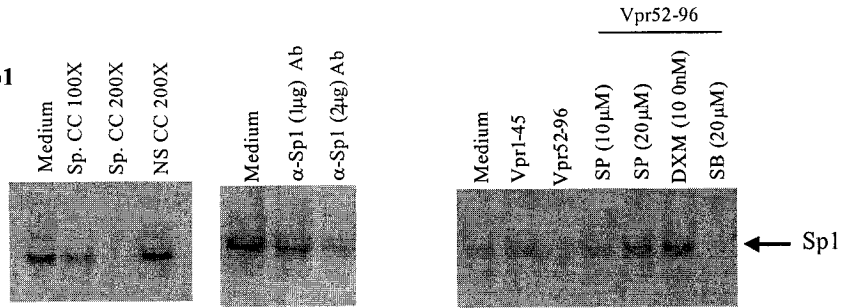
**A. Bcl2-NFκB**



**B. Bcl2-CREB**



**C. Bcl2-Sp1**



c-IAP1 promoter. The specificity of NF $\kappa$ B and CREB binding was demonstrated by competition with specific and non specific oligonucleotides and supershift analysis with respective rabbit polyclonal antibodies (Fig 4-1.9A, left and middle panel; Fig 4-1.9B, left panel). Surprisingly, Vpr52-96 peptide inhibited the binding of NF $\kappa$ B and CREB to their corresponding oligonucleotide probes. Similarly, pretreatment of Vpr52-96-stimulated cells with JNK inhibitors, SP600125 and DXM, restored the binding of both NF $\kappa$ B and CREB to their respective probes. However, pretreatment of Vpr52-96-stimulated cells with the control p38 inhibitor, SB202190 did not influence the binding of any of these transcription factors (Fig 4-1.9A and B, right panels).

These results suggest that Vpr52-96 peptide activated JNK MAPKs selectively inhibit the transcription of Bcl2 as well as c-IAP1 by inhibiting the binding of responsible transcription factors to the respective binding sites in the Bcl2 and c-IAP1 promoters, respectively.

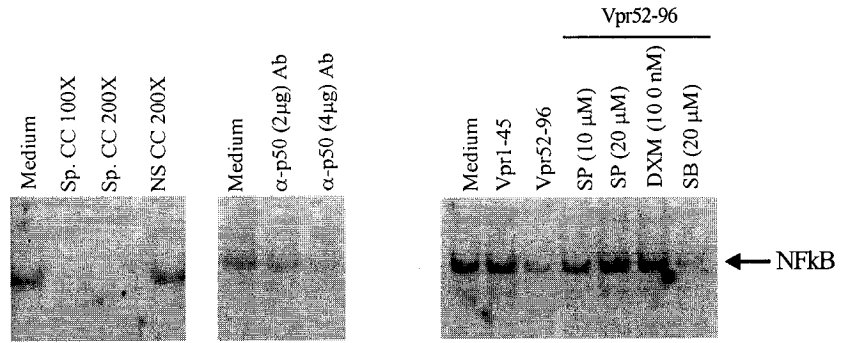
#### **Vpr52-96 peptide induced apoptosis is mediated by JNK MAPK activation in CD14+ normal human monocytes:**

I next investigated if normal human monocytes transduced with Vpr52-96 undergo a similar cell cycle arrest and whether Vpr52-96 peptide induced apoptosis through the selective activation of JNK. CD14+ purified human monocytes were treated with various concentrations of Vpr1-45 and Vpr52-96 peptides for 12 hr followed by cell cycle analysis and apoptosis as determined by PI, annexin-PI and JC staining. Similar to the results obtained with THP-1 cells, Vpr52-96 peptide in contrast to the Vpr1-45 peptide induced apoptosis in a dose dependent manner as demonstrated by PI (Fig 4-1.10A). Furthermore, Vpr52-96 peptide induced apoptosis in normal monocytes was

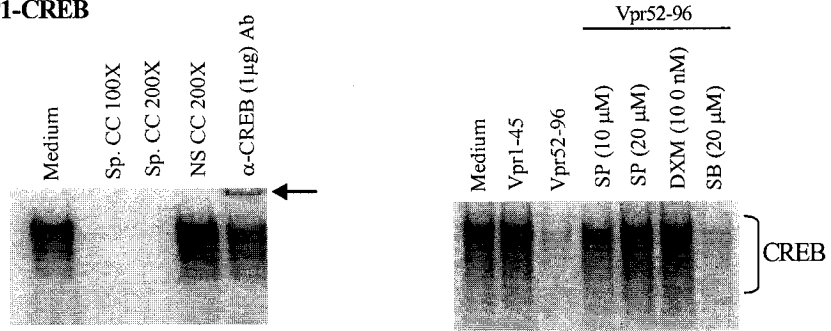
**Fig. 4-1.9: Vpr52-96-activated JNK inhibits cIAP-1 transcription by down regulating the binding of NFκB or CREB transcription factors:**

Cells ( $5 \times 10^6$ /ml) were treated with 1.5 μM of Vpr52-96 or Vpr1-45 peptides for 2 h in the presence or the absence of JNK (SP600125 and DXM) or p38 inhibitors (SB202190). Nuclear proteins (5 μg) were incubated with  $^{32}$ P-labelled oligonucleotide probes corresponding to NFκB (A), or CREB (B) sequences derived from the c-IAP1 promoter. The specificity of NFκB, and CREB binding was determined by incubating nuclear proteins with unlabelled NFκB, and CREB or non-specific oligonucleotides. The supershift analysis was performed by treating the nuclear proteins with oligonucleotide probes in the presence or the absence of anti-p50, anti-p65 NFκB, or anti-CREB antibodies. The results shown are representative of three different experiments.

**A. c-IAP1-NFκB**



**B. c-IAP1-CREB**

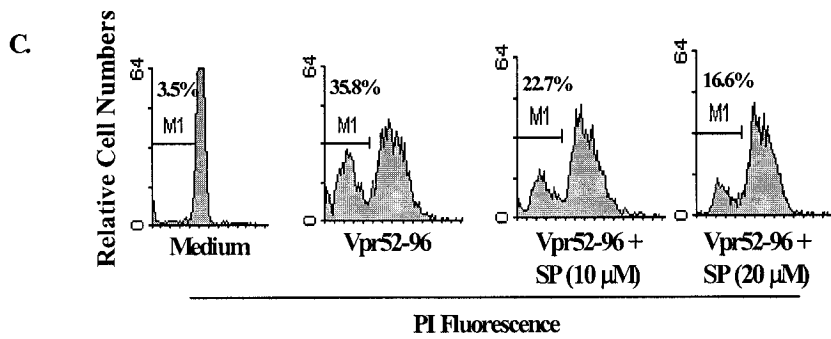
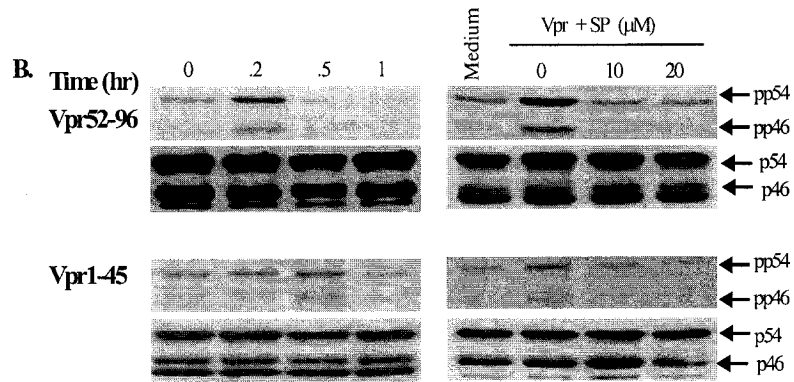
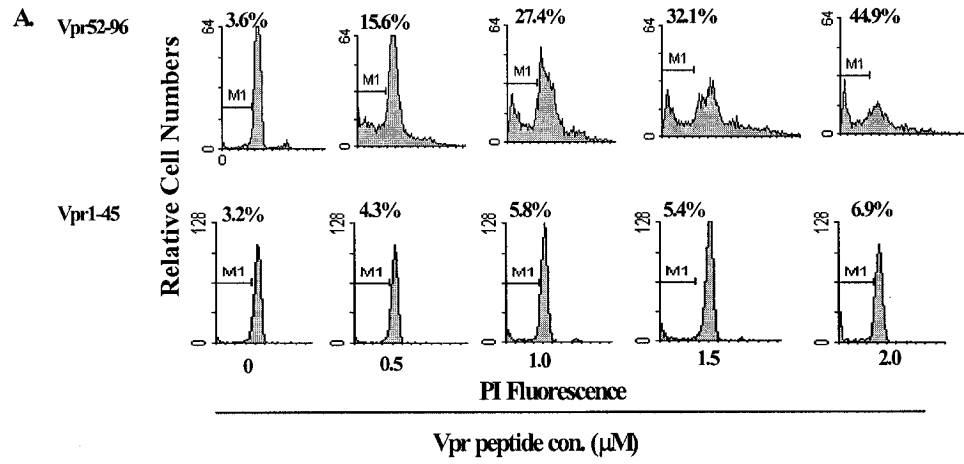


**Fig. 4-1.10: Vpr52-96-activated JNK induces apoptosis in normal human monocytes:**

**(A).** Vpr52-96-induced apoptosis in human monocytes: Monocytes ( $0.5 \times 10^6$  /ml) were stimulated with various concentrations of either Vpr52-96 or Vpr1-45 peptides for 12 h followed by staining with intracellular PI and analyzed by flow cytometry. The results shown are representative of three different experiments.

**(B).** Vpr52-96 and Vpr1-45 peptides activate p38, p42/44 and JNK MAPKs in normal human monocytes: **Left panel:** Monocytes ( $3.0 \times 10^6$ /ml) were treated with  $1.5 \mu\text{M}$  of either Vpr52-96 or Vpr1-45 peptides for 0-60 min. **Right panel:** Monocytes ( $1.0 \times 10^6$ /ml) were pretreated with SP600125 ( $0-20 \mu\text{M}$ ) for 2 h prior to stimulation with Vpr52-96 or Vpr1-45 peptides. Total proteins ( $30 \mu\text{g}$ ) were subjected to SDS-PAGE followed by Western blot analysis using anti-phospho-JNK antibodies. To ensure equal protein loading, the membranes were reprobbed with anti-JNK antibodies. The results shown are representative of three different experiments.

**(C).** Vpr52-96-activated-JNK induces apoptosis in human monocytes: Cells ( $0.5 \times 10^6$ /ml) were pretreated with SP600125 ( $0-20 \mu\text{M}$ ) for 2 h prior to stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide. After 12 h, cells were analyzed for apoptosis by intracellular PI staining and flow cytometry. The results shown are representative of three independent experiments.



found to be caspase dependent as prior treatment of cells with caspase inhibitor ZVAD-fmk resulted in a significant reduction of apoptosis (data not shown).

To determine that Vpr52-96 peptide-induced apoptosis is regulated through the activation of JNK MAPKs, I first demonstrated that both Vpr1-45 and Vpr52-96 peptides induced the phosphorylation of JNK MAPKs (Fig 4-1.10B). Subsequently I demonstrated that prior treatment of monocytes with the JNK MAPKs specific inhibitors SP600125 (Fig 4-1.10C), DXM and curcumin (data not shown) significantly reversed Vpr52-96 peptide-induced apoptosis in a dose-dependent manner as determined by PI, and annexin-PI staining (data not shown). These results suggest that Vpr52-96 peptide induces apoptosis in normal monocytes and similar to the results obtained with THP-1 cells, this apoptosis is mediated through JNK activation.

**Vpr52-96 peptide-induced apoptosis is mediated by inhibition of anti-apoptotic Bcl2 and c-IAP1 genes through JNK MAPK activation in CD14+ normal human monocytes:**

To further determine if Vpr52-96 peptide-induced apoptosis is regulated by Bcl2 and c-IAP1 genes through the activation of JNK MAPKs, freshly purified CD14+ monocytes were treated with the JNK inhibitor SP600125 for 2 hr followed by treatment with the Vpr52-96 peptide for 12 hr and 6 hr for protein (Western blotting) and mRNA (RT-PCR) analysis respectively. Unstimulated monocytes expressed constitutively both Bcl2 and c-IAP1 (Fig. 4-1.11A, B, & C). Treatment of cells Vpr52-96 peptide unlike Vpr1-45 peptide abrogated the expression of both Bcl2 and c-IAP1 in proteins and mRNA levels. Similar to the results obtained with THP-1 cells, exposure of monocytes with the JNK inhibitor SP600125 prior to treatment with the Vpr52-96 peptide restored the expression of Bcl2 and c-IAP1 genes to levels similar to that observed in

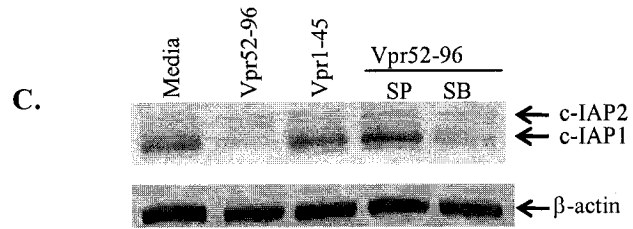
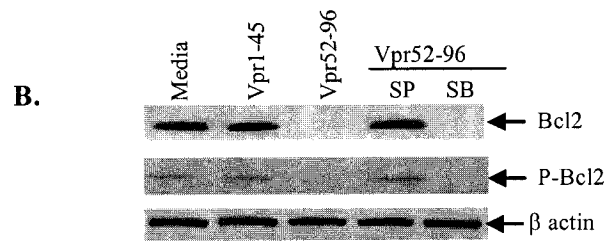
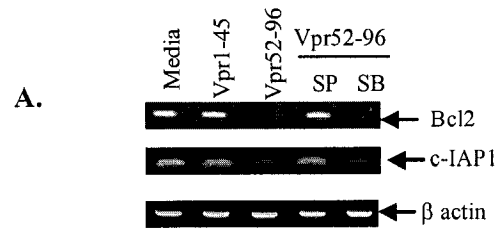
unstimulated cells (Fig. 4-1.11A, B, & C). In contrast, exposure of monocytes with the p38 inhibitor SB202190 prior to treatment with the Vpr52-96 did not affect the expression of Bcl2 and c-IAP1 genes (Fig. 4-1.11A, B, & C).

Based on all these findings, it is concluded that Vpr induced apoptosis in monocytes by downregulating anti-apoptotic Bcl2 and c-IAP1 genes through activation of JNK MAPK.

**Fig. 4-1.11: Vpr52-96-activated JNK induces apoptosis by inhibiting the expression of Bcl2 and c-IAP1 in normal human monocytes:**

**(A).** Monocytes ( $5 \times 10^6$  /ml) were stimulated with  $1.5 \mu\text{M}$  of Vpr52-96 peptides for 2 h in the presence or the absence of JNK inhibitor (SP600125) followed by RNA extraction and semiquantitative RT-PCR analysis for Bcl2 and c-IAP1 expression.

**(B, & C).** Monocytes ( $2 \times 10^6$ /ml) were pretreated with SP600125 for 2 h followed by stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 for 12 h. Cell lysates were subjected to Western blot analysis for expression of Bcl2 and phospho-Bcl2 **(B)** and c-IAP1 **(C)** using anti-Bcl2, anti-phospho-Bcl2, and anti RIAP1 antibodies, respectively. To ensure equal protein loading, the membranes were reprobbed with anti- $\beta$ -actin Abs. The results shown are representative of three independent experiments.



## **Objective # 2**

### **Signaling pathways involved in development of LPS- and TNF- $\alpha$ -mediated resistance to HIV-Vpr-induced apoptosis:**

#### **Results:**

##### **LPS-induced resistance to Vpr52-96 mediated apoptosis in human monocytic cell:**

I already demonstrated that C terminal Vpr52-96 peptide induced apoptosis in a dose dependent manner in THP-1 cells, the promonocytic cell line and in normal human monocytes isolated from healthy donors, whereas N terminal Vpr1-45 peptide at similar concentrations failed to exert apoptotic effects in both the cell types. To determine the effect of LPS on Vpr52-96 induced apoptosis, cells were stimulated with LPS for 6 hr prior to treatment with Vpr52-96 or Vpr1-45 peptides for 24 hr followed by determination of apoptosis. The results show that pretreatment of cells with LPS significantly reduced apoptosis as determined by PI and annexin/PI staining in THP-1 cell and by PI staining in monocytes (Fig. 4-2.1A, B, & C). However, stimulation of cells with LPS for less than 4 hr did not induce protection against Vpr52-96-induced apoptosis (data not shown). In contrast, when THP-1 cells and primary monocytes were stimulated with LPS for 24 hr following treatment with Vpr52-96 or Vpr1-45 peptides for 2 hr, Vpr52-96 peptide abrogated LPS-mediated resistance to Vpr52-96-induced apoptosis (Fig. 4-2.1D & E). Overall, these observations suggest that Vpr52-96 peptide induced apoptosis in both cell types and prior stimulation with LPS induced resistance to apoptosis. Furthermore, Vpr52-96 peptide attenuated LPS-induced resistance to Vpr-induced apoptosis.

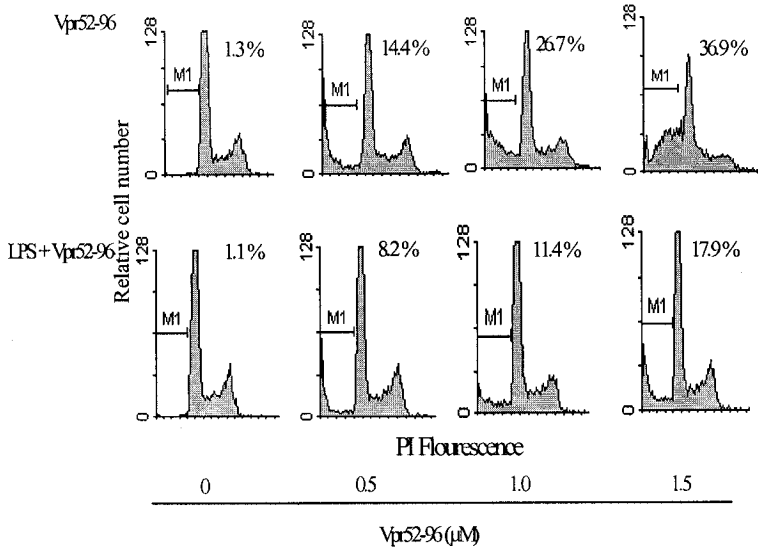
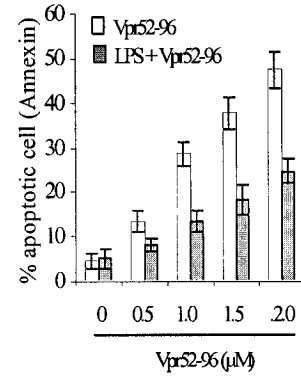
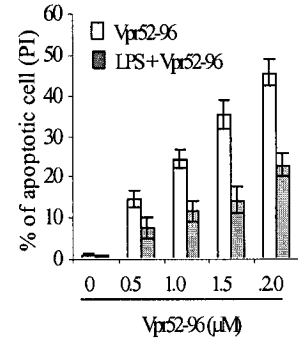
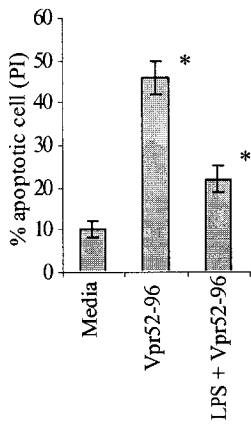
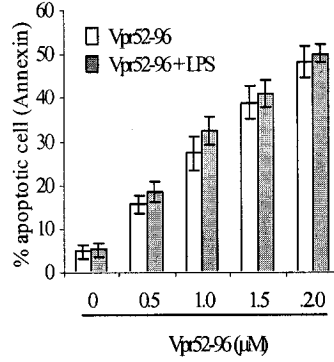
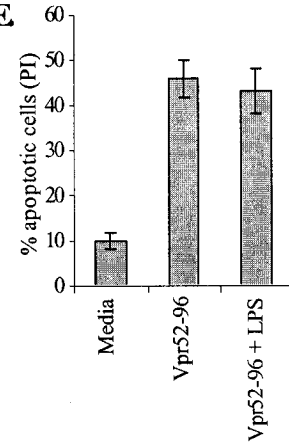
**Fig. 4-2.1: LPS induced resistance to Vpr52-96 mediated apoptosis in primary human monocytes and THP-1 cells:**

**A & B.** THP-1 cells ( $0.5 \times 10^6/\text{ml}$ ) were stimulated with LPS ( $1 \mu\text{g}/\text{ml}$ ) for 6 h followed by treatment with various concentrations of Vpr52-96 peptide for 24 h. Cells were then stained with intracellular PI for DNA content (**A, & B**), annexin-V/PI for measurement of apoptosis (**B**). The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.

**C.** Human monocytes ( $1 \times 10^6/\text{ml}$ ) were also pretreated with LPS ( $1 \mu\text{g}/\text{ml}$ ) for 6 h prior to stimulation with  $1.5 \mu\text{M}$  of Vpr52-96 peptide for 12 h. Cells were then stained with intracellular PI for DNA content. The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate (\*  $p < 0.005$ ).

**D.** THP-1 cells ( $0.5 \times 10^6/\text{ml}$ ) were stimulated with various concentrations of Vpr52-96 for 2 h prior treatment with LPS ( $1 \mu\text{g}/\text{ml}$ ) for 24 h. Cells were then stained with annexin-V/PI for measurement of apoptosis. The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.

**E.** Monocytes ( $0.5 \times 10^6/\text{ml}$ ) were stimulated with  $1.5 \mu\text{M}$  of Vpr52-96 for 2 h prior treatment with LPS ( $1 \mu\text{g}/\text{ml}$ ) for 12 h. Cells were then stained with PI for measurement of apoptosis. The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.

**A****B****C****D****E**

### **LPS induced resistance against Vpr52-96 mediated apoptosis is regulated by endogenous production of TNF- $\alpha$ :**

Since TNF- $\alpha$  is produced in response to LPS stimulation in monocytic cells, I determined whether LPS-induced protection is mediated by endogenous production of TNF- $\alpha$ . THP-1 cells and primary human monocytes were treated with various concentrations of neutralizing anti-TNF-receptor (anti-TNFR-I) antibodies followed by stimulation of cells with LPS for 6 hr. Subsequently, cells were treated with Vpr52-96 peptides for 24 hr followed by determination of apoptosis. Treatment of cells with Vpr52-96 resulted in 40-45% apoptosis, whereas prior stimulation with LPS significantly reduced the percentage of apoptotic cells to approximately 22%. However, pretreatment of cells with anti-TNFR-I antibodies significantly inhibited the LPS induced protection in both cell types suggesting the involvement of endogenous TNF- $\alpha$  in LPS-induced resistance to Vpr-mediated apoptosis (Fig. 4-2.2A). This was further confirmed by determining the protective effect of recombinant TNF- $\alpha$  on Vpr52-96-induced apoptosis in monocytic cells. THP-1 cell and human monocytes were stimulated with TNF- $\alpha$  for 6 hr prior to treatment with Vpr52-96 peptide followed by determination of apoptosis. The results in Fig.4-2.2B show that pretreatment with TNF- $\alpha$  significantly reduced Vpr52-96-induced apoptosis, as determined by PI and annexin/PI staining. Similar to the study conducted in LPS induced resistance against Vpr52-96-induced apoptosis, THP-1 cells and monocytes were also treated with Vpr52-96 for 2 hr prior to stimulation with TNF- $\alpha$  followed by measurement of apoptosis. The results show that pretreatment of cells with Vpr52-96 abrogated the protective effect of TNF- $\alpha$  to Vpr-induced apoptosis (Fig. 4-2.2C & 4-2.2D).

**Fig. 4-2.2: LPS induced resistance against Vpr52-96 mediated apoptosis is regulated by endogenous production of TNF- $\alpha$ :**

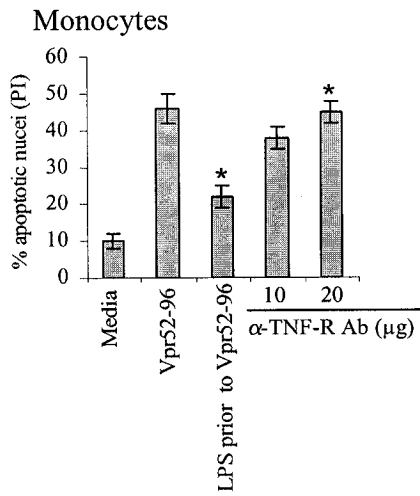
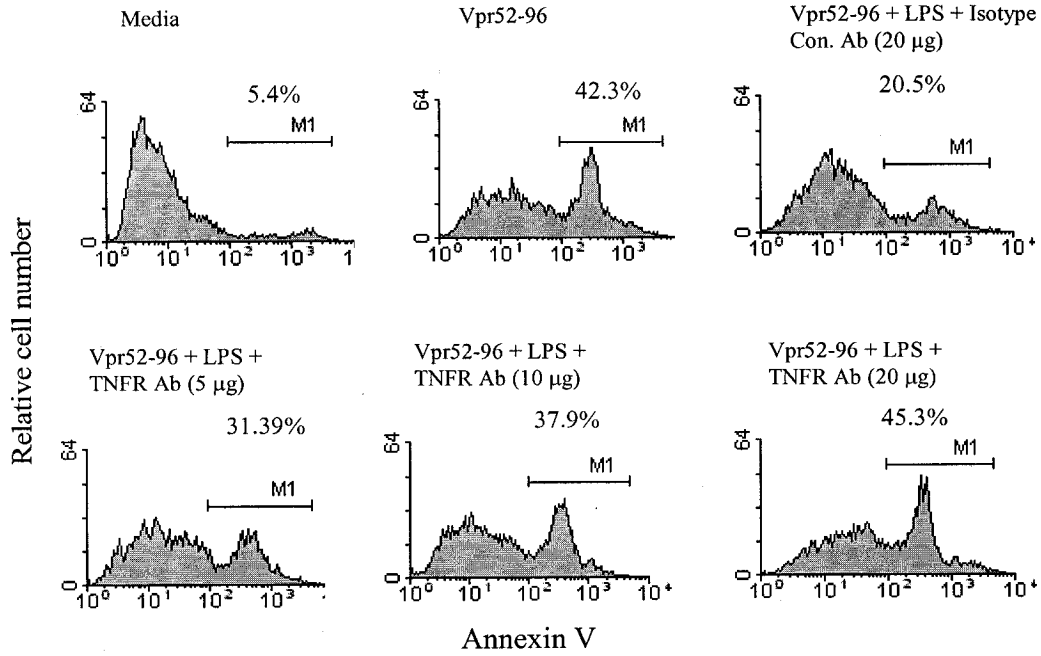
**A.** THP-1 cells or human monocytes ( $0.5 \times 10^6$ /ml) were stimulated with LPS (1  $\mu$ g/ml) for 6 h in the presence or absence of anti-TNF- $\alpha$ -R1 (10-20  $\mu$ g/ml) or isotype matched control antibodies followed by treatment with 1.5  $\mu$ M Vpr52-96 peptide for 24 h (THP-1 cell) or 12 h (monocytes). Cells were then stained with annexin-V/PI (THP-1) or PI (monocytes) for measurement of apoptosis. The results shown are representative of three different experiments (\*  $p < 0.01$ ).

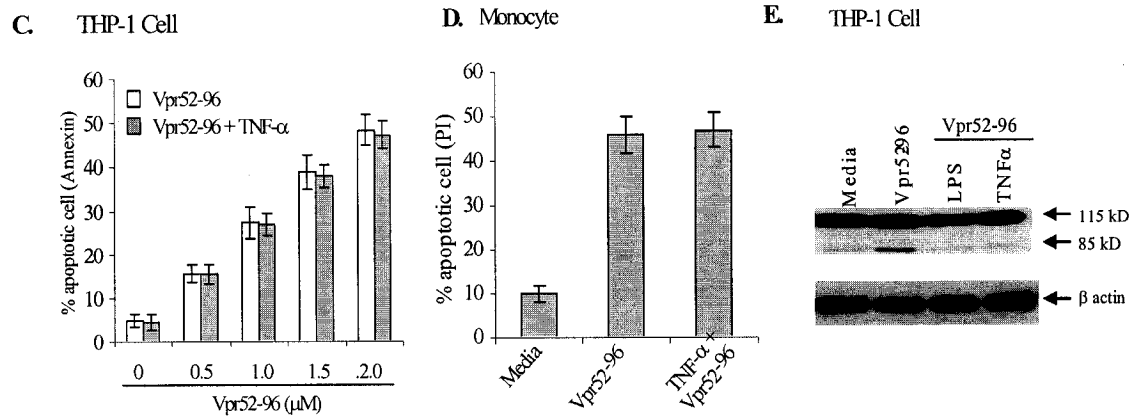
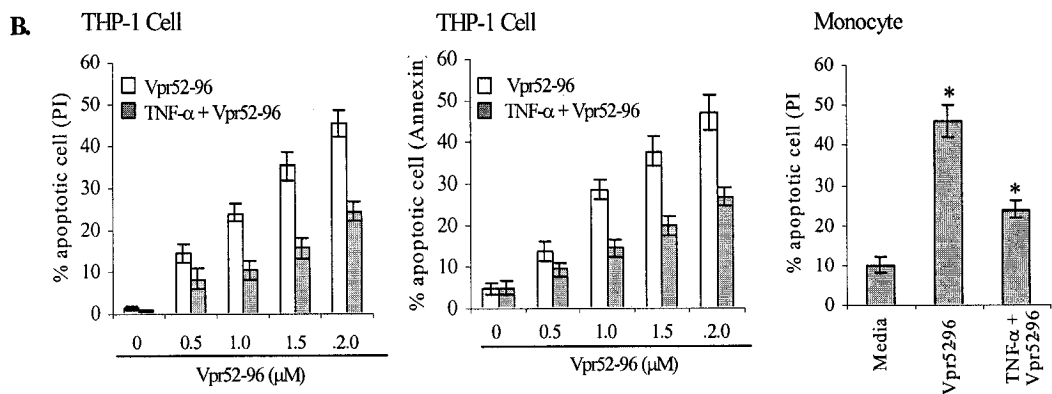
**B.** Cells ( $0.5 \times 10^6$ /ml) were stimulated with TNF- $\alpha$  (10 ng/ml) for 6 h followed by treatment with various concentrations of Vpr52-96 peptide for 24 h. Cells were then stained with intracellular PI for DNA content (**Left panel**), annexin-V/PI for measurement of apoptosis (**Middle panel**). The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate. Human monocytes ( $1 \times 10^6$ /ml) were also pretreated with TNF- $\alpha$  for 6 h prior to stimulation with 1.5  $\mu$ M of Vpr52-96 peptide for 12 h. Cells were then stained with intracellular PI for DNA content (**Right panel**). The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate (\*  $p < 0.005$ ).

**C & D.** Cells ( $0.5 \times 10^6$ /ml) were stimulated with various concentrations of Vpr52-96 for 2 h prior treatment with TNF- $\alpha$  for 24 h (THP-1 cell) or 12 h (monocytes). Cells were then stained with annexin-V/PI (THP-1) or PI (monocytes) for measurement of apoptosis. The graphs shown are a mean  $\pm$  SD of three experiments performed in triplicate.

**E.** THP-1 cells ( $1 \times 10^6$ /ml) were also pretreated with LPS/TNF- $\alpha$  for 6 h prior to stimulation with 1.5  $\mu$ M of Vpr52-96 peptide for 12 h. Cell lysates were subjected to SDS-PAGE and Western blot analysis for PARP expression by using anti-PARP antibodies. The results shown are a representative of three different experiments.

**A. THP-1 cells**





It is known that in response to apoptotic stimuli, PARP, one of the enzymes present in the nucleus that helps in repairing of DNA damage, is cleaved and it is considered as a marker of apoptosis. Our results show that treatment of cells with Vpr52-96 peptide cleaved PARP and prior treatment with LPS and/or TNF- $\alpha$  inhibited the fragmentation of PARP in THP-1 cells (Fig. 4-2.2E).

**LPS/TNF- $\alpha$  induced protection in Vpr52-96-mediated apoptosis is regulated by c-IAP2:**

My earlier results suggest LPS and TNF- $\alpha$  mediated protection against staurosporine-induced apoptosis was mediated through the anti-apoptotic gene c-IAP2 in THP-1 cells. Therefore, it is possible that c-IAP2 induction may regulate LPS and/or TNF- $\alpha$ -induced protection against Vpr52-96-mediated apoptosis. To address this question, I first demonstrated that LPS as well as TNF- $\alpha$  induced the expression of c-IAP2 gene in both primary monocytes as well as THP-1 cells. As observed earlier, low level of c-IAP2 mRNA and c-IAP2 proteins were detected in unstimulated THP-1 cells and monocytes and their expression levels increased significantly following stimulation with either LPS or TNF- $\alpha$ . To determine the involvement of c-IAP2 in LPS-/TNF- $\alpha$ -induced protection, THP-1 cells were transfected with antisense c-IAP2 or control oligonucleotides prior to stimulation with either LPS or TNF- $\alpha$  for 24 hr followed by determination of c-IAP2 expression by Western blotting and Vpr52-96 induced apoptosis. My earlier results showed that transfection of cells with antisense c-IAP2 oligonucleotides significantly inhibited the LPS- or TNF- $\alpha$ -induced expression of c-IAP2 compared to the cells transfected with control oligonucleotides (Fig. 3.1D). Similar to the results obtained with untransfected cells, LPS and TNF- $\alpha$  stimulation inhibited Vpr52-

96-induced apoptosis in cells transfected with control oligonucleotides (from 45-50% to 20-25%). In contrast, stimulation with either LPS or TNF- $\alpha$  failed to inhibit significantly Vpr52-96-induced apoptosis in cells transfected with anti-sense c-IAP2 oligonucleotides (45-50%) (Fig. 4-2.3A). These results suggest that LPS-/TNF- $\alpha$ -induced resistance to Vpr-mediated apoptosis is regulated through the induction of c-IAP2 gene in THP-1 cells. I further demonstrated that LPS induced protection against Vpr-mediated apoptosis is regulated by endogenously produced TNF- $\alpha$  through the induction of c-IAP2 gene. I already showed that prior treatment of LPS-stimulated THP-1 cells with anti-TNFR1 antibodies inhibited the induction of c-IAP2 gene compared to the cell pretreated with isotype control antibodies (Fig 3.1C). I also confirmed this finding in human monocytes (Fig. 4-2.3B).

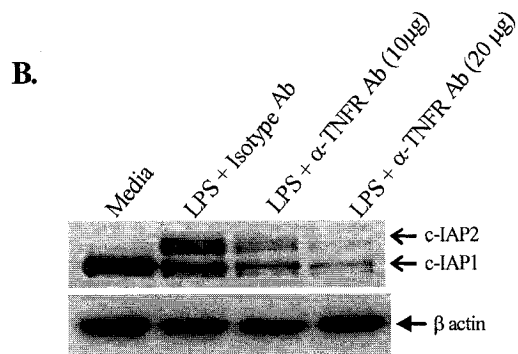
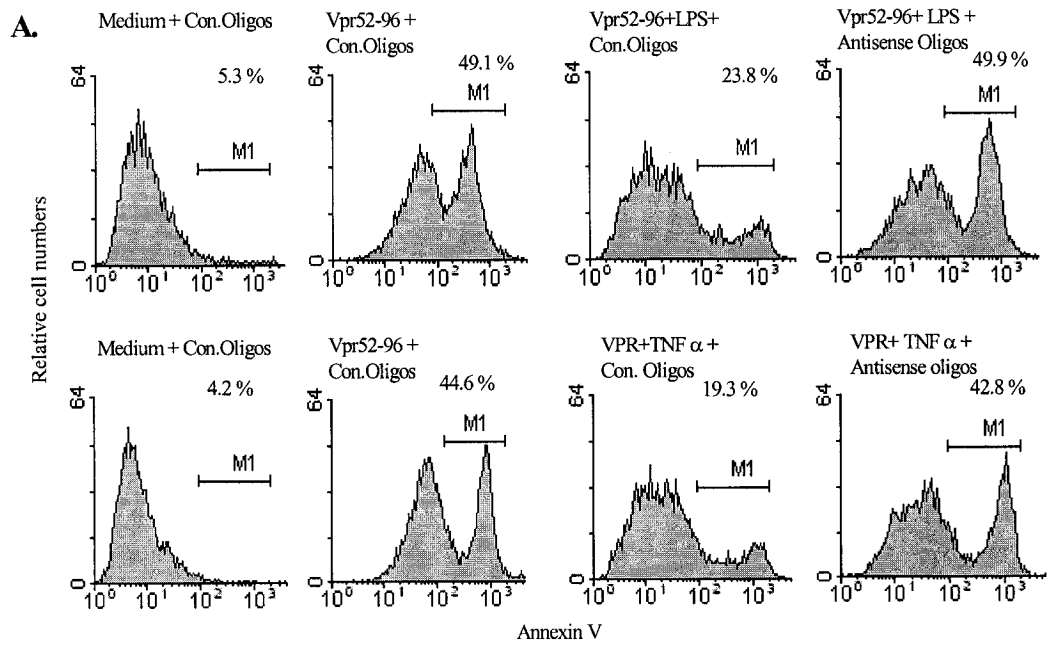
#### **Vpr52-96 inhibits LPS-/TNF- $\alpha$ -induced c-IAP2 expression in monocytic cells:**

Because the above results suggest that c-IAP2 induction regulates LPS- and TNF- $\alpha$ -induced protection against Vpr52-96-mediated apoptosis and pretreatment of cells with Vpr52-96 peptide inhibited LPS- and TNF- $\alpha$ -induced protection against Vpr52-96-mediated apoptosis, it was of interest to determine if Vpr52-96 inhibits LPS- and TNF- $\alpha$ -induced expression of c-IAP2. As expected, stimulation of cells with either LPS or TNF- $\alpha$  induced the expression of c-IAP2 in both monocytes and THP-1 cells. However, prior treatment with Vpr52-96 peptide for 2 hr inhibited LPS- and TNF- $\alpha$ -induced expression of c-IAP2 in THP-1 cells and monocytes at protein level as determined by Western immunoblotting and at the RNA level in THP-1 cell by RT-PCR (Fig. 4-2.4A). It may be pointed out that pretreatment of cells with Vpr52-96 peptide also inhibited the basal

**Fig. 4-2.3: LPS/TNF- $\alpha$  induced protection in Vpr52-96-mediated apoptosis is regulated by c-IAP2:**

**A.** THP-1 cells ( $10^6$ /ml) were transfected with either antisense (AS) c-IAP2 or control oligonucleotides followed by stimulation with LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for 6 h. Transfected and stimulated cells were treated with Vpr52-96 peptide for 24 h followed by determination of apoptotic cells by annexin/PI staining. The experiments shown are representative of three different experiments.

**B.** Monocytes ( $0.5 \times 10^6$ /ml) were stimulated with LPS (1  $\mu$ g/ml) for 6 h in the presence and the absence of anti-TNF- $\alpha$ -R1 (10-20  $\mu$ g/ml) or isotype matched control antibodies followed by treatment with 1.5  $\mu$ M Vpr52-96 peptide for 12 h. Cell extracts were prepared and c-IAP2 expression was determined by Western blot analysis. The results shown are representative of three different experiments.



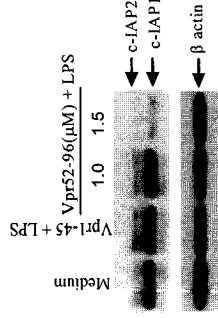
**Fig. 4-2.4:Vpr52-96 inhibits LPS-/TNF- $\alpha$ -induced c-IAP2 expression in monocytic cells:**

**A.** THP-1 cells or monocytes ( $5 \times 10^6$ /ml) were treated with various concentrations of Vpr52-96 or Vpr1-45 peptide for 2 h followed by stimulation with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$ . **Upper panel:** Cell extracts were prepared and c-IAP2 expression was determined by Western blot analysis. **Lower panel:** RNA was extracted from THP-1 cells and semi-quantitative PCR was conducted for c-IAP2. The results shown in A and B are representative of three different experiments.

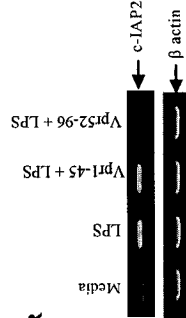
**B.** THP-1 cells or monocytes ( $5 \times 10^6$ /ml) were stimulated with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  for 6 h followed by treatment with various concentrations of Vpr52-96 or Vpr1-45 peptide. **Upper panel:** Cell extracts were prepared and c-IAP2 expression was determined by Western blot analysis. **Lower panel:** RNA was extracted from THP-1 cells and semi-quantitative PCR was conducted for c-IAP2.

**A. LPS after treatment (THP-1 cells)**

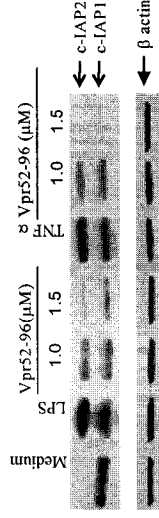
Western blotting



RT-PCR

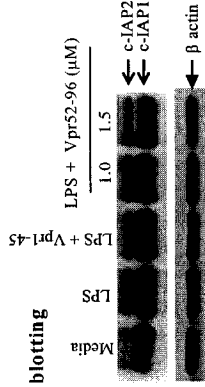


**Monocytes**

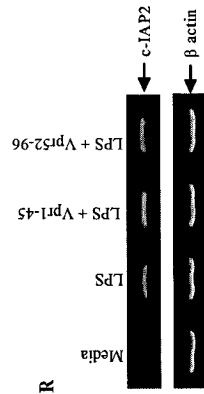


**B. LPS prior treatment (THP-1 cells)**

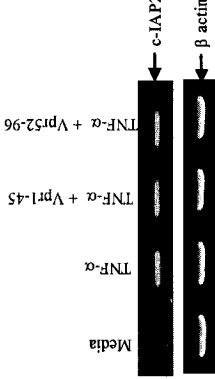
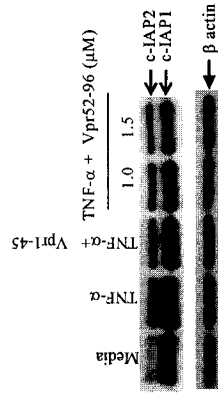
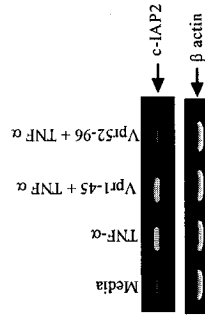
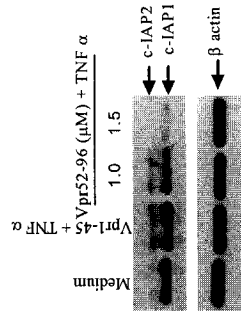
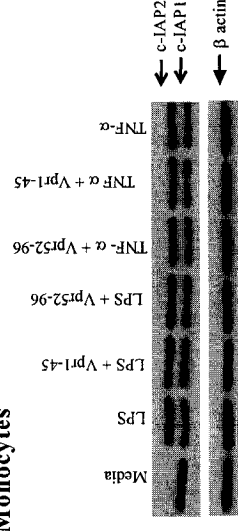
Western blotting



RT-PCR



**Monocytes**



levels of c-IAP1 in both monocytes and THP-1 cells. In contrast, if cells were treated with Vpr52-96 peptide following stimulation with either LPS or TNF- $\alpha$ , the expression of c-IAP2 was not inhibited at RNA (THP-1 cell) as well as protein level (monocyte and THP-1 cell) even when Vpr peptide was used at a highest concentration of 2  $\mu$ M (Fig. 4-2.4B). These results suggested that LPS- and TNF- $\alpha$ -induced protection against Vpr52-96-mediated apoptosis may be regulated, at least in part, through the induction of anti-apoptotic c-IAP2 gene. Furthermore, Vpr52-96 peptide may inhibit LPS and TNF- $\alpha$ -induced protection by inhibiting c-IAP2 induction.

#### **LPS/TNF- $\alpha$ induced activation of CAMKII confers protection to Vpr52-96 induced apoptosis:**

I have previously demonstrated that CaM/CAMKII regulates LPS- and TNF- $\alpha$ -induced expression of c-IAP2 in THP-1 cells. To determine whether CaM/CAMKII also regulates c-IAP2 expression in primary human monocytes, pharmacological inhibitors specific for calcium influx (EGTA), calmodulin (W-7), and CAMKII (KN-93) were employed. The results show that EGTA, W-7 and KN-93 inhibited LPS- as well as TNF- $\alpha$ -induced expression of c-IAP2 in monocytes (Fig. 4-2.5C).

Since c-IAP2 induction has been shown to induce resistance to staurosporine-induced apoptosis, it was of interest to determine the role of calcium signaling and in particular the role of CaM/CAMKII in LPS- and TNF- $\alpha$ -induced resistance to Vpr52-96-mediated apoptosis in primary human monocytes and THP-1 cells. THP-1 cells and monocytes were treated with pharmacological inhibitors specific for the calcium signaling such as calcium chelator EGTA for 2 hr prior to stimulation with LPS and TNF- $\alpha$  for 6 hr. Subsequently cells were treated with various concentrations of Vpr52-96

or Vpr1-45 peptides for 24 hr followed by analysis for apoptosis. As expected, stimulation with either LPS or TNF- $\alpha$  inhibited Vpr52-96-induced apoptosis in both THP-1 cells (Fig. 4-2.5A) and monocytes (Fig. 4-2.5B). Significantly, prior treatment of cells with EGTA reversed the LPS/TNF- $\alpha$  mediated inhibition of Vpr52-96 induced apoptosis in both monocytes and THP-1 cells (Fig. 4-2.5A and 4-2.5B). Elevations in cytoplasmic calcium concentrations occur following stimulation by diverse stimuli that activate voltage or ligand-gated calcium channels in the plasma membrane or following release of calcium present in intracellular stores, mainly in the endoplasmic reticulum (ER). The role of receptor-mediated entry of extracellular Ca<sup>2+</sup> was studied by employing SKF-96365. To determine whether calcium release from the ER regulates LPS- and TNF- $\alpha$ -induced resistance to Vpr-mediated apoptosis, we employed 2-APB, an inhibitor of the IP3 receptor which blocks the release of calcium from the ER by blocking IP3 receptor-gated channels. Treatment with SKF prior to stimulation with LPS or TNF- $\alpha$  reversed the LPS- as well as TNF- $\alpha$ - mediated inhibition of Vpr52-96-induced apoptosis in THP-1 cells (Fig. 4-2.5A). However, prior treatment with 2-APB did not affect Vpr52-96-induced apoptosis (Fig 4-2.5A).

Calmodulin (CaM), a major calcium receptor, is present in both cytoplasmic and nuclear compartments. The calcium/CaM complex regulates several downstream targets including protein kinases and phosphatases. To investigate the role of CaM, a specific calmodulin inhibitor, W-7, was employed. One major family of calcium/CaM effectors is the calmodulin-dependent protein kinases (CAMK), which includes a multifunctional kinase, CAMKII. To gain further insight into the role of CaM, we examined the involvement of CAMKII by employing the CAMKII-specific inhibitor, KN-93. Results

show that calmodulin and CAMKII inhibitors significantly reversed the protection induced by LPS- and TNF- $\alpha$  in THP-1 cells and human monocytes (Fig 4-2.5A and 4-2.5B). It may be pointed out that pretreatment of cells with inhibitors specific for p38 (SB202190), p42/44 ERK (PD98059), JNK MAPKs (SP600125), PI3K (Ly294002), (data not shown) and calcineurin such as FK506 and Cyclosporin A did not affect the level of protection induced by LPS and TNF- $\alpha$  in THP-1 cells (Fig 4-2.5A).

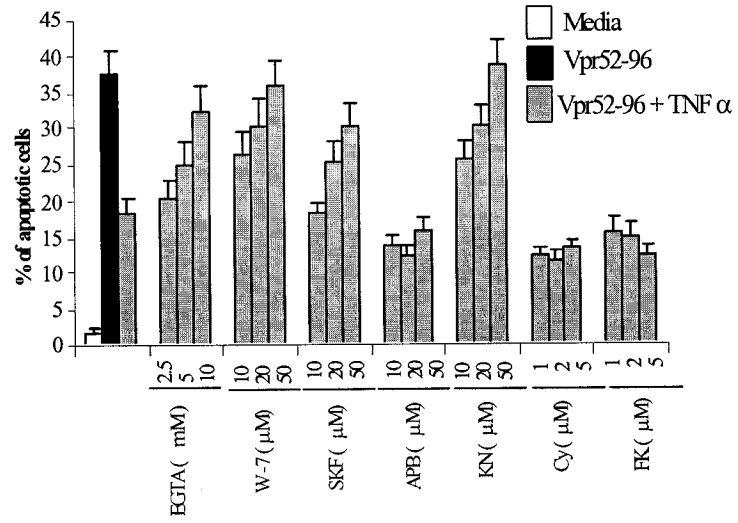
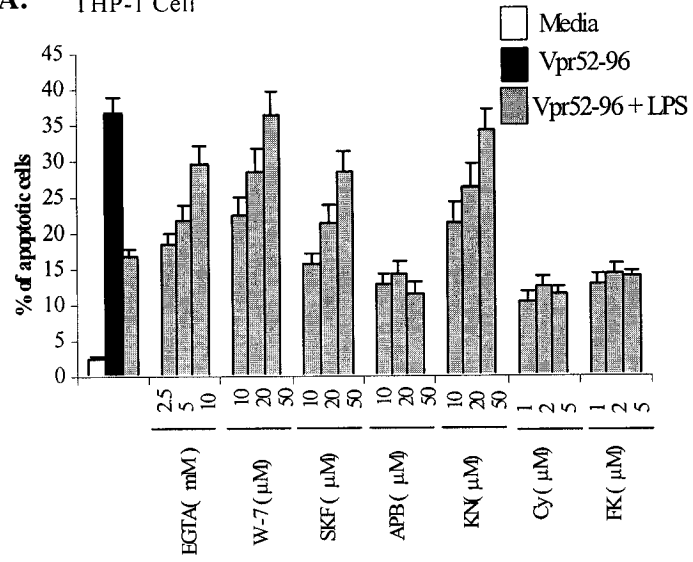
To confirm the involvement of CAMKII in LPS- and TNF- $\alpha$ -mediated inhibition of Vpr52-96-induced apoptosis, THP-1 cells were transfected with DN-CAMKII plasmid. After 24 hr, transfected cells were stimulated with either LPS or TNF- $\alpha$  followed by determination of c-IAP2 expression and analysis of Vpr52-96-induced apoptosis. My earlier results showed significant inhibition of c-IAP2 expression in cells transfected with DN-CAMKII plasmid following LPS as well as TNF- $\alpha$  stimulation compared to the cells transfected with the control vector (Fig. 3.6C). Stimulation with either LPS or TNF- $\alpha$  inhibited Vpr52-96-induced apoptosis in cells transfected with control vector. In contrast, transfection of cells with DN-CAMKII construct reversed the LPS- (from 21 to 43%) and TNF- $\alpha$ -mediated (from 20 to 40%) inhibition of Vpr52-96-induced apoptosis (Fig. 4-2.6). Overall, these results suggest that LPS and TNF- $\alpha$  induce protection against Vpr52-96-mediated apoptosis by c-IAP2 through CAMKII activation.

**Fig. 4-2.5: LPS-/TNF- $\alpha$ -mediated resistance to Vpr52-96 induced apoptosis is regulated through the activation of CaM/CAMKII:**

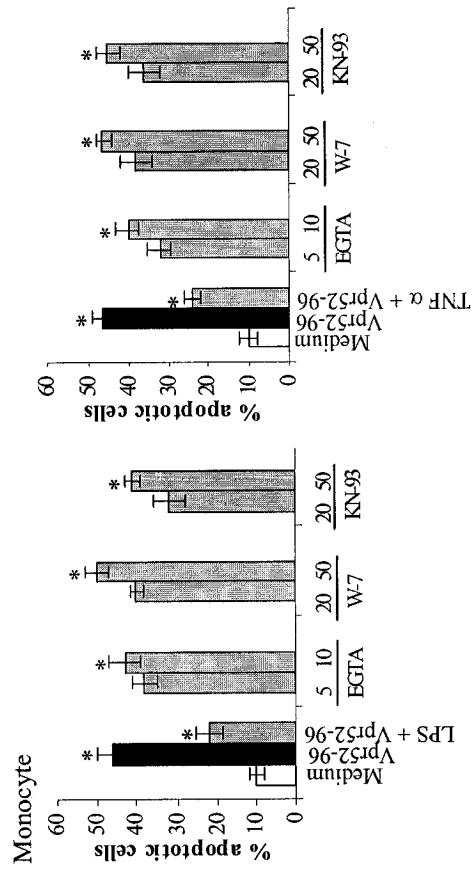
**A.** THP-1 cells ( $0.5 \times 10^6$ /ml) were stimulated with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for 6 h in the presence or absence of various concentrations of calcium signaling inhibitors such as EGTA, W-7, SKF, APB, KN-93, Cyclo, and FK506 followed by treatment with 1.5  $\mu$ M Vpr52-96 peptide for 24 h. Cells were then stained with intracellular PI for measurement of DNA content. The graphs shown are a mean  $\pm$  SD of three different experiments.

**B & C.** Monocytes ( $0.5 \times 10^6$ /ml) were stimulated with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for 6 h in the presence or absence of various concentrations of calcium signaling inhibitors such as EGTA, W-7, and KN-93 followed by treatment with 1.5  $\mu$ M Vpr52-96 peptide for 12 h. Cells were then stained with intracellular PI for measurement of DNA content. The graphs shown are a mean  $\pm$  SD of three different experiments (\*  $p < 0.001$ ). Cell extracts were used to detect c-IAP2 expression by Western blot. The experiments shown are representative of three different experiments.

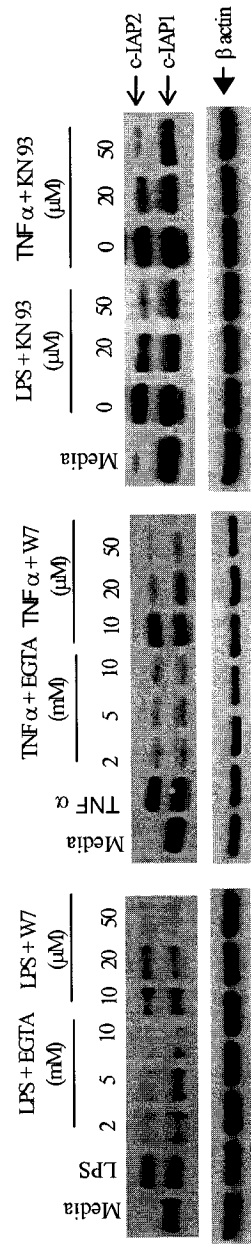
**A. THP-1 Cell**



**B.**

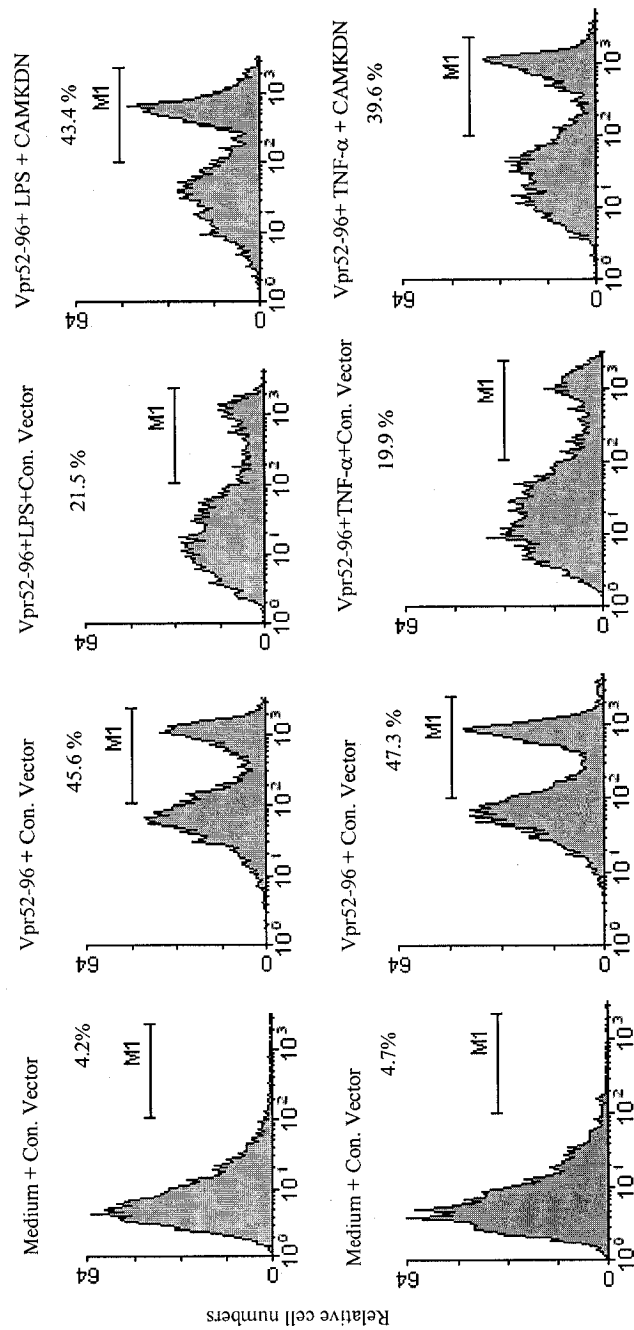


**C.**



**Fig. 4-2.6: LPS-/TNF- $\alpha$ - induced activation of CAMKII confers protection to Vpr52-96 induced apoptosis:**

THP-1 cells were transfected with either DN-CAMKII or control vector and cultured for 24 h, followed by stimulation with either LPS (1  $\mu$ g/ml) or TNF- $\alpha$  (10 ng/ml) for another 6 h. Cells were then treated with Vpr52-96 for 24 h followed by determination of apoptotic cells by annexin/PI staining. The results shown are representative of three different experiments.



Annexin V

**Vpr52-96 inhibits LPS- and TNF- $\alpha$ -induced resistance to Vpr52-96-mediated apoptosis by blocking LPS- and TNF- $\alpha$ -induced calcium influx, CAMKII phosphorylation and c-IAP2 transcription in human monocytic cells:**

***Vpr52-96 interferes with the LPS- and TNF- $\alpha$ -induced calcium influx and CAMKII phosphorylation:***

Since Vpr52-96 treatment prior to stimulation of monocytic cells with either TNF- $\alpha$  or LPS inhibited LPS- and TNF- $\alpha$ -mediated c-IAP2 expression (Fig 4-2.4A and 4-2.4B), it is likely that Vpr52-96 may interfere with the LPS- and TNF- $\alpha$ -induced CaM/CAMKII pathway to inhibit LPS-/TNF- $\alpha$ -mediated protection against Vpr52-96-induced apoptosis. I first determined if Vpr52-96 interferes with the LPS- and TNF- $\alpha$ -induced calcium pathway, and in particular the calcium influx, cells were treated with Vpr52-96 followed by stimulation with LPS or TNF- $\alpha$  and measurement of calcium flux at various times. Both LPS as well as TNF- $\alpha$  induced calcium influx at 12 and 8 min post stimulation, respectively, and treatment with EGTA inhibited LPS- and TNF- $\alpha$ -induced calcium influx to the basal level in THP-1 cells (Fig. 4-2.7A). LPS- and TNF- $\alpha$ -induced calcium influx was inhibited by Vpr52-96 in a dose dependent manner (Fig. 4-2.7A). In contrast, pretreatment of cells with Vpr1-45 did not have any effect on LPS- or TNF- $\alpha$ -induced calcium influx in THP-1 cells (Fig 4-2.7A). Similar results were obtained when monocytes were treated with Vpr peptides prior to stimulation with either LPS or TNF- $\alpha$  (data not shown). To determine if Vpr52-96 inhibited LPS- and TNF- $\alpha$ -induced CAMKII activity, THP-1 cells were treated with Vpr52-96 for 2 hr followed by stimulation with either LPS or TNF- $\alpha$  and measurement of CAMKII activity. Vpr52-96 inhibited LPS- and TNF- $\alpha$ - induced CAMKII activity (Fig 4-2.7B).

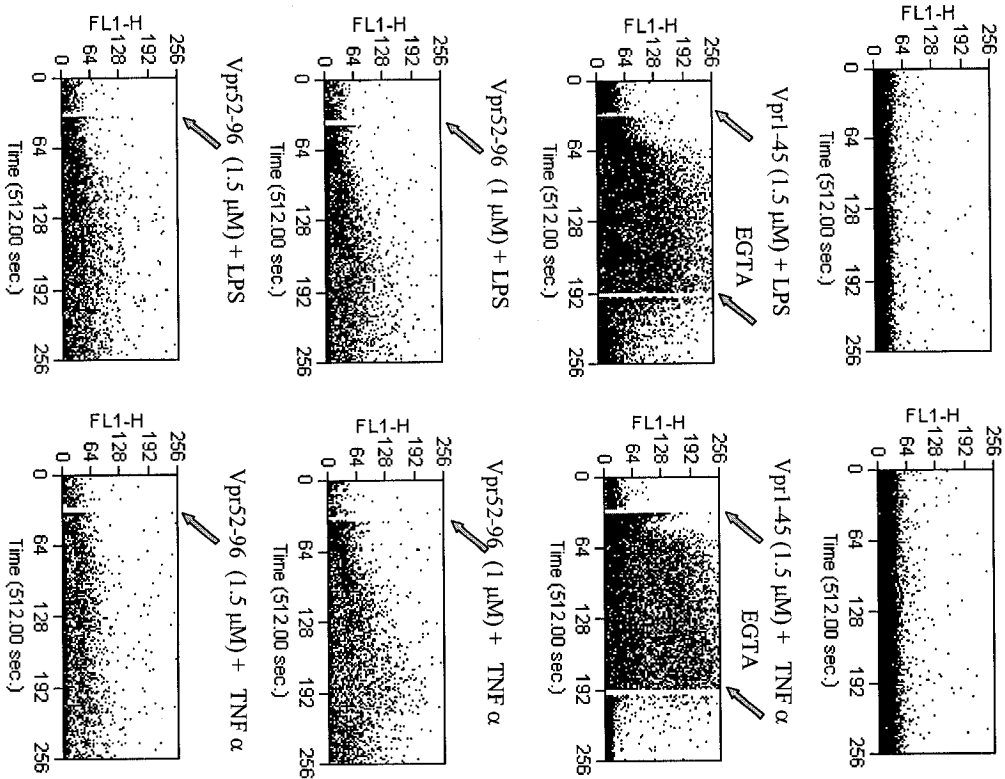
**Fig. 4-2.7: Vpr52-96 interferes with the LPS- and TNF- $\alpha$ -induced calcium influx and CAMKII activity in human monocytic cells:**

**A.** THP-1 cells ( $0.5 \times 10^6$ /ml) treated with Vpr52-96 peptide for 2 h followed by loaded with Fluo3/AM. Cells were then stimulated with either LPS or TNF- $\alpha$  and the resulting Ca<sup>2+</sup> influx was measured by flow cytometric analysis. **Top panel:** Baseline Ca<sup>2+</sup> levels in unstimulated cells. **2<sup>nd</sup> panel:** Stimulation with LPS/TNF- $\alpha$  followed by the addition of EGTA. **3<sup>rd</sup> and 4<sup>th</sup> panels:** Treatment with Vpr52-96 peptide prior to stimulation with LPS/TNF- $\alpha$ . The results shown are representative of three different experiments.

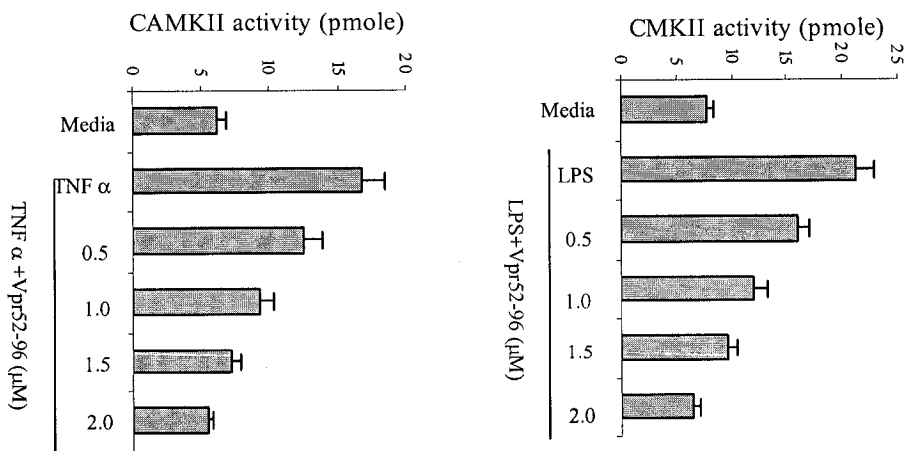
**B.** THP-1 cells ( $2.0 \times 10^6$ /ml) were pretreated with Vpr52-96 for 2 h followed by stimulation of cells with either LPS or TNF- $\alpha$  for 30 min. CAMKII activity was assayed from total cell proteins utilizing a peptide substrate (KKALRRQETVDAL) specific for CAMKII. The results shown represent the mean  $\pm$  S.D. of three independent experiments.

A.

Fluo-3



B.



***Vpr52-96 inhibits LPS-induced c-IAP2 transcription in human monocytic cells:***

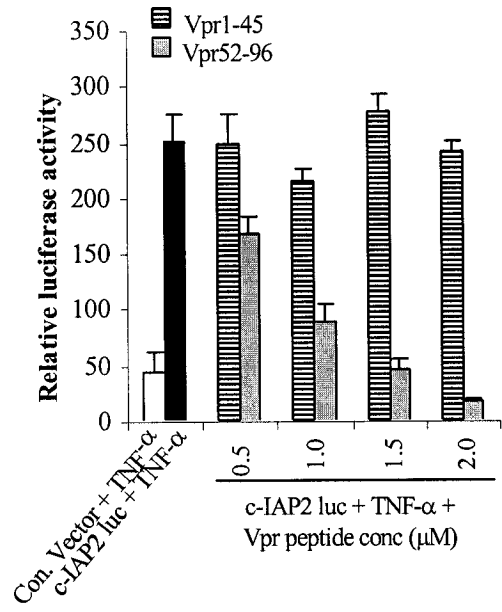
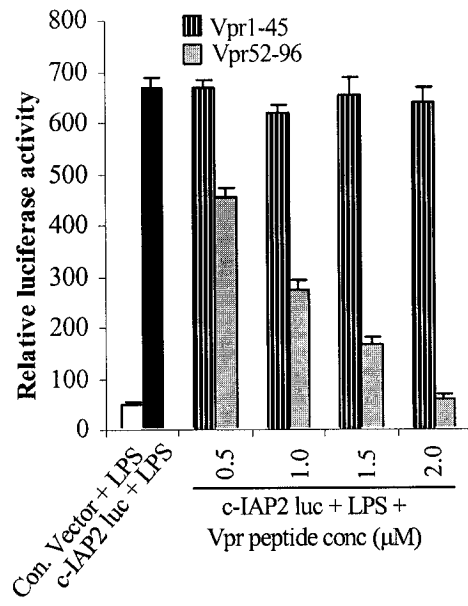
NF $\kappa$ B has been shown to play a critical role in c-IAP2 transcription following LPS and TNF- $\alpha$  stimulation in monocytic cells [11]. To determine whether Vpr52-96 inhibits c-IAP2 transcription by inhibiting NF $\kappa$ B activation, THP-1 cells were transfected with human c-IAP2 promoter (-606 to + 121 bp) linked to the luciferase reporter construct. Subsequently, transfected cells were stimulated with either LPS or TNF- $\alpha$  in the presence or absence of Vpr peptides. Stimulation of cells with either LPS or TNF- $\alpha$  significantly enhanced c-IAP2 promoter activity compared to the cells transfected with the control vector. (Fig 4-2.8). Vpr52-96 treatment prior to LPS or TNF- $\alpha$  stimulation significantly inhibited c-IAP2 promoter activity whereas pretreatment with Vpr1-45 peptide did not have any effect on luciferase activity (Fig. 4-2.8).

***Vpr52-96 inhibits binding of NF $\kappa$ B to its binding sites in the c-IAP2 promoter in LPS- and TNF- $\alpha$ -stimulated monocytic cells:***

To further confirm that Vpr52-96 inhibits LPS-/TNF- $\alpha$ -induced c-IAP2 gene transcription by inhibiting the binding of NF $\kappa$ B to the c-IAP2 promoter, the nuclear extract harvested from LPS- and TNF- $\alpha$ -stimulated cells in the presence and absence of Vpr peptides were analyzed for binding of NF $\kappa$ B to the oligonucleotide probes containing NF $\kappa$ B sequences corresponding to their sites in the c-IAP2 promoter. There are at least two NF $\kappa$ B binding sites in the c-IAP2 promoter that have been implicated in transcription. Stimulation of cells with either LPS or TNF- $\alpha$  induced the binding of NF $\kappa$ B to the oligonucleotide probes containing NF $\kappa$ B site # 1 as well as site # 3 (Fig. 4-2.9). I have already demonstrated in my earlier study the specificity of NF $\kappa$ B binding by

**Fig. 4-2. 8: Vpr52-96 inhibits LPS-induced c-IAP2 transcription in human monocytic cells:**

THP-1 cells ( $10^6$ /ml) were transiently cotransfected with 5  $\mu$ g of pc-IAP2pr-GL3B (c-IAP2 luc) and 3  $\mu$ g of  $\beta$ -galactosidase plasmids. After 24 h, cells were treated with either Vpr1-45 or Vpr52-96 peptides for 2 h followed by stimulation with either 1  $\mu$ g/ml LPS or 10 ng/ml TNF- $\alpha$  for 24 h. Following incubation, luciferase and  $\beta$ -galactosidase activities were determined. Luciferase activity was normalized for  $\beta$ -galactosidase activity to give relative luciferase units (RLU).

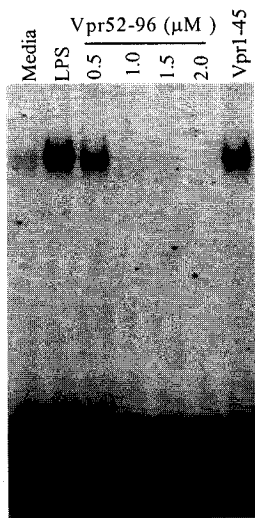


cold competition with specific and non specific oligonucleotides and by supershift analysis using anti NF $\kappa$ B-p50 and p65 antibodies (Fig. 3.10). Further, treatment of THP-1 cells with Vpr52-96 peptide for 2 hr prior to stimulation with either LPS or TNF- $\alpha$  inhibited the binding of NF $\kappa$ B to its oligonucleotide probes in a dose dependent manner (Fig. 4-2.9). In contrast, prior treatment of cells with Vpr1-45 peptide did not have any effect on NF $\kappa$ B binding (Fig. 4-2.9). Taken together, these results suggest that Vpr52-96 inhibits LPS- and TNF- $\alpha$ -induced resistance to Vpr52-96-mediated apoptosis by blocking LPS- and TNF- $\alpha$ -induced calcium influx, CAMKII phosphorylation and c-IAP2 transcription in human monocytic cells.

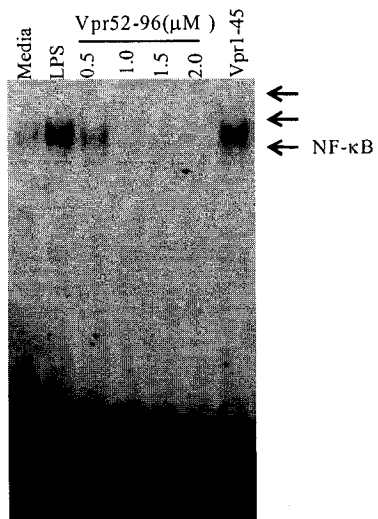
Based on all these findings, my results suggest that LPS-/TNF- $\alpha$ -induced resistance to Vpr52-96 mediated apoptosis is due to c-IAP2 upregulation via activation of CAMKII through NF $\kappa$ B.

**Fig. 4-2. 9: Vpr52-96 inhibits binding of NFκB to its binding sites in the c-IAP2 promoter in LPS- and TNF-α-stimulated monocytic cells:**

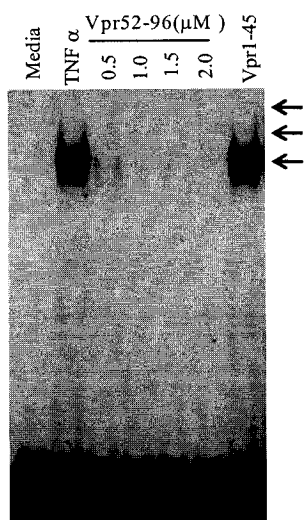
THP-1 cells ( $5 \times 10^6$ /ml) were treated with either Vpr1-45 or Vpr52-96 peptides for 2 h followed by stimulation with either 1 μg/ml LPS or 10 ng/ml TNF-α for 60 and 45 min, respectively. Nuclear proteins (5 μg) were incubated with  $^{32}$ P-labeled oligonucleotide probes corresponding to NF-κB site 1 and 3 sequences derived from the c-IAP2 promoter. The samples were run in 5% non denaturing polyacrylamide gel, dried and autoradiographed. The results shown are representative of three different experiments.



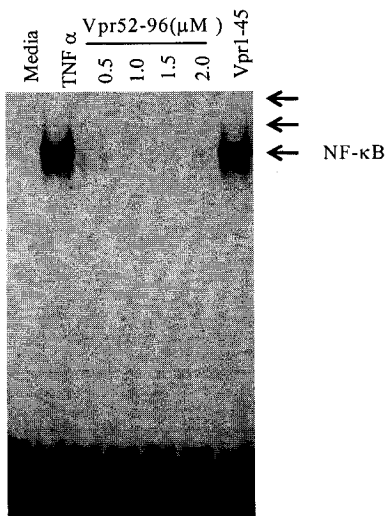
NF- $\kappa$ B site # 1



NF- $\kappa$ B site # 3



NF- $\kappa$ B site # 1



NF- $\kappa$ B site # 3

## **Discussion:**

HIV is known to cause apoptosis in CD4+ T cells and other cell types including neuronal cells, and neutrophils and plays a key role in HIV pathogenesis [90]. However, monocytes/macrophages unlike CD4+ T cells survive HIV replication and serve as a major reservoir of HIV in lymphoid and extralymphoid tissues at all stages of the disease [8]. The inability to eliminate persistently infected monocytic cell reservoirs in HIV-infected patients despite highly active anti-retroviral therapy poses a major hurdle in curing the disease [332-336]. Based on my preliminary results, I believe that the pro-inflammatory cytokine, TNF- $\alpha$  which is known to enhance HIV replication and is produced following HIV infection may be a key to protect monocytic cells from the cytopathic effects of HIV. This may promote the development and maintenance of these cells as viral reservoirs.

Among various proteins involved in inducing apoptosis in HIV infection, Vpr plays an important role being packaged in great quantities into the virion nucleocapsid and is also expressed late in the infection suggesting the importance of this protein throughout the viral life cycle [12;13]. HIV Vpr is believed to cause cell death in several cell types including CD4+ T cells and neuronal cells [34;95;129]. In this study, I used C terminal Vpr peptide (Vpr52-96) which mimics the apoptosis inducing property of Vpr and the N terminal end (Vpr1-45) as control. First of all, I delineated the mechanism involved in Vpr induced apoptosis in monocytes and monocytic cell line. My results revealed that Vpr52-96 induced apoptosis in a caspase dependent manner by inducing mitochondrial membrane permeabilization. I also demonstrated that activation of JNK MAPK downregulates anti-apoptotic genes such as c-IAP1 and Bcl2 by inhibiting the

respective transcription factors which lead to apoptosis. Further, I have shown that LPS/TNF- $\alpha$  induces protection to Vpr52-96-mediated apoptosis and it is regulated by upregulation of one of the anti-apoptotic genes c-IAP2 through activation of CAMKII in monocytes and a monocytic cell line. These two important findings are discussed as below in separate sections.

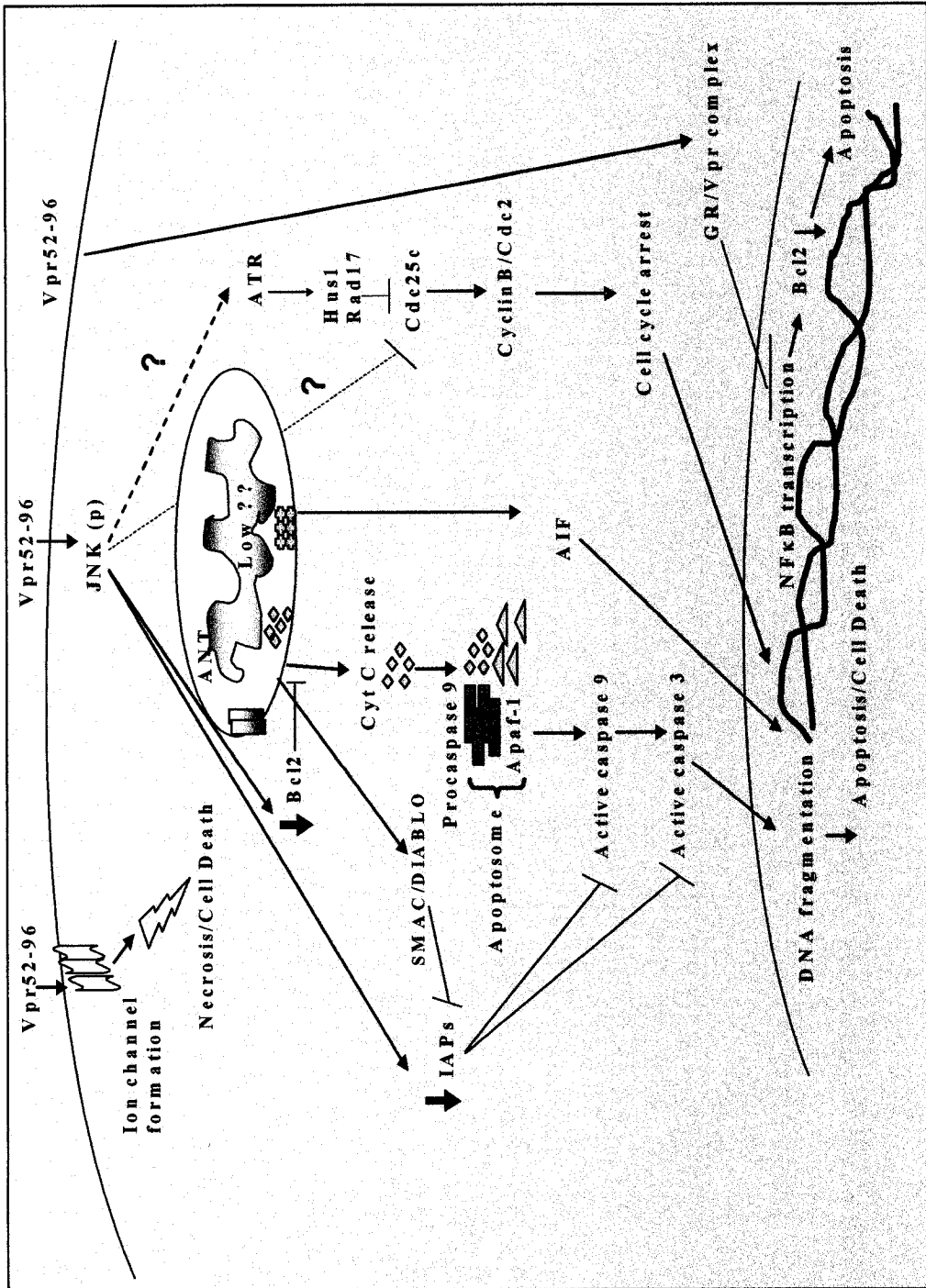
### **Signaling pathways involved in Vpr induced apoptosis:**

The primary aim of this study was to investigate the signaling pathways, particularly the role of MAPKs, and the transcription factors involved in the regulation of Vpr-induced apoptosis in human monocytic cells. My results suggest that Vpr52-96-induced apoptosis in normal human monocytes and promonocytic THP-1 cells occurs in a caspase-dependent manner. Although both Vpr1-45 and Vpr52-96 peptides induced phosphorylation of p38, ERK, and JNK MAPKs, Vpr52-96-induced apoptosis was regulated selectively through JNK activation. Furthermore, Vpr-52-96-induced apoptosis was attributed to the down regulation of anti-apoptotic genes Bcl2 and c-IAP1 through the activation of upstream JNK MAPKs (Fig. 4-3.1).

It is well established that cell cycle arrest occurs by interfering with the activity of the Cdc2-cyclin B1 complex, a central regulator of the G2 to mitosis transition [348]. In general, this complex is inactivated by Wee1 kinase and activated by Cdc25C phosphatase [348]. Vpr mediates cell cycle arrest by phosphorylation and inactivation of Cdc25C phosphatase via activating the ATR DNA damage response pathway [115;349]. The Rad17 and Hus1 proteins involved in the ATR pathway were shown to be required for cell cycle arrest by Vpr [350]. Vpr was also shown to bind Cdc25C directly and

**Fig. 4-3.1: HIV-Vpr induced apoptosis by JNK-MAPK in human monocytes:**

Entry of Vpr into the monocytic cells induces JNK activation resulting in transcriptional inhibition of c-IAP1 and Bcl2 expression, activation of caspases, and apoptosis. Vpr is known to activate ATR DNA damage pathway that acts on Cdc25C through Hus1 and Rad17. This process leads to inactivation of cyclin B and cell cycle arrest [115;349-351]. Vpr is also known to bind glucocorticoid receptor and downregulates NFκB regulated anti-apoptotic gene expression and induces apoptosis [127;352]. Smac released from mitochondria inhibits the activation of c-IAPs which may result in the activation of caspase cascade and apoptosis.



inhibit Cdc25C phosphatase activity [349;351], perhaps blocking cyclin-B1-Cdc2 redundantly with the ATR pathway. Recently, Jacotot *et al.* demonstrated that Vpr52-96-induced apoptosis may occur through a direct effect on the mitochondrial permeability transition pore complex (PTPC) and specifically on the mitochondrial adenine nucleotide translocator (ANT), a component of the PTPC [101]. This event leads to permeabilization of the outer mitochondrial membrane with consequent release of apoptosis inducing factor and cytochrome C [101;102]. Cytochrome C interacts with Apaf-1 and procaspase 9 to create an apoptosome, the caspase activation complex that causes activation of other caspases resulting in apoptosis [101;102;120;121;123]. My results suggest that Vpr52-96 peptide caused a dramatic reduction of mitochondrial membrane potential in monocytic cells in a caspase-dependent manner.

Although numerous studies have implicated the JNK pathway in pro-apoptotic as well as anti-apoptotic cellular functions [136;353], there is little information on the role of MAPKs in Vpr-mediated cell cycle arrest and apoptosis. Recently, Vpr-induced cell cycle arrest was shown to be associated with down regulation of ERK MAPK pathway in a 293 fibroblast cell line [138]. My results suggest that Vpr-induced apoptosis in normal human monocytes and THP-1 cells is regulated through the activation of JNK MAPKs. Pretreatment of cells with JNK inhibitors SP60025, dexamethasone, and curcumin or transfection with JNK-specific siRNAs significantly inhibited Vpr-induced apoptosis. Although MAPKs have been reported to regulate HIV replication in T cells and latently infected cells [137;354], this is the first report describing a novel pathway involving JNK activation in Vpr-induced apoptosis.

The JNK group of MAPK is encoded by three genes: *jnk1* and *jnk2* genes which are ubiquitously expressed, and the *jnk3* gene, expressed primarily in the heart, testis, and brain [235]. Targeted disruption of *jnk1* or *jnk2* genes results in mice that exhibit defects in apoptosis, development and functions of effector T cells, and cytokine production [136;355]. However, disruption of both *jnk1* and *jnk2* genes resulted in embryonic death [135;136;356]. Although a distinct role for JNK-1 and JNK-2 in apoptosis, immunological and developmental processes is not clear at present, some studies have suggested a differential involvement for JNK-1 and JNK-2 [135;136;357;358]. I employed siRNAs specific for JNK-1 and JNK-2, both of which prevented Vpr-mediated cell death to equal levels suggesting redundancy between the two JNK isoforms at least with respect to Vpr-induced apoptosis in monocytic cells.

I have also demonstrated that Vpr-induced apoptosis was mediated by the down regulation of anti-apoptotic Bcl2 gene. Bcl2 and its closest homologues, BclXL and Bclw, potently inhibit apoptosis in response to many signaling pathways [342;359;360]. Bcl2 has been shown to protect cells from Vpr-induced apoptosis most likely by regulating inner and outer MMP through interactions with major components of PTPC such as ANT in the inner membrane, and the voltage dependent anion channels in the outer membrane and/or through autonomous channel-forming activities [101;102;123;124]. Vpr was shown to physically and functionally interact with the ANT104-116 site in ANT, consequently converting ANT into a non-specific pore leading to inner MMP which triggers matrix swelling, outer membrane rupture, and permeable to cytochrome C [101;102].

There is substantial agreement that anti-apoptotic c-IAP1 and c-IAP2 genes endow cells with protection against a number of apoptotic stimuli [85;168]. In my earlier studies, I demonstrated a critical role for c-IAP2 in conferring resistance to staurosporine-induced apoptosis in human monocytic cells [11]. Herein, I show that Vpr-induced apoptosis in monocytic cells may be mediated by inhibition of c-IAP1 expression in addition to that of Bcl2. How IAPs confer anti-apoptotic signals has been recently investigated. IAPs regulate the caspase cascade by binding to caspase 3 and 7 and by inhibiting the activation of procaspase 8 and 9 [168]. c-IAP1 was also shown to inhibit apoptosis through noncaspase mechanisms such as via activation of NF $\kappa$ B and JNK MAPK [195]. In addition, c-IAPs were suggested to obstruct apoptosis through binding to the IAP antagonists such as SMAC [361] or interfering with the signaling pathway initiated by TNF- $\alpha$  by interacting with TRAF through the BIR1 (Baculoviral IAP Repeat 1) domain [362].

JNK can phosphorylate Ser/Thr-Pro motifs in the activation domains of various transcription factors such as c-Jun, Jun-B, Jun-D, activating transcription factor-2, PU.1, Sp-1, and Ets-2 [136;285;363;364]. My results suggest that Vpr52-96-activated JNK causes down regulation of transcription factors involved in the regulation of Bcl2 and c-IAP1 gene transcription. Bcl2 transcription is regulated by NF $\kappa$ B, Sp-1 and CREB [151], whereas c-IAP1 transcription was shown to involve activation of NF $\kappa$ B and CREB transcription factors [199]. Selective activation of JNK by Vpr52-96 but not Vpr1-45 peptides resulted in inhibition of binding of corresponding NF $\kappa$ B and CREB transcription factors to their binding sites, and inhibition of JNK activity restored this binding and thus transcription of Bcl2 and c-IAP1 genes. These observations suggest specific interaction

of Vpr52-96 peptide with member(s) of the JNK MAPKs family or with any of these transcription factors either alone or as a complex in the cytoplasm to prevent their translocation into the nuclei. The identity of the JNK family member and/or the transcription factor involved in binding with Vpr52-96 peptide remains to be investigated. Nonetheless, Vpr has been shown to engage with a number of host cellular proteins to promote cell cycle arrest such as VprBP, a protein believed to interfere with Vpr-mediated arrest by sequestering Vpr in the cytoplasm [365] and the human homologue of MOV34, a proteosomal subunit [366].

Recently, glucocorticoid receptor complex was identified as an intracellular target for Vpr [366-368] suggesting a possible involvement of these receptors in Vpr52-96-induced apoptosis. The observations that glucocorticoids and Vpr inhibited NF $\kappa$ B induction suggest a role for glucocorticoid receptors in Vpr-mediated apoptosis [127]. However, unlike glucocorticoids that are known to inhibit JNK activity [285], Vpr52-96 induced JNK phosphorylation in my study. Therefore, it seems unlikely that Vpr52-96 induces apoptosis in monocytic cells through glucocorticoid receptors, although I can not rule out this possibility at present.

### **Signaling pathways involved in development of LPS- and TNF- $\alpha$ -mediated resistance to HIV-Vpr-induced apoptosis:**

Monocytes/macrophages survive HIV-induced cytopathic effects and acts as a major source of viral reservoir. However, the mechanism underlying the development of resistance to apoptosis remains unknown. In this study, I have demonstrated that HIV-Vpr induces apoptosis in human monocytes and monocytic cell lines. However, I also showed that bacterial endotoxin (LPS) and the pro-inflammatory cytokine, TNF- $\alpha$  that is produced in

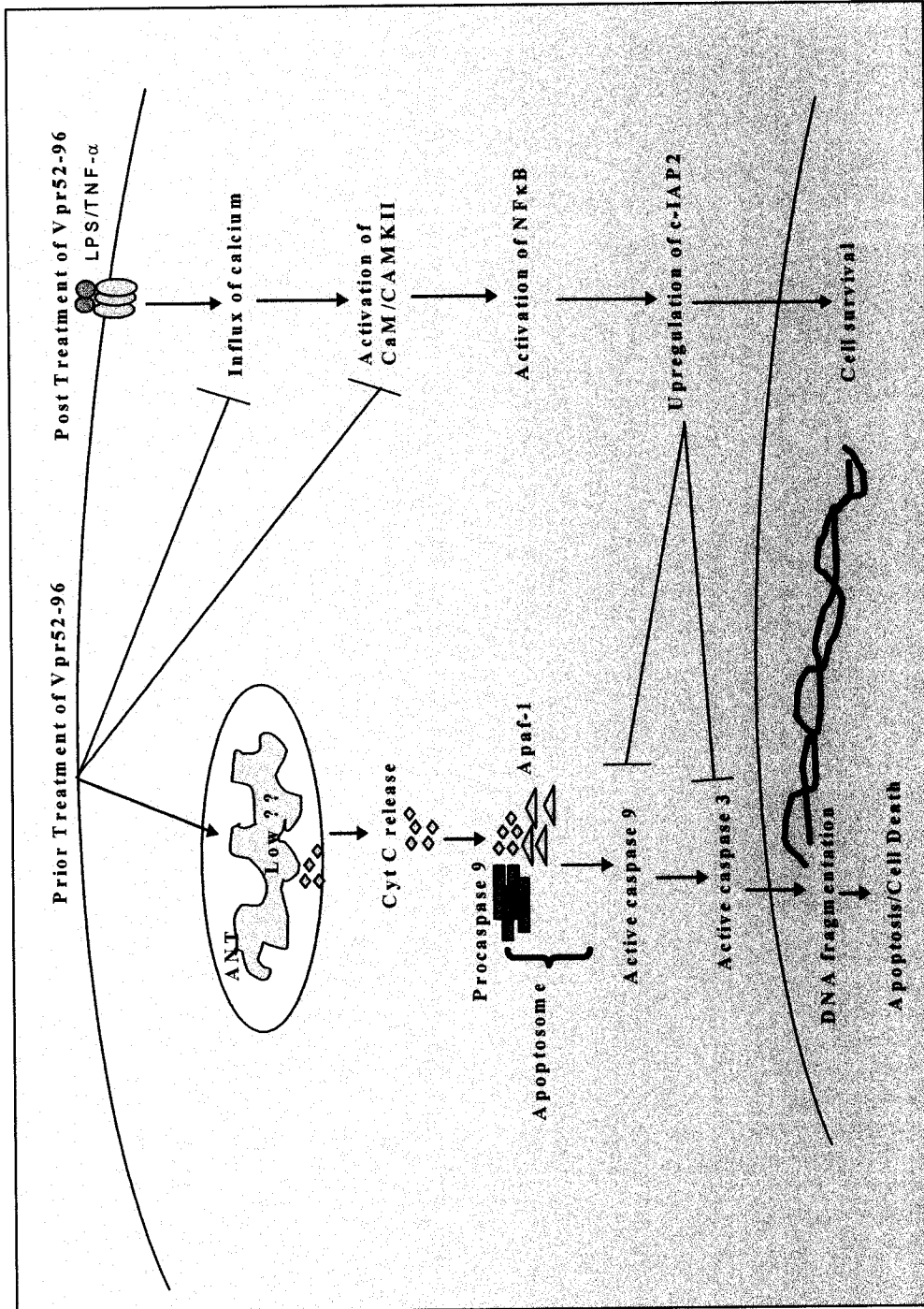
abundance during HIV infection, play a key role in inducing anti-apoptotic survival signals in human monocytic cells by inducing the expression of anti-apoptotic c-IAP2 gene through the activation of CaM/CAMKII and its down stream effector NF $\kappa$ B. In contrast, if cells are treated with Vpr52-96 prior to LPS or TNF- $\alpha$  stimulation, it abrogates LPS- and TNF- $\alpha$ -induced resistance to apoptosis by inhibiting calcium influx, activation of CAMKII and NF $\kappa$ B and eventually c-IAP2 expression (Fig. 4-3.2).

LPS, a structural component of the outer membrane of Gram-negative bacteria has been shown to prevent monocyte apoptosis [141;369]. There is evidence to suggest that LPS-induced resistance to apoptosis may be mediated by the c-IAP family of anti-apoptotic genes [190]. The c-IAP1 and c-IAP2 are key regulators of apoptosis and are overexpressed in many cancer cell lines. It is interesting to observe that c-IAP2 is selectively induced following stimulation of primary monocytes and THP-1 cells with either LPS or TNF- $\alpha$ . In this study, I show for the first time that specific inhibition of c-IAP2 by antisense oligonucleotides or the pharmacological inhibitors specific for CaM/CAMKII reversed LPS- and TNF- $\alpha$ -mediated protection from Vpr52-96-induced apoptosis. These results suggest a key role for c-IAP2 in the development of resistance to apoptosis in human monocytic cells.

c-IAP2 is known to inhibit apoptosis by interacting with initiator as well as effector caspases including caspases 3, 7, and 9 in various cell types [85]. In addition, c-IAP2 appears to be a part of the signaling complex recruited to the cytoplasmic domain of TNF-R by binding to the TRAF-1/TRAF-2 heterocomplexes and functions to suppress caspase-8 activation [161;164;168]. Since I have previously demonstrated that Vpr52-96-induced apoptosis in human monocytic cells is caspase-dependent, it is likely that c-

**Fig. 4-3.2 LPS/TNF- $\alpha$  induced resistance to HIV-Vpr mediated apoptosis:**

As shown in the figure, LPS- and TNF- $\alpha$ -mediated resistance to Vpr-induced apoptosis is regulated by induction of c-IAP2 through activation of calcium signaling pathway, particularly CAMKII. However, pretreatment of cell with Vpr peptide no more provide protection by blocking calcium influx, activation of CAMKII and NF $\kappa$ B, and induction of c-IAP2.



IAP2 is inducing resistance to Vpr52-96 mediated apoptosis by interacting with caspases. c-IAP2 is also known to interfere in the apoptosis process in a caspase-independent manner by interacting with TRAF-6. Therefore, it is possible that TNF- $\alpha$ -induced resistance to apoptosis may be mediated in a caspase-independent manner through c-IAP2 interactions with TRAF-6.

It is well established that calcium signaling plays a key role in mediating transcription of a variety of cellular genes [244]. In general, binding of a ligand to its receptor induces influx of calcium which in turn leads to release of calcium from endoplasmic reticulum [244;298]. CaM is highly conserved 17 kD protein associated either with membrane, cytoplasm or nucleus. It binds to four calcium ions and as a consequence of calcium binding, it undergoes a conformational change that renders it active to bind the target proteins with high affinity [299]. CAMKII is one of the key targets for CaM binding [247;299]. CaM is also an activator of Ser-Thr-phosphatase, calcineurin. It is activated by increase in intracellular calcium levels and is essential for translation of calcium signals into the nuclei and gene transcription [247;300]. In this study, I have demonstrated for the first time that LPS- and TNF- $\alpha$ -induced c-IAP2 expression is regulated by CaM/CAMKII in primary human monocytes in addition to the THP-1 cells described earlier. By employing specific inhibitors and the dominant negative mutants, my results suggest that LPS- and TNF- $\alpha$ -induced resistance to Vpr52-96-mediated apoptosis in primary human monocytes and THP-1 cells is regulated selectively by CaM and CAMKII activation. It is known that NF $\kappa$ B plays a key role in c-IAP2 transcription [191]. My results also show that NF $\kappa$ B activation plays a key role in LPS- and TNF- $\alpha$ -induced resistance to Vpr-mediated apoptosis in primary human monocytes as well as THP-1 cells.

The precise intracellular pathway responsible for inducing resistance to Vpr52-96-mediated apoptosis remains unclear at the present moment. As mentioned, Vpr52-96 interacts with mitochondrial protein, ANT [101], following which apoptogenic factors such as AIF, Smac, and Cyt-c, are released to deliver apoptotic signals [47;64;370]. It is possible that prior stimulation of cells with LPS or TNF- $\alpha$  may interfere with the process of Vpr internalization and/or its interaction with the mitochondrial protein ANT, and subsequent release of apoptotic factors. Since Vpr52-96-activated JNK was found to cause apoptosis in monocytic cells, it is possible that Vpr52-96 may not be able to activate JNK MAPK in TNF- $\alpha$ /LPS prestimulated monocytic cells.

My results also show that Vpr52-96 if treated prior to LPS/TNF- $\alpha$  stimulation, abrogated LPS- and TNF- $\alpha$ -induced c-IAP2 expression as well as protection against Vpr52-96-induced apoptosis. These results suggested that Vpr interfered with the LPS- and TNF- $\alpha$ -induced signaling pathway responsible for c-IAP2 induction and survival of monocytic cells. I have demonstrated for the first time that Vpr52-96 inhibited LPS- and TNF- $\alpha$ -induced calcium influx, activation of CaM and CAMKII, its down stream effector NF $\kappa$ B, and eventually c-IAP2 transcription. How Vpr blocks LPS-/TNF- $\alpha$ -induced calcium influx is not known. Since entry of Vpr is receptor independent, it is possible that internalization of Vpr through cell membrane may disturb the integrity of the cell surface receptors responsible for binding to either LPS or TNF- $\alpha$ , and consequent blocking of calcium entry in monocytic cells.

In summary, my results suggest for the first time that JNK activated selectively by the HIV-Vpr peptide plays a critical role in the induction of cell death in normal human monocytes and leukemic THP-1 cells. In view of studies suggesting the role of HIV

Vpr52-96 peptide as a potential therapeutic anti-proliferative agent against malignancies [119;371;372], my results showing inhibition of Bcl2 and c-IAP1 expression provide a broad basic mechanism for Vpr-induced apoptosis. Since deregulation of the JNK pathway has been implicated in cancer and other diseases including Alzheimer's and Parkinson's diseases [135;357;358], investigation of the molecular mechanisms that govern the role of the JNK pathway in apoptosis should provide insight into its biological functions and strategies to target this pathway for prevention and treatment of human diseases and cancer.

The results of my study demonstrate for the first time induction of resistance to apoptosis by a HIV accessory protein, Vpr, in primary human monocytes and a monocytic cell line following stimulation with LPS or endogenously produced TNF- $\alpha$ . Therefore, monocytes of HIV-infected patients may have a reduced propensity to undergo apoptosis at least in part due to the protective effect of TNF- $\alpha$  produced in the intracellular milieu following HIV infection or as a result of the inflammatory immune responses in the patients. Since TNF- $\alpha$  is known to enhance HIV replication, its production following HIV infection may enhance monocytic cell survival and provide an intracellular environment independent of HIV cytopathic effects to stimulate viral transcription and formation of potent viral reservoirs. I have also demonstrated that an anti-apoptotic gene, c-IAP2 plays a critical role in LPS and TNF- $\alpha$ -induced survival of human monocytic cells. Moreover, inhibition of c-IAP2 expression by antisense oligonucleotides or the pharmacological inhibitors specific for CaM/CAMKII reversed LPS- and TNF- $\alpha$ -mediated protection from Vpr52-96-induced apoptosis. These results further suggest that strategies based on suppression of c-IAP2 induction by agents known

to inhibit CaM/CAMKII/NF $\kappa$ B signaling pathways may be helpful in controlling HIV reservoir formation and in general prevent infection with pathogenic intracellular organisms and associated inflammatory responses.

# **Chapter V**

## *Conclusion & Future direction*

Monocytic cells are productively infected by HIV, however, they survive HIV infection and act as a major source of viral reservoir. The mechanism by which HIV enhances monocytic cell survival is largely unknown. The main goal of my study was to investigate the molecular mechanisms involved in regulation of resistance to apoptosis in human monocytic cells in general and in particular against HIV infection. My results suggest that Vpr, one of the accessory proteins of HIV induces apoptosis in monocytic cells and pretreatment of cells with LPS/TNF- $\alpha$  mediates protection to HIV-Vpr-induced apoptosis. Subsequently, I elucidated the intracellular signaling pathways involved in HIV-Vpr-mediated apoptosis and the resistance induced by LPS and TNF- $\alpha$  in normal human monocytic cells and promonocytic cells (THP-1) using Vpr1-45 and Vpr52-96 peptides.

The main aim of my first objective was to elucidate the intracellular signaling pathways involved in LPS-/TNF- $\alpha$ -induced resistance to apoptosis in human monocytes. I have demonstrated that c-IAP2, one of the anti-apoptotic genes is involved in inducing resistance to staurosporine mediated apoptosis in monocytic cells. c-IAP2 was shown to be induced in response to LPS and TNF- $\alpha$ , whereas the level of c-IAP1 remained unchanged in monocytic cells. It is likely that c-IAP1 plays a role in spontaneous survival of THP-1 cells and it may not be involved in LPS- and TNF- $\alpha$ -induced anti-apoptotic activity. The involvement of XIAP, one of the IAPs that provides protection was ruled out since it was not inducible in LPS/TNF- $\alpha$  stimulation of monocytic cells. The involvement of the Bcl2 family of anti-apoptotic proteins including Bcl2, BclXL, Mcl, and A1 could not be ruled out at this stage. It is likely that any one of them may also be involved in inducing resistance. However, there is at least one report demonstrating that

Bcl2 is not inducible in response to LPS. LPS/TNF- $\alpha$  induced resistance by other members of IAP and Bcl2 family of genes in monocytic cell needs further investigation.

In an attempt to understand the mechanism underlying LPS/TNF- $\alpha$ -induced expression of c-IAP2 and subsequent development of resistance to apoptosis in human monocytic cells, I investigated the role of MAPKs and PI3K. My results suggest that neither MAPKs nor PI3K is involved in LPS-/TNF- $\alpha$ -induced c-IAP2 expression. These results prompted me to investigate the upstream signaling molecules such as calcium in c-IAP2 induction and resistance to apoptosis. I have demonstrated that LPS-/TNF- $\alpha$ -induced c-IAP2 and its associated anti-apoptotic activity is regulated selectively by the calcium signaling pathway, particularly CaM/CAMKII protein kinase through activation of NF $\kappa$ B. To determine the involvement of transcription factors in c-IAP2 induction, gel shift assays were conducted. It will be of interest to perform chromatin immunoprecipitation (CHIP) assays to confirm the results. Further, it is to be determined whether the link between CAMKII and NF $\kappa$ B operates directly through activation of I $\kappa$ B or whether there are some other intermediate molecules involved in this activation process.

The molecular mechanism involved in the regulation of c-IAP1 expression is not clear at present. My results suggest that constitutive expression of c-IAP1 may be regulated selectively by the calcium pathway as its expression was down-regulated by EGTA, SKF, and W-7. However, c-IAP1 does not seem to be regulated by the CAMKII pathway as its inhibitor KN-93 inhibited LPS-/TNF- $\alpha$ -induced expression of c-IAP2 alone. The regulation of c-IAP1 in spontaneous survival of monocytes needs further investigation.

In my earlier studies, I used staurosporine to induce apoptosis in monocytic cells. Since staurosporine is not a physiological trigger, I used HIV-Vpr synthetic peptide to induce apoptosis in my second objective. I demonstrated that Vpr52-96-induced apoptosis in monocytic cells by activating JNK through the mitochondrial pathway in a caspase-dependent manner. However, the mechanism by which Vpr52-96-activated JNK induces apoptosis through the mitochondrial pathway is not known and needs further investigation. It is known that Vpr52-96 interacts with ANT in the inner mitochondrial membrane through which it has been suggested to release apoptogenic factor(s) such as AIF, Smac and/or Cyt-c to induce apoptosis. It is to be determined if JNK activation by Vpr influences Vpr-ANT interactions resulting in induction of apoptosis. Vpr peptides were recently shown to enter mitochondria. Keeping in view our results showing the involvement of Vpr-activated JNK through the mitochondrial pathway in inducing apoptosis, it is of interest to determine if Vpr-activated JNK enters into mitochondria and induces apoptosis by regulating the release of apoptogenic factor(s) from the mitochondria. Since Vpr induces apoptosis in T lymphocytes and neurons, I would also like to know if similar signaling pathways like monocytes are involved in Vpr-induced apoptosis.

I demonstrated that Vpr-induced apoptosis in monocytes was mediated by down regulation of anti-apoptotic Bcl2 and c-IAP1 genes through activation of JNK. IAPs are known to regulate the caspase cascade by binding to caspase 3, and 7 and by inhibiting the activation of procaspase 9. c-IAP1 has also been shown to inhibit apoptosis through non-caspase mechanisms such as via activation of NF $\kappa$ B and JNK MAPKs. It would be interesting to determine the non-caspase mechanism used by c-IAP1 in inducing

resistance to apoptosis. The possibility of XIAP and other anti-apoptotic factors involvement in Vpr-induced apoptosis also need to be investigated. How JNK activation downregulated Bcl2 and c-IAP1 is not known. It is speculated that downregulation may occur by direct interaction between these molecules or through involvement of any intermediate molecules.

Vpr has been shown to inhibit Cdc25 phosphatases to induce cell cycle arrest. It is likely that Vpr52-96-activated JNK may also induce cell cycle arrest by influencing cyclin-Cdc2 interactions and could be a subject of future investigations.

My third objective regarding the protective effect to Vpr induced apoptosis revealed that the Vpr-mediated apoptotic effect was reversed by pretreatment of cells with either LPS or TNF- $\alpha$  produced endogenously following LPS stimulation. These observations suggest that TNF- $\alpha$ , a cytokine that enhances HIV replication and is known to be produced following HIV infection, may be one of the critical factors responsible for protection of monocytic cells against the apoptotic effects of Vpr and thereby promotes viral reservoir formation and maintenance. Therefore, it would be interesting to determine if HIV-infected monocytes have a reduced propensity to undergo apoptosis at least in part due to TNF- $\alpha$ . Further, I demonstrated the involvement of c-IAP2 in LPS-/TNF- $\alpha$ -mediated resistance to Vpr-induced apoptosis through activation of CAMKII.

Interestingly, my results also demonstrate that Vpr interferes with the LPS-/TNF- $\alpha$ -induced resistance by inhibiting calcium influx, CAMKII activation, and translocation and activation of NF $\kappa$ B essential for c-IAP2 induction. However, the mechanism underlying the interference of Vpr in LPS-/TNF- $\alpha$ -induced resistance in apoptosis is not clearly known. It is most likely that Vpr disturbs cell surface receptors such as CD14 and

TLR4 which are essential for LPS binding and needs further investigation. Recently several groups have identified a novel mitochondrial anti-viral signaling protein (MAVS), which plays an important role in inducing NF $\kappa$ B stress response and antiviral type-I interferon response [373;374]. It is likely that Vpr may cause cleavage/disruption of MAVS protein which in turn may cause disruption of NF $\kappa$ B signaling and impaired expression of anti-apoptotic genes such as Bcl2/IAPs and apoptosis.

I have conducted my studies using HIV-Vpr peptides in monocytes. It will be of interest to reproduce these findings with recombinant Vpr protein or intracellularly expressed Vpr. It is to be determined if dendritic cells and monocyte derived macrophages which act as viral reservoir are protected against HIV-Vpr induced apoptosis in a manner similar to human monocytic cells. Further, to confirm the involvement of IAPs in inducing resistance, drugs acting specifically on IAP proteins may be used to determine the impact on survival of monocytic cells and eventual destruction of HIV carrying virus reservoir.

Overall, my findings suggest that LPS and the LPS induced proinflammatory cytokine TNF- $\alpha$  play an important role in HIV pathogenesis. Since LPS-/TNF- $\alpha$ -induced resistance to HIV-Vpr-mediated apoptosis in monocytes is mediated by c-IAP2 upregulation, manipulating signaling molecules involved in c-IAP2 regulation such as calcium and CAMKII may help in clearing the viral reservoir from monocytes.

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## PUBLICATION IN REFERRED JOURNAL:

- **Mishra S**, Mishra JP, and Kumar A. 2007. A critical role for anti-apoptotic c-IAP2 gene in LPS and TNF- $\alpha$ -induced resistance to HIV-Vpr-mediated apoptosis in human monocytic cells. **Journal of Biological Chemistry (Submitted)**
- Ma W\*, **Mishra S\***, Gee K, Mishra JP, Nandan D, Reiner NE, Angel JB, and Kumar A. 2007. Cyclosporin A and FK506 inhibit IL-12p40 production through the calmodulin/calmodulin-dependent protein kinase-activated PI3K in LPS-stimulated human monocytic cells. **Journal of Biological Chemistry. March 8, Epub ahead of print (\* co-author)**
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