Involvement of Egr-1/RelA Synergy in Distinguishing T Cell Activation from Tumor Necrosis Factor-\(\alpha\)-induced NF-\(\kappa\)B1 Transcription

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Summary

NF-\(\kappa\)B is an important transcription factor required for T cell proliferation and other immunological functions. The NF-\(\kappa\)B1 gene encodes a 105-kD protein that is the precursor of the p50 component of NF-\(\kappa\)B. Previously, we and others have demonstrated that NF-\(\kappa\)B regulates the NF-\(\kappa\)B1 gene. In this manuscript we have investigated the molecular mechanisms by which T cell lines stimulated with phorbol 12-myristate 13-acetate (PMA) and phytohemagglutinin (PHA) display significantly higher levels of NF-\(\kappa\)B1 encoding transcripts than cells stimulated with tumor necrosis factor-\(\alpha\), despite the fact that both stimuli activate NF-\(\kappa\)B. Characterization of the NF-\(\kappa\)B1 promoter identified an Egr-1 site which was found to be essential for both the PMA/PHA-mediated induction as well as the synergistic activation observed after the expression of the RelA subunit of NF-\(\kappa\)B and Egr-1. Furthermore, Egr-1 induction was required for endogenous NF-\(\kappa\)B1 gene expression, since PM A/PHA-stimulated T cell lines expressing antisense Egr-1 RNA were inhibited in their ability to upregulate NF-\(\kappa\)B1 transcription. Our studies indicate that transcriptional synergy mediated by activation of both Egr-1 and NF-\(\kappa\)B may have important ramifications in T cell development by upregulating NF-\(\kappa\)B1 gene expression.

T cell activation results in a rapid activation of NF-\(\kappa\)B (1, 2) which appears to play an important role in T cell proliferation, partly because of the involvement of this transcription factor in the upregulation of the IL-2 and cognate receptor (IL-2R) genes (3). NF-\(\kappa\)B was originally described to be composed of heterodimeric subunits of p50 and p65 proteins (1, 2) and is typically found in the cytoplasm of cells as an inactive precursor complex with an inhibitor protein, \(1\kappa\)B (4). The NF-\(\kappa\)B1 gene product p105 is processed into the DNA-binding subunit of p50 through a mechanism that requires serine phosphorylation (5) and the induction of an ATP-dependent ubiquitin-proteasome pathway (6, 7). Cellular activation leads to an increase in NF-\(\kappa\)B1 transcripts, p105 processing, and subsequent p50 accumulation in both fibroblasts and in T cells (5, 8).

Although little is known about the regulation of NF-\(\kappa\)B1 in T lymphocytes, its expression has been demonstrated to be essential for proliferation after costimulation through CD2 or CD28 receptors (9). Recently, it has been demonstrated that lymphocytes derived from p50−/− deficient mice display defects in immune responses (10). In addition Sha et al. (10) noted that T cells derived from these animals were unable to effectively proliferate in response to TCR and CD28 costimulation. Although disruption of the NF-\(\kappa\)B1 gene did not result in lethality, possibly because

\(\text{NF-}\kappa\text{B2}/\text{p52 could substitute for p50, these studies strongly suggest that the p50 DNA-binding component of NF-}\kappa\text{B is critical for T cell proliferation.}

Analysis of the NF-\(\kappa\)B1 promoter revealed several NF-\(\kappa\)B DNA-binding sites within the upstream regulatory region which are capable of binding p50 homodimers, p50/p65, or p50/c-Rel heterodimers and, in part, account for the ability of NF-\(\kappa\)B to regulate NF-\(\kappa\)B1 gene expression (11, 12). Although the NF-\(\kappa\)B1 promoter has been shown to require NF-\(\kappa\)B for activity, it is presently unclear whether NF-\(\kappa\)B needs other transcription factors to mediate a transcriptional response. This is especially important because on many responsive promoters NF-\(\kappa\)B alone is insufficient at activating transcription (2). T cell stimulation mediated by the addition of either PMA and PHA or TNF-\(\alpha\) results in an increase in NF-\(\kappa\)B1 expression (13). Both stimuli activate NF-\(\kappa\)B nuclear translocation and DNA-binding within 15 to 30 min (14); however, phorbol esters in combination with mitogens result in a greater accumulation of NF-\(\kappa\)B1 transcripts (11, 13). Our research demonstrates that full PMA/PHA-mediated activation of the NF-\(\kappa\)B1 promoter not only required the NF-\(\kappa\)B transcription factor, but also the activation of the early growth response gene product (Egr-1)1. Egr-1, also known as NGFI-A, Zif268, Krox-24, and Tis 8, is transiently induced during the activation of T

1Abbreviations used in this paper: Egr-1: early growth response gene product; EMSA, electromobility shift assay.
cells from the G0 to G1 phase in response to various cellular stimuli (15), has been recently demonstrated to be required for T cell proliferation, and is known to regulate transcription of several genes (15-17). Our data establishes Egr-1 and R eA as important transcription factors capable of synergistically transactivating the NF-κB1 promoter.

Materials and Methods

Cell Culture and Transient Transfection Analysis. CEM cells were cultured in RPMI 1640 medium containing 10% FCS and antibiotics. Cells were stimulated by supplementing their growth medium with either PMA and PHA (Sigma Chemical Co., St. Louis, MO) to a final concentration of 50 ng/ml and 5 μg/ml, respectively, or TNF-α (10 ng/ml; Promega Corp., Madison, WI). Transfections were by electroporation (11) and luciferase or chloramphenicol acetyl-transferase assays were performed as previously described (11, 18, 19).

Plasmid Constructs and Site-directed Mutagenesis. Both the NF-κB1 promoter constructs, p50HS- and p50SS-CAT, were previously described (11). The Sp5-, HIS-, and AS-CAT constructs were generated by digesting the p50HS-CAT reporter with HindIII, and SpFI, HinfI, or ApoI, respectively. The SSLUC reporter plasmid was generated by cloning the StuI/SmaI fragment from p50HS-CAT into the pGLO2 basic reporter containing the luciferase gene (Promega Corp.). The StuI/SmaI fragment of the NF-κB1 promoter was subjected to site-directed mutagenesis using a two-staged PCR (20). The mNLUC construct, containing the disrupted 289-bp NF-κB site, was made using a 5′ primer (5′-ATGTAACCTGAGACACGCTTTAAATGGAATAAAGTA-3′) and a 3′ primer (5′-AGGCGCATCAGCCGCGGCCTCGGCAGCA-3′) in the first round of amplification and two internal primers (5′-AGGCGCTTCTTCTGGAACCTTGAATACCGCTTCCAG-3′ and 5′-CTGAGGCCGATTCAGCTTCCAGGTGAA-3′) which mutated the κB element to a HindIII site. The NF-κB1 promoter sequences containing a site-directed mutation within the Egr-1 DNA binding site (mELUC) was created using the same 5′ and 3′ primers described above plus two internal primers (5′-GCCGCACGACGCGAAATCCGGGAGTTAGTTCGC-3′ and 5′-GACCTCTACCTCCGGACTTTCCGCCGTCGCAATGCA-3′) which destroyed both the SPI/Egr-1 motif and created a unique EcoRI site. The mELUC construct was created by mixing the mutant Egr-1 oligos described above and using the mNLUC fragment as a template. The PCR amplified NF-κB1 promoter fragments were cloned into the SSLUC construct by replacing the wild-type PvuII/SmaI fragment with the corresponding site-directed mutant promoter sequences. Nucleotide sequences of mN, mE, and mNELUC constructs were confirmed by sequence analysis.

Northern Blot and Electrophoresis Mobility Shift Analysis. Total cellular RNA was isolated from CEM cells using the RNeasy total RNA kit (Qiagen, Inc., Chatsworth, CA). No. 189) was purchased from Santa Cruz Biotechnology (Santa Cruz, CA).

Generation of Stable Cell Lines. The full-length human Egr-1 cDNA was cloned into the EcoR1 site of the CMV-5 expression vector in the antisense orientation. CEM cells were cotransfected with either CMV-AsEgr-1 or with the CMV-5 control vector in the presence of pcDNA-3.1 Neo (Invitrogen, San Diego, CA). Transfected cells were grown in complete RPMI-1640 medium supplemented with 1.5 mg/ml of Geneticin (GIBCO BRL, Gathersburg, MD) and resistant clones were isolated. RNA protection assays were performed using the RPA II kit (Ambion, Inc., Austin, TX) to ensure that the CEM/AsEgr-1 cells were expressing the CMV-driven antisense human Egr-1 transcript.

Results and Discussion

Differential Expression of NF-κB1 mRNA After PMA/PHA- or TNF-α-Stimulation. To determine whether differential expression of NF-κB1 mRNA was observed after stimulation by PMA and PHA or TNF-α, Northern blot analysis was performed on total cellular RNA isolated from the human T cell line, CEM. As shown in Fig. 1 A, NF-κB1 mRNA began to accumulate within 1 h of stimulation with PMA and PHA, and by 4 h a significant induction (10-fold) was observed in CEM cells. Although TNF-α-stimulated cells also displayed increases in NF-κB1 transcripts with similar kinetics, a substantially lower accumulation of mR NA was observed over the 4-h time course.

Identification of the NF-κB1 Promoter Region Required for PMA/PHA-R e spon sive U pregulation. To determine whether the increase in NF-κB1 mRNA, seen in Fig. 1 A, was due to transcriptional upregulation of the promoter and not due to PMA/PHA-induced message stabilization, CEM cells were transiently transfected with the p50HS-CAT NF-κB1 promoter construct and stimulated with either PMA/PHA or TNF-α for 24 h. As shown in Fig. 1 B, the NF-κB1 promoter (p50HS-CAT) was strongly activated in CEM cells after PMA/PHA stimulation, but only weakly after TNF-α addition, suggesting that PMA/PHA-mediated activation of the NF-κB1 promoter was through a transcription-dependent mechanism.

To localize the PMA/PHA-responsive region within the NF-κB1 promoter, a series of deletion promoter constructs were made. CEM cells were transiently transfected with each reporter construct and then either stimulated with PMA/PHA or with TNF-α. As shown in Fig. 1 B, no significant difference in stimulation was observed between the HS-, the SS-, or the Sp5-CAT constructs. However, the HIS-CAT reporter, which lacked the −289 NF-κB site, displayed a significant decrease in NF-κB1 promoter activity after stimulation by either PMA/PHA or TNF-α. The AS-CAT reporter, lacking both the −103 and −11 kb sites, was greatly diminished in response to PMA/PHA- and TNF-α-mediated activation (Fig. 1 B). Collectively, this data indicates that the region between the SpFI site (−425)
and the ApoI site (-9) was critical for both inducers, but that PMA/PHA stimulation resulted in a higher fold activation than TNF-α. Based on the deletion analysis of the NF-κB1 promoter, these results suggest that both stimuli may use NF-κB, but that the PMA/PHA stimulation must activate additional transcription factors not induced by TNF-α.

The NF-κB1 promoter contains an Egr-1 consensus site and T cells stimulated with PMA and PHA, but not TNF-α, display Egr-1 DNA binding. Computer analysis of the SphI/ApoI fragment of the NF-κB1 promoter identified potential DNA-binding motifs for five different transcription factors including AP-1, E2F, Egr-1, NF-κB, and SP1. Of these, NF-κB, Egr-1, and AP-1 are known to display increased transactivation potential after PMA stimulation (2, 15, 21). Since PMA/PHA and TNF-α both activated NF-κB, we excluded this transcription factor as the nuclear factor responsible for differentially regulating the NF-κB1 promoter.

In addition, the putative AP-1 site located in the NF-κB1 promoter was not found to affect PMA-induced transactivation of the NF-κB1 promoter (12). To test whether extracts from PMA/PHA-stimulated cells would display Egr-1 binding, EMSAs were performed. As shown in Fig. 2A, a 32P double stranded oligonucleotide probe corresponding to the 68-bp Egr-1 site within the NF-κB1 promoter bound a nuclear protein which was present in PMA/PHA-stimulated cell extracts (lane 2), but not in unstimulated cell extracts (lane 1). This DNA–protein complex could also be

**Figure 1.** NF-κB1 gene expression and promoter analysis in CEM cells after PMA/PHA or TNF-α stimulation. (A) RNAs were isolated from CEM cells after addition of either PMA/PHA (50 ng and 5 μg/ml) or TNF-α (10 ng/ml) over the time course indicated. RNAs were detected using a 32P-labeled NF-κB1-specific probe. Transcripts encoding N-κB1 were quantitated by densitometric scanning autoradiograms and the fold accumulation of mRNA was calculated after normalization to β-actin. (B) Schematic of the NF-κB1 promoter depicting the Egr-1 and NF-κB binding sites. CEM cells were transfected with either the HS-CAT reporter or with various deletion constructs (SS-, SpS-, HS-, and AS-CAT). 18 h after transfection, cells were stimulated with either PMA/PHA (50 ng and 5 μg/ml) or TNF-α (10 ng/ml) and CAT activity was analyzed. Transfection experiments were performed in triplicate and the mean fold induction and the standard deviations are shown.

**Figure 2.** Identification of an Egr-1 DNA binding site within the NF-κB1 promoter. (A) Nuclear extracts were isolated from CEM cells after a 2 h PMA/PHA stimulation in either the absence or presence of cycloheximide (50 μg/ml, 30 min pretreatment). Nuclear extracts (5 μg) were incubated with a 32P-labeled probe corresponding to the 68-bp Egr-1 site. Competition assays and antibody supershift experiments were performed by preincubating nuclear extracts (15 min) with either unlabeled mutant Egr-1 (mEgr-1) or wild-type Egr-1 oligonucleotide (50 ng total) before the addition of probe. Lane 1, unstimulated cells; lane 2, PMA/PHA for 2 h; lane 3, PMA/PHA + wild-type Egr-1 oligo; lane 4, PMA/PHA + mEgr-1 oligo; lane 5, PMA/PHA + Egr-1–specific antibody; lane 6, pretreatment with cycloheximide (30 min) + PMA/PHA for 2 h. SS indicates the position of the Egr-1–antibody supershift complex; NS identifies nonspecific bands. (B) Nuclear proteins from CEM cells were isolated after addition of either PMA/PHA or TNF-α over the indicated time course and EMSAs were performed. As shown in Fig. 2A, a 32P double stranded oligonucleotide probe corresponding to the 68-bp Egr-1 site within the NF-κB1 promoter bound a nuclear protein which was present in PMA/PHA-stimulated cell extracts (lane 2), but not in unstimulated cell extracts (lane 1). This DNA–protein complex could also be
competed with an excess of wild-type unlabeled oligonucleotide (lane 3), but not by equal concentrations of a corresponding mutant Egr-1 site (lane 4). Moreover, this complex contained Egr-1 protein since incubation with an Egr-1-specific antibody completely supershifted the nuclear protein bound to the 32P-probe (lane 5). Pretreatment with cycloheximide, which has been previously demonstrated to block PMA-mediated increases in Egr-1 protein (15), prevented the detection of Egr-1-specific binding (lane 6). Although we do not effectively detect SP1 binding under our EMSA conditions (Fig. 2A), we observed constitutive SP1 binding in nuclear extracts isolated from CEM cells using a modified binding protocol (data not shown). Since SP1 binding to the −68 site was constitutive and completely independent of cellular stimulation mediated by either PMA/PHA or TNF-α (data not shown), we chose to focus on the inducible binding of the Egr-1 transcription factor.

To elucidate whether differential Egr-1 binding was observed in T cells after the addition of either PMA/PHA or TNF-α, nuclear proteins were isolated from stimulated CEM cells over a 4 h time course and EMSAs were performed using the NF-κB1 Egr-1 consensus site. After stimulation with PMA/PHA, Egr-1 binding begins to appear within 30 min and continues to increase at both 1 and 2 h with a slight decrease seen at 4 h (Fig. 2B). Interestingly, no Egr-1 binding was observed in CEM cell extracts after TNF-α stimulation (Fig. 2B). However, both PMA/PHA- and TNF-α-stimulated CEM cells demonstrated NF-κB-specific binding after the addition of each inducer, confirming that CEM cells were capable of responding to TNF-α (data not shown). Identical results to those obtained in the CEM cell line were demonstrated in Jurkat T cells (data not shown). Collectively, these results indicate that the −68 site located in the NF-κB1 promoter is capable of binding the Egr-1 transcription factor and that, unlike PMA/PHA stimulation, TNF-α fails to stimulate Egr-1 binding in T cell lines.

Efficient PMA/PHA-responsive activation of the NF-κB1 Promoter Requires the Egr-1 DNA Binding Site. To determine whether Egr-1 is required for PMA/PHA responsive activation of the NF-κB1 promoter, site-directed mutagenesis was performed. Since the NF-κB1 promoter is regulated directly by NF-κB (11, 12), we chose to mutate the −289 κB motif alone or in combination with the −68 Egr-1 binding site. The four luciferase NF-κB1 promoter constructs included (a) SSLUC, the wild-type construct, (b) mNLUC, which contained a mutated NF-κB site at position −289, (c) mELUC, which contained the disrupted 68-bp Egr-1 site, and (d) mNLUC, which contained mutated NF-κB and Egr-1 sites. As shown in Fig. 3A, site-directed mutagenesis of the Egr-1 binding element (mELUC) significantly diminished PMA/PHA-responsive activation of the NF-κB1 promoter, but had very little or no effect on TNF-α-mediated stimulation. In contrast, mutating the NF-κB −289 site alone had very little effect on either PMA/PHA- or TNF-α-induced activation (data not shown). These results in conjunction with the promoter deletion studies (shown in Fig. 1B) would strongly suggest that other κB binding sites (namely −103 and −11) are important for transcriptional activation. Recently, McElhinny et al.
transactivation of the with both RelA and Egr-1 resulted in a potent synergistic by the overexpression of Egr-1. Interestingly, transfection strongly transactivated after cotransfection with the RelA 5 site plays an important role in the activation of this gene in T lymphocytes.

NF-κB and Egr-1 Transcription Factors Synergistically Transactivate the NF-κB Promoter. To further explore the ability of each of these transcription factors to activate the NF-κB promoter, the wild-type as well as the site-directed mutant reporters were cotransfected with the empty expression plasmid or with constructs encoding either R elA, the p65 subunit of NF-κB, Egr-1, or a combination of both. As shown in Fig. 3 B, the SSLUC reporter was strongly transactivated after cotransfection with the R elA encoding expression construct, but only weakly activated by the overexpression of Egr-1. Interestingly, transfection with both R elA and Egr-1 resulted in a potent synergistic transactivation of the NF-κB promoter. Although the −289 κB site was important for R elA-mediated transactivation, mutagenesis of this element did not affect activation by Egr-1, nor did it affect R elA/Egr-1 synergy (Fig. 3 B). This result would suggest that, in the presence of Egr-1 binding, other κB sites located within the NF-κB promoter are used for the synergistic response. Unlike the mELUC reporter, mutagenesis of the Egr-1 site (mELUC) resulted in a significant reduction in R elA+, Egr-1+, and R elA/Egr1-mediated activation of the NF-κB promoter (Fig. 3 B). However, disruption of both the −289 and −68 sites (mELUC) did not further diminish R elA/Egr1-mediated synergy. This would suggest that overexpression of both of these transcription factors may indirectly lead to the activation of the NF-κB promoter by upregulating other trans-acting elements, or that Egr-1 (like NF-κB) recognizes other DNA-binding sites within the NF-κB promoter. Collectively, co-transfection studies strongly suggest that the Egr-1 DNA binding site is critical for both Egr1-mediated transactivation and for R elA/Egr1-dependent synergy. Although the R el homology domain of R elA has been shown to be responsible for protein–protein interactions with transcription factors outside of the NF-κB/R el family (23–26), we were unable to demonstrate a physical interaction between R elA and Egr-1, nor were we able to generate synergistic transactivation mediated by these factors using either a 3AR κB or 3AR-Egr1 CAT reporter (data not shown).

Egr-1 Complements TNF-α to Stimulate the NF-κB Promoter. To determine whether the difference between PM A/PHA- and TNF-α-stimulated NF-κB1 gene expression was due to the inability of TNF-α to activate Egr-1, CEM cells were transfected with the SSLUC reporter along with the empty vector control or with the Egr-1 expression construct and 24 h later cells were stimulated with PM A/PHA or TNF-α. As shown in Fig. 3 C, the fold increase between cells transfected with the vector control or with the Egr-1 expression construct was comparable to previous experiments while PM A/PHA-stimulated cells (coexpressing Egr-1) displayed the highest level of NF-κB1 activation. Interestingly, cells transfected with Egr-1 and stimulated with TNF-α displayed a significant increase in promoter activity, compared to TNF-α-stimulated cells transfected with the vector control. The ability of Egr-1 to augment TNF-α-mediated activation of the NF-κB1 promoter was a direct effect since the transcriptional synergy was not observed with the mELUC construct containing the disrupted Egr-1 binding site (data not shown). These results demonstrate that the Egr-1 transcription factor can complement TNF-α-mediated stimulation of the NF-κB1 promoter. Furthermore, our data suggests that the inability of TNF-α to activate Egr-1 may account for the difference between PM A/PHA- and TNF-α-mediated NF-κB1 gene expression in T cells.

Endogenous NF-κB1 Gene Expression Is Affected in T Cells Expressing Antisense Egr-1 RNA. To determine the importance of the Egr-1 transcription factor on endogenous NF-κB1 gene expression, we developed a CEM cell line which constitutively expressed antisense human Egr-1 RNA. Total RNAs were isolated from either CEM/Asegr1 cells (which express the human Egr-1 antisense RNA) or from CEM/CMV control cells (which harbor the empty expression vector) after the addition of either PM A/PHA or TNF-α over the time course indicated. As shown in Fig. 4 A, CEM/Asegr1 cells did not display significant increases in NF-κB1 transcripts until 4 h after PM A/PHA addition, while the control cells (CEM/CMV) responded within 1 to 2 h with similar kinetics as the parental CEM cell line (Fig. 1 A). Interestingly, TNF-α-stimulated CEM/Asegr1 cells demonstrated a reduction in NF-κB1 transcripts 30 min after activation. Although TNF-α does not activate Egr-1, it would appear that under conditions in which endogenous Egr-1 levels are reduced (as with CEM/Asegr1 cells), TNF-α stimulation represses NF-κB1 transcription (Fig. 4 A). Although the level of Egr-1 protein in the CEM/Asegr1 cells after PM A/PHA stimulation was significantly lower (fivefold) than protein levels observed in the control line, the antisense Egr-1 transcripts were not able to completely block PM A/PHA-mediated increases in Egr-1 protein (Fig. 4 B). Perhaps for this reason CEM/Asegr1 cells are still able to display PM A/PHA-responsive upregulation of NF-κB1 transcripts but with slower kinetics.

In this paper we have demonstrated that to achieve full activation of the NF-κB1 promoter, T cell signals require not only the activation of NF-κB, but also the Egr-1 transcription factor. Interestingly, it appears that the potent activation of NF-κB DNA binding activity by TNF-α is insufficient at inducing high levels of NF-κB1 transcription. This is consistent with the recent report that activation of NF-κB binding by TNF-α is insufficient at activating VCAM-1
transcription in some cells, but the co-activation of NF-κB and IRF-1 in endothelial cells functions to stimulate transcription (27, 28). Moreover, like NF-κB, Egr-1 is a relatively poor activator of NF-κB1 transcription. Thus, it is the combined action of NF-κB and Egr-1, both of which alone result in weak activation, that functions to synergistically stimulate the NF-κB1 promoter. A number of NFκB-responsive genes have been characterized and found to require Egr-1 DNA binding motifs for maximum transactivation. Such genes include TNF-α, IL-2, and ICAM-1 (17, 29, 30).

In T cells, TNF-α does not fully upregulate its own promoter, presumably because of the inability of cytokines to activate Egr-1 (17). However, primary human fibroblasts and macrophage cell lines display dramatic increases in Egr-1 after TNF-α stimulation (15). Collectively, these studies would suggest that the synergistic potential mediated by the NF-κB and Egr-1 transcription factors are not only restricted by the type of stimuli, but also may depend on the particular cell type. Thus, it appears that the functional interaction of NF-κB and Egr-1 in the context of a promoter is likely to mediate critical aspects of T cell signaling and potentially other important aspects of cellular growth control. The potential synergy between NF-κB and Egr-1 may explain, at least partially, the requirements for these transcription factors in T cell proliferation with NF-κB1 being a critical downstream target for Egr-1.

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