

Regulation of NF- κ B by the HTLV-1 Tax Protein

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The Tax protein encoded by the human T-cell leukemia virus type 1 (HTLV-1) activates viral gene expression via the ATF/CREB pathway. Tax also induces a variety of cellular genes through activation of the transcription factor NF- κ B. The ability of Tax to activate the NF- κ B pathway plays an essential role in HTLV-1-induced cellular transformation. This review briefly summarizes the remarkable discoveries of the past several years that have greatly advanced our knowledge on signal-mediated activation of the NF- κ B pathway. It highlights our current understanding of how viral agents like Tax modulate cellular signaling machinery to activate the NF- κ B pathway.

HTLV-1 Tax protein NF- κ B

HTLV-1 AND Tax

Human T-cell leukemia virus type 1 (HTLV-1) induces the proliferation of CD4-positive human T cells and is the etiological agent for the aggressive malignancy of activated CD4-positive T cells termed adult T-cell leukemia (35,85,102,120,121). Unlike most oncoviruses, HTLV-1 does not contain a cellular oncogene but instead utilizes the virus-encoded transactivator, Tax, to transform human T cells [for a review see (88)]. Tax is able to transform cultured cells (86,95,100) and can also induce tumors in transgenic mice (47,81).

HTLV-1 gene expression is controlled by the viral long terminal repeat (LTR), which contains three 21-bp repeat regulatory elements that are crucial for Tax-mediated increases in gene expression (23,34). Though Tax itself does not specifically bind to DNA, it interacts with members of the ATF/CREB family of transcription factors and facilitates their increased binding affinity to the 21-bp repeats (9,14,19,84,109,116,118,124). In addition, Tax is able to interact with the cellular coactivator CREB binding protein (CBP) on the HTLV-1 21-bp repeats (64). The Tax/CREB/CBP ternary complex may act as a scaffold to recruit

additional regulatory components to the HTLV-1 LTR for viral gene expression (2,41).

The ability of Tax to activate diverse cellular genes may contribute directly to increases in T-cell proliferation early in the course of HTLV-1 infection that ultimately leads to lymphocyte transformation and to the development of adult T-cell leukemia. Cellular genes that are regulated by Tax include those involved in T-cell activation and growth such as the interleukin-2 (IL-2) gene and the gene encoding the alpha chain of IL-2 receptor (IL-2R α) (29,54,71,94). Activation of cellular gene expression by Tax is thought to be manifested primarily through the NF- κ B pathway. Both HTLV-1-infected and Tax-transfected T lymphocytes contain increased levels of NF- κ B in the nucleus (65). In addition, Tax colocalizes with NF- κ B in subnuclear regions that contain specific RNA transcripts from a promoter containing NF- κ B binding sites (16,17,91). This suggests that Tax may function as a transcriptional cofactor acting cooperatively with NF- κ B in the nucleus. However Tax-mediated NF- κ B activation is thought to be primarily regulated at the level of NF- κ B nuclear translocation (42,57,65,97,99). Induction of NF- κ B nuclear migration by Tax occurs in the cytoplasm. For

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example, a Tax mutant defective in nuclear transport is still able to activate NF- κ B-dependent transcription (82). The topic of Tax-mediated activation of NF- κ B nuclear transport will be further discussed in later sections.

NF- κ B REGULATION

NF- κ B comprises a family of homo- and heterodimeric transcription factors. These proteins were first identified as transcriptional regulators that bind to the enhancer elements in the kappa light-chain gene in murine B lymphocytes (92). Subsequently, it was found that it is a ubiquitous transcription factor present in nearly all types of human cells. Homologous proteins have been also found in species like insects (33,55,96).

In mammalian cells, NF- κ B comprises at least five members including NF- κ B1 (p50 and p105), NF- κ B2 (p52 and p100), RelA (p65), RelB, and c-Rel (6–8,10,40,93,108) (Fig. 1A). These proteins share a conserved amino-terminal Rel homology domain (RHD) of 300 amino acids that confers DNA binding, dimerization, and nuclear transport. RelA, RelB, and c-Rel contain divergent carboxy-terminal transactivation domains. The p50 and p52 proteins are the proteolytically processed forms of p105 and p100, respectively, and contain the amino-terminal RHD. The carboxy-terminus of the precursor proteins p105 and p100 contains ankyrin-like motifs and can act as inhibitors (see below) that interact with NF- κ B and prevent its nuclear translocation. Active forms of NF- κ B are commonly heterodimers that usually consist of p65 (RelA) and p50. Other subunits, such as RelB, c-Rel, and p52, may also be part of active NF- κ B heterodimers. Different forms of NF- κ B may activate different sets of target genes or be involved in tissue-specific activation.

NF- κ B can function in conjunction with other transcription factors such as AP1 (activation protein 1) and NF-IL-6 (nuclear factor of interleukin-6) [(1) and references therein]. Cellular genes activated by NF- κ B are involved in the regulation of the immune and inflammatory response [for recent reviews see (11,40)] in addition to other functions including the regulation of cell growth, apoptosis, and virus replication (46,104,110,111). These genes include those encoding proinflammatory cytokines such as TNF- α , IL-1, IL-6; chemotactic cytokines (chemokines) such as IL-8 that attract inflammatory cells to sites of inflammation; enzymes that generate mediators of inflammation; immune receptors such as the IL-2 receptor alpha chain (IL-2R α); immunoregulatory molecules such as MHC class I and II, TCR- α and - β ,

IL-2, and β interferon (IFN- β); adhesion molecules that play a key part in the initial recruitment of leukocytes to sites of inflammation; acute phase response proteins; transcription factors such as c-myc, p53, the NF- κ B subunits NF- κ B1 and NF- κ B2, and the NF- κ B inhibitors I κ B α and I κ B ϵ (11,40,83). Due to its ability to activate such diverse and important regulatory genes, NF- κ B has become one of the most extensively studied transcription factors.

REGULATION OF NF- κ B ACTIVATION

Products of a number of genes that are regulated by NF- κ B can also stimulate its activation. For example, the proinflammatory cytokines IL-1 and TNF- α activate the NF- κ B pathway and can also be activated by NF- κ B (7,93). This positive feedback loop may amplify and perpetuate the inflammatory response in the absence of exogenous stimuli and thus contribute to the pathogenesis of chronic inflammatory disorders (11). In addition, genes encoding specific NF- κ B inhibitory proteins like I κ B α are also transactivated by NF- κ B through κ B recognition sequences in their promoter regions (22,98). Free I κ B proteins can enter the nucleus, interact with NF- κ B, and cause dissociation of preformed NF- κ B–DNA complexes (122). These altogether provide a negative feedback loop that may contribute to specifically timed activation of NF- κ B-responsive gene expression.

The most striking feature involved in activating NF- κ B is a process that occurs in the cytoplasm and involves the degradation of a family of inhibitory proteins known as I κ B (5,108). In most cells, NF- κ B is sequestered by I κ B proteins in the cytoplasm. I κ B interaction with NF- κ B masks the NF- κ B nuclear localization signal and keeps NF- κ B retained in the cytoplasm (12,38,45). Upon stimulation of cells by a variety of agents including TNF- α , I κ B α is rapidly phosphorylated at residues Ser32 and Ser36 (Fig. 1B) or similar positioned amino-terminal serine phosphorylation sites in either I κ B β and I κ B ϵ (20,21,31,101,112). The phosphorylated form of I κ B is subject to polyubiquitination and 26S proteasome-mediated proteolytic degradation to result in NF- κ B nuclear translocation and activation of gene expression (24,31). Numerous agents can trigger this process, including proinflammatory cytokines in addition to a variety of stimuli such as bacterial lipopolysaccharide (LPS), viral products like the Tax protein, mitogens like phorbol esters, UV light, and oxidants (6,63,93). Interestingly, phosphorylation of the I κ B protein at these specific serine sites appears to be an important juncture at which all of these stimulatory pathways converge. Identification of the inducible kinases that

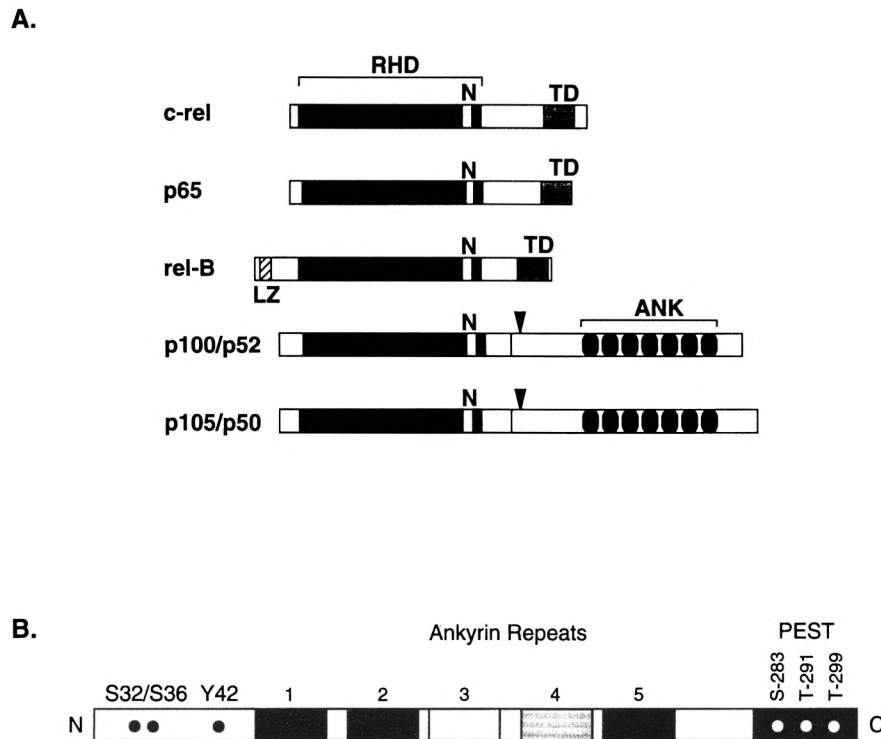


FIG. 1. Schematic of NF- κ B and I κ B α . (A) A schematic of the NF- κ B family of proteins is shown with the Rel homology domain (RHD), the transactivation domain (TD), the nuclear localization signal (N), and the ankyrin repeats (ANK) indicated. (B) The I κ B α protein is indicated with the position of serine residues 32 and 36, the five ankyrin repeats, and potential phosphorylation sites in the C-terminal PEST domain indicated.

result in amino-terminal phosphorylation of I κ B and their regulation is a major issue in understanding NF- κ B regulation.

I κ B KINASES: IKK α AND IKK β

The first reports about a putative I κ B kinase described the partial purification and characterization of a high molecular weight (~700 kDa) kinase complex isolated from untreated HeLa cells. This kinase phosphorylated Ser32 and Ser36 of I κ B α in an ubiquitination-dependent manner and could be activated by treatment of cells with the phosphatase inhibitor okadaic acid (24). The activity of a similar kinase complex was stimulated by treatment of cells with TNF- α or treatment of the purified kinase complex with the MAP3K family member MEKK1 (mitogen-activated protein kinase/extracellular signal-regulated kinase kinase 1) (66). MEKK1 activates the c-Jun N-terminal kinase/stress activated protein kinase (JNK/SAPK) pathway leading to activation of AP1 in response to TNF- α treatment of cells (30,90,115). The fact that MEKK1 increases NF- κ B-mediated gene expression in transfected cells and stimulates phosphorylation of I κ B α in vitro (49,66) has led to speculation

that the signal transduction pathways leading to I κ B phosphorylation might involve components of the MAP kinase pathway. This possibility is supported by an independent discovery that another MAP3K homolog protein, NIK (NF- κ B inducing kinase), binds to both the TNF receptor-associated protein TRAF2 and the IL-1 receptor-associated protein TRAF6. Thus, NIK may be a common mediator of both TNF- α and IL-1 signal transduction pathways (70).

The first kinase that specifically phosphorylates I κ B α was discovered using a yeast two-hybrid screen with NIK as the bait (87). The protein identified was a previously isolated kinase termed CHUK (later renamed as IKK α or IKK1) (28,75). Several observations suggest that this kinase is a NIK-activated I κ B kinase that links TNF- α - and IL-1-induced signal transduction cascades to NF- κ B activation (87). First, overexpression of CHUK activates an NF- κ B-dependent reporter gene. Second, a catalytically inactive mutant of CHUK is a dominant-negative inhibitor of TNF- α -, IL-1-, TRAF-, and NIK-induced NF- κ B activation. In addition, CHUK interacts with I κ B α and specifically phosphorylates I κ B α on both serine resi-

dues 32 and 36. Finally, the phosphorylation of I κ B α by CHUK is greatly enhanced by NIK costimulation.

Shortly after the discovery of IKK α , a second IKK (IKK β or IKK2) was identified by utilizing a cDNA database to search for genes having homology with CHUK or IKK α (113). Independent studies by several groups resulted in the biochemical characterization and molecular cloning of both IKK α and IKK β from the 700–900-kDa IKK complex isolated from TNF- α -treated HeLa cells (32,74,123). These two kinases share 51% amino acid sequence homology and both contain a kinase domain, a leucine zipper domain necessary for dimerization, and a helix–loop–helix domain presumably involved in interactions with essential regulatory subunits (74,123). Though both proteins can undergo homotypic or heterotypic dimerization, the heterodimer form has been suggested to be the predominant state of this kinase (113).

Given that both immunoprecipitates containing IKK (32,74,123) and recombinant IKK α and IKK β (67) can phosphorylate I κ B α and/or I κ B β at specific serine residues, these proteins are likely to be bona fide I κ B kinases. Furthermore, the activity of both kinases can be stimulated by NIK and either IL-1 or TNF- α treatment. Dominant-negative IKKs or NIK can also inhibit TNF- α - and IL-1-induced NF- κ B activation. Although both proteins contribute to I κ B kinase activity (113,123), IKK β appears to be a more potent I κ B kinase than IKK α (74,113). In addition, the substrate specificity of the two IKK subunits for I κ B α and I κ B β appears to be slightly different (113).

The question of whether both NIK and MEKK1 are direct upstream kinases that regulate IKK activity is not clear at the present time. Evidence supporting a direct role for NIK in IKK activation is based on the fact that IKK α and IKK β associate with NIK both in vivo and in vitro (27,87,113). NIK is also detected in the 700-kDa IKK complex (27). Transfection experiments demonstrate that NIK can activate IKK α and IKK β activity (87,113). However, no evidence has been presented that demonstrates that IKK activation is directly mediated by NIK.

Data indicate that MEKK1 might be a direct activator of IKK kinase activity (67,117). In one study (67), MEKK1 was shown to induce the in vivo activation of both IKK α and IKK β . In addition, MEKK1 is present in the inducible, high-molecular-weight I κ B kinase complex (74). Treatment of the IKK complex with purified MEKK1 induces phosphorylation of IKK α in vitro (67). Conversely, it was shown that incubation of purified catalytic domain of MEKK1 with IKKs increases IKK α but not IKK β phosphorylation of I κ B α (117). Furthermore, recombinant MEKK1 is able to phosphorylate IKK β in vitro

(117). The discrepancy regarding whether MEKK1 only activates IKK β or both IKK α and IKK β may be due to differences in the experimental methods used in these different studies. Further studies are needed to determine whether NIK, MEKK1, or other kinases are all directly involved in the phosphorylation and activation of IKKs and whether NIK and MEKK1 have different substrate specificity.

CHARACTERIZATION OF COMPONENTS OF THE IKK COMPLEX

One interesting feature of the IKK α and IKK β kinases is that they exist in a large complex with several other components including MEKK1, NIK, RelA, p50, and I κ B α (27,74,89). The identification of several novel proteins that are not kinases yet are presented in the IKK complex (27,74,89,114) suggests that these proteins may have regulatory functions. A protein designated IKK γ was found in an IKK complex purified using a monoclonal antibody against IKK α (89). Molecular cloning and sequencing indicated that IKK γ was composed of several potential coiled-coil motifs and interacts preferentially with IKK β to activate the IKK complex. An IKK γ carboxy-terminal truncation mutant that still binds to IKK β blocks the activation of IKK β in response to TNF- α but has only a small effect on basal kinase activity. Using genetic complementation experiments with cell lines that were unresponsive to stimuli that activate NF- κ B (114), a protein designated NEMO (NF- κ B Essential Modulator) was identified. NEMO is the mouse homologue of IKK γ . Thus, IKK γ /NEMO has been suggested to be a mediator that connects the IKK proteins with upstream activators.

A second regulatory component was recently identified in an IKK complex purified from IL-1-treated cells and was named IKAP (IKK-complex-associated protein) (27). IKAP interacts directly with NIK, IKK α , and IKK β and potentially regulates the activity of these three kinases. It has been suggested that IKAP functions as a scaffold protein, which is involved in the formation of the IKK complex. Indeed, the highest level of IKK activity is achieved when NIK, IKK α , and IKK β are coexpressed together with IKAP in transfected cells. The role of another protein that chromatographed with IKK was identified as MAP kinase phosphatase-1 (74). The function of this protein in regulating IKK activity remains to be elucidated.

It is plausible to speculate that the IKK complex may act as an intrinsic control system that involves both positive and negative regulatory mechanisms. IKK α and IKK β receive signals transmitted by a va-

riety of pathways activated by different stimuli. At the same time, their activation leads to upregulation of diverse NF- κ B-dependent genes involved in a variety of functions. Thus, it is expected that IKK complex must have a highly sophisticated regulatory machinery. This machinery must have the ability to intrinsically regulate itself in order to process as well as to transmit information to allow diverse biological events to occur. In this scenario, it may not be surprising that the catalytic subunits of IKK α and IKK β are contained within a large protein complex together with several different regulatory components. As suggested in a recent review (4), a large protein complex may not be easily accessible to low-molecular-weight inhibitory molecules that can readily downregulate the IKK pathway.

ASPIRIN INHIBITS IKK β KINASE ACTIVITY

Because NF- κ B is one of the key factors that regulates the immune and inflammatory response, determining the specific pathways that modulate its activity is critical for better understanding the pathogenesis of immune and inflammatory disorders (Fig. 2). Potentially this will provide new insights for designing highly specific and potent drugs. We will use the following example to illustrate how recent advances in our knowledge in signal-mediated NF- κ B activation has allowed us to better understand the effects of the widely used drug, aspirin.

Some nonsteroidal anti-inflammatory drugs

(NSAIDs), such as aspirin and other aspirin-like agents, block NF- κ B activity (43,62) by preventing the degradation of I κ B (62). This function of aspirin is independent of its effects on inhibiting cyclo-oxygenase activity and therefore prostaglandin synthesis (106,107). Because IKK α and IKK β are key proteins in regulating I κ B α protein levels in response to various stimuli, it was possible that these kinases are a direct target for aspirin-like agents. One recent study from our laboratory has clearly demonstrated such a link (119). Both aspirin and its derivative sodium salicylate, but not the cyclo-oxygenase inhibitor indomethacin, markedly reduce IKK β kinase activity and NF- κ B activation. The effect of these drugs is due to their direct binding to IKK β but not IKK α , to inhibit ATP binding.

Tax-MEDIATED NUCLEAR TRANSPORT OF NF- κ B

Studies have suggested that Tax-mediated activation of NF- κ B is due to inducing a process in the cytoplasm of cells that triggers NF- κ B nuclear localization. Two mechanisms have been proposed to be involved in this process. Tax has been reported to directly interact in the cytoplasm with the NF- κ B precursors p100 and p105 (15,48,59,78). These proteins can function as cytoplasmic inhibitors of RelA nuclear localization through their ankyrin repeats. This interaction may overcome the cytoplasmic sequestration of p65 by p100 and p105, to permit the cyto-

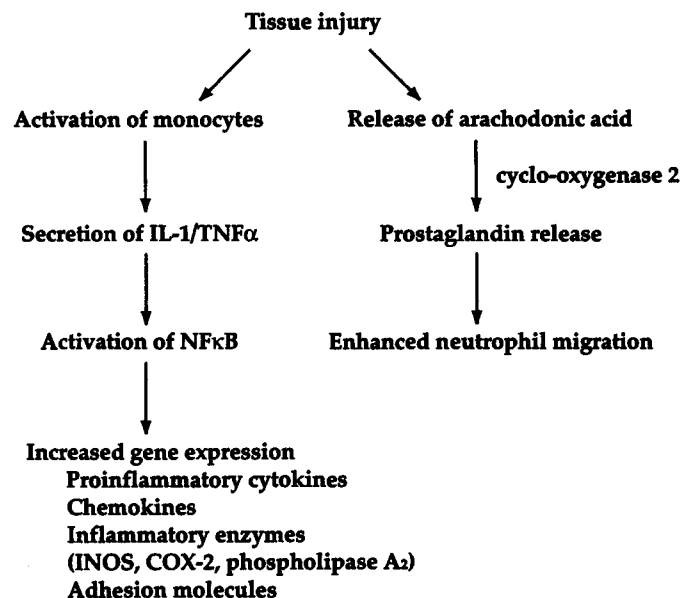


FIG. 2. Pathogenesis of the inflammatory response. Two major pathways that mediate the inflammatory response are indicated. One pathway leads to the generation of prostaglandins and is catalyzed by cyclo-oxygenase 2 whereas the other pathway is mediated by activation of NF- κ B.

plasmic release and nuclear transport of p65 (15,59, 76,77).

Alternatively, Tax may activate a signal transduction pathway that leads to phosphorylation and degradation of I κ B. The constitutive nuclear translocation of NF- κ B, which is associated with increased phosphorylation and degradation of both I κ B α and I κ B β , is found in both HTLV-1-infected and Tax-transfected cells. This suggests that Tax may induce the nuclear localization of NF- κ B by acting prior to or at the level of I κ B phosphorylation (20,42,58,65,73,97). Furthermore, I κ B mutants lacking the two N-terminal serine sites phosphorylated by IKK are resistant to Tax-mediated degradation (20,58). This indicates that Tax is directly involved in induction of a specific kinase activity necessary for I κ B phosphorylation/degradation.

Recent advances in the characterization of the IKK complex has made it possible to study mechanisms involved in Tax activation of I κ B phosphorylation. This research has been focused mainly on addressing the following questions. Dose Tax regulate the same signal transduction pathways that are directed by cytokine? What is the molecular target for Tax in regulating I κ B phosphorylation? What is the mechanism? Studies by our lab and several other groups have shown that IKK activity is stimulated in cells that either stably or transiently produce the Tax protein [(26,39,103,117); Li et al., unpublished results]. Kinase-defective mutants of IKK β effectively block Tax-mediated increases in NF- κ B-dependent gene transcription (39,103,117). This suggests that Tax plays a role in modulating IKK activity during NF- κ B activation.

Stimulation of the IKK activity by Tax could be due to a direct effect on either IKK or their upstream activators. The possibility that the IKK molecules are a direct target for Tax in NF- κ B activation arises from observations using immunoprecipitation studies of Tax from HTLV-1-infected cells. These studies indicate that Tax associates with specific kinase activity that phosphorylates I κ B α on serine residues 32 and 36, suggesting that Tax can directly interact with the IKKs (26).

Several other observations have led to the conclusion that Tax acts at steps upstream of IKKs (39,103,117). Because we were unable to detect a direct interaction between Tax and IKK, we analyzed a number of regulatory proteins previously demonstrated to be involved in activation of the NF- κ B pathway, including NIK, MEKK1, the TNF receptor associated protein TRAF2, and the small GTPases Rac2, CDC42, RhoA (117). Studies using dominant-negative mutants of these regulatory proteins show that only the kinase-defective MEKK1 mutant effec-

tively blocks Tax activation of NF- κ B-dependent gene expression. A dominant-negative NIK protein also results in a modest level of inhibition, whereas the other proteins did not have any effect. Conversely, the dominant-negative MEKK1 protein did not efficiently inhibit NF- κ B-dependent gene expression induced by TNF- α , whereas a dominant-negative mutant of either NIK and TRAF2 strongly blocked TNF- α -mediated gene activation. This suggests that whereas only NIK is directly involved in TNF- α -induced IKK activation, MEKK1 and/or NIK may both be involved in Tax-mediated activation of the NF- κ B pathway.

A direct and specific interaction between Tax and the amino-terminus of MEKK1 occurs both *in vitro* and *in vivo* (117). A Tax mutant defective in activation of gene expression via the NF- κ B pathway is not capable of interacting with MEKK1. This suggests that MEKK1 is the direct target of Tax to result in activation of IKK kinase activity. Tax is able to stimulate MEKK1 kinase activity to phosphorylate downstream kinases as well as increase its autophosphorylation. Expression of both Tax and MEKK1 results in enhanced NF- κ B activation, further suggesting that Tax activation of the NF- κ B pathway might be mediated by direct effects on MEKK1.

It has been suggested that MEKK1 may act as a direct upstream effector of IKKs (67) and that IKK β might be a preferential substrate involved in mediating the Tax-dependent activation (117). Overexpression of MEKK1 enhanced the kinase activity of both endogenous and coexpressed IKK β but not IKK α (117). Given the fact that dominant-negative IKK β , but not IKK α , mutants are able to interfere with activation of NF- κ B-dependent gene expression in the presence of MEKK1 (117), MEKK1 was a likely target for Tax activation of IKK. MEKK1 can phosphorylate IKK β and this may increase its ability to phosphorylate I κ B (117). It is possible that Tax may induce a conformational change in MEKK1 that increases its enzymatic activity. Although NIK is exclusively an activator of the NF- κ B pathway, MEKK1 acts at the convergence between the JNK and NF- κ B pathways (60). It is tempting to think that Tax may be able to alter MEKK1 substrate specificity so that phosphorylation of IKK β becomes its primary target (Fig. 3).

However, MEKK1 is obviously not the only target for Tax. NIK appears to be also involved in Tax-mediated NF- κ B activation (39,103,117). It is possible that NIK and MEKK1 function coordinately in Tax-stimulated NF- κ B activation. Whether or not NIK and MEKK1 act directly as upstream IKK kinases, and how Tax affects their enzymatic activities

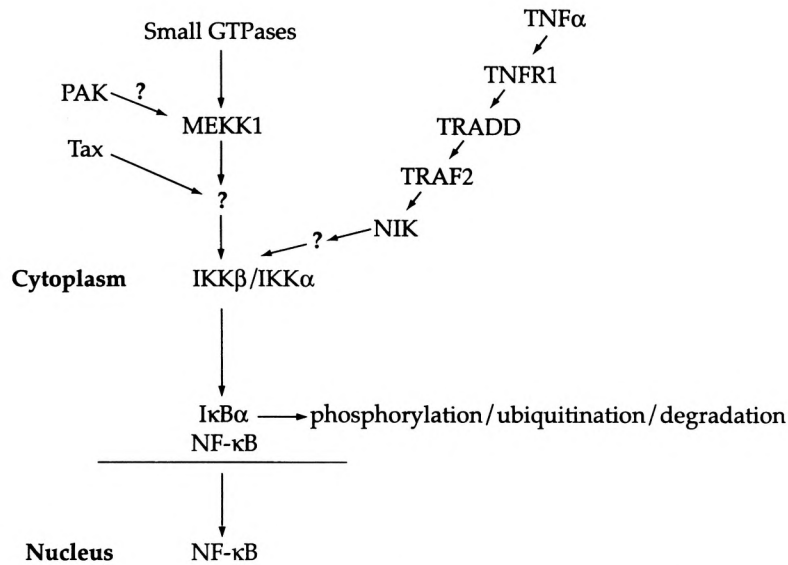


FIG. 3. Schematic of signal transduction pathways leading to NF- κ B activation. The TNF- α pathway leading to activation of NF- κ B is indicated as is a second pathway through MEKK1 that is the likely target for Tax activation.

and substrate specificity, will need further investigation.

What other mechanisms could Tax utilize to activate NF- κ B? In an attempt to answer this question, we recently isolated an IKK complex from HTLV-1-infected cells. The activity of both IKK α and IKK β in this complex is much higher than that in complexes isolated from uninfected cells. Surprisingly, both kinases are found in a much lower molecular weight complex in HTLV-1-infected cells compared to the high-molecule-weight IKK complex found in both unstimulated (24) and cytokine-induced cells (32,74) (Li et al., unpublished). Furthermore, the active IKK complex did not contain substantial quantities of MEKK1, NIK, and Tax. These findings suggest that IKKs are possibly removed from the large molecular weight complex during the process of Tax activation (Fig. 4).

Apparently Tax uses a distinct mechanism to initiate and maintain activation of IKKs. This likely involves modifying the composition of the IKK complex. The mechanism that Tax uses to modify the IKK remains to be determined. Once the IKK complex is induced, maintaining it in the constitutively active state would be the simplest way to maintain high levels of IKK activity. This model may explain the persistent NF- κ B activation by Tax that results from constitutive IKK activation (26). Once the IKK complex is stimulated, maintaining this activity would be a way for HTLV-1 to establish a persistent infection in a continuously proliferating environment.

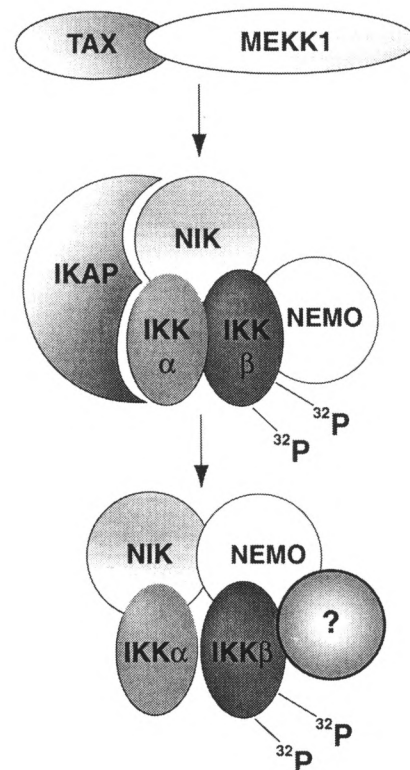


FIG. 4. Model for Tax modification of the NF- κ B pathway. Tax interaction with MEKK1 leads to phosphorylation of IKK β and the loss of potential inhibitory proteins in the IKK complex.

NF- κ B AND APOPTOSIS

NF- κ B is involved in protecting cells from programmed cell death. Cells responsive to TNF- α and IL-1, strong activators of the NF- κ B pathway, become resistant to cell killing induced by these cytokines (104). This indicates that TNF- α and IL-1 can activate cell mechanisms that promote as well as antagonize cell death. Furthermore, certain stimuli leading to programmed cell death can also activate NF- κ B (7,8,93,108). The direct role of NF- κ B as an anti-apoptotic factor was first proposed because disruption of the p65/RelA locus in mice results in embryonic death concomitant with massive apoptosis in liver (13). In addition, inhibition of NF- κ B nuclear transport enhances cell killing (104) by a variety of different apoptotic stimuli (110). This implicates a feedback loop in which NF- κ B activation suppresses signals needed to induce cell death.

Studies have now begun to address the mechanisms by which NF- κ B antagonizes apoptosis. These studies involve molecular dissection of cell surface receptors containing death domains (e.g., TNFR1) (51–53,69) and determining the functional interaction between NF- κ B and apoptotic factors (72,111). Through the TNF- α receptor, TNFR1, TNF- α elicits an unusually wide spectrum of cellular responses leading to inflammation, cellular proliferation, and apoptosis through activating different effectors. These effects are mediated by distinct pathways and are determined by factors recruited to the TNFR1 complex. Recruitment of FADD (Fas-associated death domain) (25,44,52) to the complex results in apoptosis as a consequence of activation of an apical apoptotic protease associated with TNFR1, namely caspase-8 (also called FLICE or MACH) (18,79). Interaction with the signal transducers RIP (receptor interacting protein) (51,80) and TRAF2 (52,69) leads to both JNK and NF- κ B activation (61). However, activation of NF- κ B, but not JNK, protects cells from TNF- α -mediated cell apoptosis (69,105). MEKK1 and NIK may be activated and/or recruited by RIP and TRAF2 by yet unidentified mechanisms (60).

It has been suggested that the NF- κ B protection of cells from apoptosis is, at least in part, mediated by suppression of caspase-8 activity (111). Caspase-8 functions at the apex of the apoptotic cascade and transmits death signals by activating downstream proteases (3,18,79). Using cell lines in which the nuclear transport of NF- κ B was inhibited, it was demonstrated that the activity of caspase-8 was substantially induced by TNF- α (111) and that NF- κ B activation suppresses the initiation of apoptosis (104,105,111). NF- κ B induces the expression of genes encoding the

TNFR1-associated proteins including TRAF1 and TRAF2, and the suppressors of caspase-1-induced apoptosis, c-IAP1 and c-IAP2 (111). These four proteins together provide maximum protection against TNF- α -induced apoptosis. Furthermore, activation of TRAF1, TRAF2, c-IAP1, and c-IAP2 expression is associated with inhibition of the caspase-8 activity (111). Therefore, NF- κ B-mediated suppression of TNF- α -induced apoptosis is, at least in part, through activation of a group of genes whose products function cooperatively at the earliest checkpoint of apoptosis. This finding also provides a reason why the synthesis of new proteins is required for NF- κ B-mediated prevention of apoptosis and is consistent with earlier findings that induced resistance to cell killing in response to TNF- α is enhanced in the presence of inhibitors of protein synthesis (50).

NF- κ B is also able to interfere with the activity of oncogenic Ras to suppress p53-independent apoptosis (72). NF- κ B is activated in response to oncogenic Ras (36) and this activation is largely due to stimulation of the transcription function of RelA/p65 subunits, but not through its induced nuclear transport (37). Regulation of NF- κ B by oncogenic Ras may play an important role in the early stages of tumorigenesis as a large number of antiapoptotic proteins are expressed in tumor cells.

It is also important to note that specific proteins can be involved in both pro- and antiapoptotic responses. Involvement of NF- κ B in proapoptotic pathways in certain cell types in response to particular stimuli has been reported (56,68).

CONCLUDING REMARKS

The past few years have been remarkable times for discoveries in NF- κ B activation. The transmission of signals from the cell surface that lead to the activation of gene expression is much better understood than ever before. The link between NF- κ B activation and the etiology of human cancers has just begun to be understood. The molecular cloning of the I κ B kinases and characterization of the IKK complex have opened up new avenues of future research. Based on our knowledge of cytokine-stimulated IKK activation process, the responses to other stimuli including viral agents can now be studied in a much more direct manner. We are beginning to understand how oncoproteins such as the HTLV-1 Tax protein interact with cellular factors to activate cellular signal transduction pathways and modulate NF- κ B activity. Further understanding of the IKK complex will likely demonstrate how this complex transmits information for specific cellular responses such as inflammation,

immune function, and cellular survival. Components in the IKK complex could be potential therapeutic targets to treat human disorders involving abnormalities in cellular proliferation. Finally, understanding

the molecular targets for Tax in the IKK complex will be beneficial to better understand cellular regulation and to develop potential new treatments for human malignancy.

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