NIK Controls Classical and Alternative NF-κB Activation and Is Necessary for the Survival of Human T-cell Lymphoma Cells

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Abstract

Purpose: Peripheral T-cell lymphomas (PTCL) are a heterogeneous entity of neoplasms with poor prognosis, a lack of effective therapies, and a largely unknown molecular pathology. Deregulated NF-κB activity has been associated with several lymphoproliferative diseases, but its importance in T-cell lymphomagenesis is poorly understood. We investigated the function of the NF-κB–inducing kinase (NIK), in this pathway and its role as a potential molecular target in T-cell lymphomas.

Experimental Design: We used immunohistochemistry to analyze the expression of different NF-κB members in primary human PTCL samples and to study its clinical impact. With the aim of inhibiting the pathway, we used genetic silencing of NIK in several T-cell lymphoma cell lines and observed its effect on downstream targets and cell viability.

Results: We showed that the NF-κB pathway was activated in a subset of PTCLs associated with poor overall survival. NIK was overexpressed in a number of PTCL cell lines and primary samples, and a pivotal role for NIK in the survival of these tumor cells was unveiled. NIK depletion led to a dramatic induction of apoptosis in NIK-overexpressing cell lines and also showed a more pronounced effect on cell survival than inhibitor of kappa B kinase (IKK) knockdown. NIK silencing induced a blockage of both classical and alternative NF-κB activation and reduced expression of several prosurvival and antiapoptotic factors.

Conclusions: The results of the present study indicate that NIK could be a promising therapeutic target in these aggressive malignancies. Clin Cancer Res; 19(9); 2319–30. ©2013 AACR.

Introduction

Peripheral T-cell lymphomas (PTCL) are a heterogeneous family of non-Hodgkin lymphomas often associated with an aggressive clinical course and poor outcome. First-line standard therapy is based on the combination chemotherapy regimens usually used in B-cell lymphomas or solid tumors. As these regimens generally have poor response or high rates of recurrence, there is a need to develop targeted therapies based on the signaling pathways that are abnormally expressed in these T-cell malignancies (1, 2).

Deregulated NF-κB activity plays a key role in the development of multiple malignancies. Thus, constitutive activation of NF-κB signaling has been observed in various tumor types, including lymphomas, leukemias, and solid tumors (3, 4). The NF-κB signaling pathway regulates the transcription of many genes involved in cancer initiation and progression events, such as apoptosis, proliferation, angiogenesis, and metastasis, and hence, several lymphoma types rely on NF-κB activity for their proliferation and survival (4, 5). Genetic changes leading to constitutive activation of the pathway have been detected in several hematologic tumors, emphasizing its importance in the pathogenesis of these malignancies (6–9).

NF-κB can be activated either through the classical (canonical) pathway or the alternative (noncanonical) pathway. Briefly, activation of the classical pathway generally requires the activation of the IκB kinase (IKK) complex, which phosphorylates the inhibitory protein IκB. Phospho-IκB is then degraded, releasing NF-κB (p65/p50/p105/p100) which translocates to the nucleus and activates the transcription of several target genes (2). On the other hand, alternative NF-κB activation occurs in the absence of IκB phosphorylation, but involves the activation of the NIK kinase and NF-κB–inducing kinase (NIK). NIK is a pivotal regulator of NF-κB activation and is frequently deregulated in various hematologic malignancies (2). In this review, we will focus on the role of NIK in T-cell lymphomas and discuss its potential as a therapeutic target.
Peripheral T-cell lymphomas (PTCL) are aggressive malignancies presenting poor clinical outcome. There are currently no effective treatments or targeted therapies available for these patients. Thus, studies aimed to elucidate the mechanisms contributing to these tumors and to identify new therapeutic targets are required to improve their dismal prognosis. Here, we show for the first time that primary PTCLs expressing nuclear NF-κB are characterized by a significantly worse clinical outcome compared with NF-κB-negative tumors, supporting a rationale for the exploration of NF-κB-interfering strategies. We further identify NF-κB–inducing kinase (NIK) as a novel potential therapeutic target in T-cell lymphomas and show that targeting NIK might be more effective than previously suggested inhibitor of kappa B kinase (IKK) inhibition. This study opens up opportunities for further translational studies and will hopefully contribute to the future development of new targeted drugs useful in PTCL.

results in nuclear translocation of mainly p50/p65 heterodimers through the phosphorylation of IκB and p105 by the inhibitor of kappa B kinase (IKK) complex. Activation of the alternative pathway results in nuclear accumulation of p52/RelB heterodimers and depends on the activation of the NF-κB–inducing kinase (NIK) and IKKα phosphorylation (reviewed in ref. 10). NIK (MAP3K14) is a serine/threonine kinase described as critical for the activation of the alternative pathway by inducing phosphorylation of IKKα and p100, leading to p100 processing with subsequent p52 generation and nuclear translocation (11, 12). Nevertheless, the involvement of NIK in the activation of the classical pathway has also been noticed (13, 14). Signals from CD40, B-cell activating factor receptor (BAFF-receptor), and lymphotxin β receptor have been shown to induce NIK-dependent NF-κB activation (15–18). In multiple myeloma, several genetic abnormalities, such as deletions and inactivating mutations of the TNF receptor–associated factor 3 (TRAF3), have been shown to lead to the stabilization of NIK (19). Similarly, in B-cell lymphomas, activating mutations in the BAFF-receptor are known to activate NF-κB in a NIK-dependent manner (20). Knockdown of NIK in several types of malignancies, such as multiple myeloma, diffuse large B-cell lymphoma (DLBCL), adult T-cell leukemia, and melanoma, has been associated with antitumor effects (14, 16, 21, 22), suggesting that NIK could be a therapeutic target in some cancers. However, whether NIK is involved in NF-κB activation and tumorigenesis or not is dependent on the cell type and cellular context and has not been studied in PTCL. Cutaneous T-cell lymphoma cell lines and primary samples undergo apoptosis upon treatment with the proteasome inhibitor bortezomib or an IKKβ inhibitor (23–25), suggesting that NF-κB inhibition could be used as a therapeutic strategy. However, most studies have only addressed the classical pathway, leaving the alternative pathway poorly described. There are no specific NF-κB inhibitor drugs in clinical use for PTCL today, indicating a need for more detailed studies, the identification of new targets, and the development of novel specific inhibitors in the pathway.

In the present study, we show that both the alternative and classical NF-κB pathways are activated in a subset of primary PTCL samples associated with poor clinical outcome. To block the NF-κB signaling pathway in PTCL, we showed a key role for NIK as a regulator of both pathways and showed that NIK-depleted PTCL cells present strongly reduced cell viability. These results highlight NIK as an attractive molecular target in T-cell lymphomas.

Materials and Methods

Patient samples and cell lines

Use of patient samples in this study was approved by the Clinical Research Ethics Committee of Hospital Universitario Marqués de Valdecilla (HUMV; Santander, Spain). Tumor biopsies before treatment were obtained from the CNIO Tumour Bank Unit. T cells from peripheral blood of healthy donors or patients with Sézary syndrome were isolated through negative selection using the RosetteSep Kit (StemCell Technologies). The proportion of T cells (CD3⁺) in the samples was checked by flow cytometry and ensured to be more than 90%. For the gene expression data in primary samples, 37 frozen PTCL cases were used, including 19 PTCL-not otherwise specified (PTCL-NOS), 15 angioimmunoblastic T-cell lymphomas (AITL), and 3 anaplastic large cell lymphomas (ALCL). The human T-cell lymphoma cell lines DERL-7 (hepatosplenic γ-δ T-cell lymphoma) and SR-786 (ALCL) were obtained from the German Collection of Microorganism and Cell Cultures (DSMZ). HuT 78 (Sézary syndrome), HH (cutaneous T-cell lymphoma), and MJ (PTCL, HTLV-positive) were obtained from the American Type Culture Collection, and the cell line My-La (Mycosis fungoides) was obtained from the European Collection of Cell Cultures. All cell lines were previously authenticated (year 2010–2011) by DSMZ.

Immunohistochemistry

Tissue microarrays of paraffin-embedded tumor biopsies or cell lines were used for immunohistochemistry and evaluated by the pathologists participating in the project (M.A. Piris and S. Montes-Moreno). Cases presenting nuclear staining in more than 20% of tumor cells were considered positive, grade 1 (pos +), whereas cases with strong nuclear staining in more than 50% of cells were considered positive, grade 2 (pos ++). Antibodies and conditions are summarized in Supplementary Table S1.

Survival and correlation analyses

The Kaplan–Meier method applying the log-rank test was used to estimate the differences in overall survival (OS) between NF-κB–positive and -negative cases in a series of 77
patients with PTCL (Table 1). Samples presenting nuclear staining of NF-κB (p52, p50, RelB, p65, or c-Rel) in more than 50% (poss +++) of tumor cells were considered positive for NF-κB. Multivariate survival analysis including relevant clinical parameters (see Table 1) was conducted using a Cox regression analysis. To determine the independence of variables, the Pearson χ² test was used. Values of P < 0.05 were considered statistically significant.

**Quantitative RT-PCR**
RNA was isolated using the RNeasy Mini Kit (Qiagen). cDNA was synthesized from 500-μg DNase-treated RNA with SuperScript II Reverse Transcriptase (Invitrogen) and random primers. Human GUSB and 18S expression were used as endogenous controls in samples and cell lines.

**Immunoblotting**
Protein was extracted using radioimmunoprecipitation assay (RIPA) lysis buffer supplemented with protease and phosphatase inhibitors, and Western blot analysis was conducted following standard protocols. For NIK detection, cell lines were treated for 3 hours with 20 μmol/L proteasome inhibitor MG132 (Sigma). MG132 was exclusively added to cells for NIK detection, and separate untreated cells were collected to detect other proteins. Western blot analyses were quantified using the ImageJ program (National Institutes of Health, Bethesda, MD).

**Gene expression microarray analyses**
All gene expression experiments used 4 × 44 K Whole Human Genome Oligo Microarrays (Agilent Technologies, Inc.). For gene expression analysis of primary PTCL samples, 37 frozen biopsies were used, and the Gene Set Enrichment Analysis (GSEA) tool (http://www.broad.mit.edu/gsea/) was applied to classify the expression profiles into functional pathways. The gene sets correlated with MAP3K14 (NIK) expression in primary samples were identified using Pearson correlation. Gene sets with a false discovery rate (FDR) < 0.10 were considered significant. The microarray data are available at the Gene Expression Omnibus under accession number GSE36172. After NIK knockdown in cell lines, pellets were collected 48 hours after siRNA transfection and RNA was extracted. Three independent experiments were carried out in My-La and SR-786 cell lines, and each sample was hybridized onto a separate microarray. The gene sets up- or downregulated in NIK knockdown cells were identified with the GSEA tool by applying a limma t test (FDR < 0.10). Genes differentially expressed between control cells and NIK knockdown cells were identified using a paired t test (http://pomelo2.bioinfo.cnio.es) and visualized using Gene Cluster and Treeview (http://rana.lbl.gov/EisenSoftware.htm).

**RNA interference**
siRNAs against MAP3K14 (NIK), IKKB (IKKβ), and CHUK (IKKα), or a nontemplate control (NTC; 100 nmol/L stealth siRNA; Invitrogen) were used for genetic silencing. siRNAs were introduced into the cells by microinjection (Microinjector MP-100; Digital Bio).

**NF-κB–binding activity**
Nuclear cell fractions were isolated using the BioVision Nuclear/Cytosol Fractionation Kit (BioVision), and 5 μg of nuclear extract was used to quantify the NF-κB transcription activation using the ELISA-based TransAM NF-κB Family Transcription Factor Assay Kit (Active Motif), following the manufacturer’s instructions. Nuclear extracts were plated in triplicate.

**Cell viability and cell-cycle analysis**
Cell viability and cell cycle were assessed in a FACS Canto II flow cytometer (BD Biosciences), and FlowJo software (FlowJo version 7.6.1; TreeStar Inc.) was used for data quantification. Cells staining negative for Annexin V–allophycocyanin conjugate (APC) and 4′,6-diamidino-2-phenylindole (DAPI) were considered viable. To estimate the number of cells in each stage of the cell cycle, cells were fixed with ethanol and stained with propidium iodide.

**Table 1. Characteristics of patients included in the survival analysis**

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Abbreviations: ECOG, Eastern Cooperative Oncology Group; IPI, International Prognostic Index; LDH, lactate dehydrogenase.
Reagent information, primer sequences, and additional protocols are described in the online Supplementary Data.

Results

Nuclear NF-kB is present in primary PTCL samples and is associated with worse clinical outcome

Even though NF-kB activation has been reported in PTCL, there are few studies of patient material, and the expression pattern of the various NF-kB members has not been described in detail. We conducted immunohistochemistry on paraffin-embedded tissues from patients with the most common types of PTCL: AITL, ALCL, and PTCL-NOS, to examine the nuclear expression of NF-kB. Nuclear expression of components defining both the classical (p50 and c-Rel) and alternative (p52 and RelB) pathways (Fig. 1A and B) was detected in the majority of PTCLs. To represent different levels of NF-kB expression, 2 positivity thresholds were used: 20% (pos +) and 50% (pos ++) positive nuclei. Surprisingly, the commonly used marker for NF-kB activation, p65, showed only cytoplasmic expression in most cases, suggesting that other factors of the family are more frequently involved in NF-kB signaling in PTCL. A subset of cases expressed highly elevated levels of NF-kB, (pos ++), being most frequent in the CD30-positive ALCLs. Moreover, a significant positive correlation (P < 0.05) was established between nuclear p50 and p52 expression (Fig. 1C), indicating frequent activation of both pathways in the same sample.

Contradictory results have been reported for the clinical correlation of NF-kB in different tumors (5, 26–28). To estimate the impact of nuclear NF-kB expression on the clinical outcome of patients with PTCL, we did a Kaplan–Meier analysis to compare the OS between NF-kB–positive and –negative tumors in a series of 77 PTCL cases (Fig. 1D; see patient characteristics in Table 1). Tumors with more than 50% positive nuclei for any NF-kB factor were considered positive. Similar thresholds have previously been used for immunohistochemistry of NF-kB in other studies in the lymphoma field (6, 28, 29). Only PTCL-NOS and AITL subtypes were included in the survival analysis, as these patients did not present any significant difference in basal OS due to PTCL subtype (Supplementary Fig. S1). When NF-kB was taken into account, however, patients with NF-kB–positive tumors had a significantly worse OS compared with those in the NF-kB–negative group (log-rank test; P = 0.003) with a 2-year OS of 41.7% compared with 67.9%, respectively. NF-kB activation in PTCL was still significantly associated with inferior OS when the impact of other clinical covariates was taken into account, although the International Prognostic Index (IPI) was still a more accurate estimate of prognosis in our series (Supplementary Table S2). The observation that NF-kB signaling is activated in a subset of T-cell lymphomas with very poor clinical outcome suggests the merit of evaluating NF-kB inhibition strategies in these tumors.

NIK is overexpressed in PTCL cell lines and primary samples, and its expression is correlated with NF-kB activation

Because NIK is involved in the activation of NF-kB in some cells and settings, we examined whether NIK was involved in NF-kB activation in T-cell lymphomas. We observed a remarkable overexpression of NIK mRNA in several PTCL cell lines and primary Sézary syndrome samples compared with T lymphocytes from healthy donors (Fig. 2A). The cell lines expressing high levels of NIK mRNA also expressed elevated protein levels of NIK (Fig. 2B). Although DERL-7 lacked nuclear expression of alternative NF-kB factors (p52 and RelB), the other cell line with low NIK levels, HuT 78, expressed both nuclear p52 and RelB (Supplementary Table S3). However, HuT 78 expresses a truncated form of p100 (Fig. 2B), which has previously been described to activate the alternative pathway in a NIK-independent manner (30). To detect NIK protein levels in primary PTCL samples, we tested a handful of different NIK antibodies in paraffin-embedded tissues, but none of these provided consistent results. For that reason, we used gene expression microarray data to compare the expression of NIK (MAP3K14) and NF-kB target genes (6) in a series of 37 PTCL samples. Using GSEA, we found a significant positive correlation between the expression of NIK and NF-kB target genes (Fig. 2C), suggesting that NIK may be involved in NF-kB signaling in these tumors. Other gene sets significantly correlated with the expression of NIK are listed in Supplementary Table S4.

NIK is involved in both classical and alternative NF-kB signaling in T-cell lymphomas

Whether NIK participates in classical NF-kB pathway activation as well as in alternative pathway regulation is currently unclear. To study the role of NIK in NF-kB signaling in T-cell lymphoma cells, we knocked down NIK using 2 different siRNAs in 2 PTCL cell lines (My-La and SR-786). The 2 siRNA sequences induced different levels of knockdown efficiencies (Fig. 3A), allowing us to study the effect of a dose-dependent decrease in NIK. As expected, the levels of p52 were reduced and the levels of p100 were initially increased after NIK knockdown, indicating an attenuation of p100 processing. We also observed a similar but somewhat delayed decrease of p50 levels and an increase in the levels of p105, linking NIK to the regulation of classical NF-kB activation as well (Fig. 3A and C and Supplementary Fig. S2). Figure 3B confirms that the knockdown of NIK gave rise to decreased nuclear levels of both p52 and p50. The NF-kB DNA-binding activity of all 5 proteins, measured by TransAM ELISA assay, was decreased, supporting a role for NIK in both classical and alternative NF-kB regulation in PTCL (Fig. 3D).

NIK is necessary for the survival of PTCL cell lines with high NIK levels

According to our data, My-La and SR-786 are characterized by NIK overexpression and an active NF-kB pathway
We measured cell viability after NIK silencing in these cells by flow cytometry using Annexin V and DAPI staining. NIK knockdown led to a dramatic increase in cell death compared with NTC-transfected cells, suggesting that NIK is necessary for the survival of these cells. The cell death observed after NIK knockdown increased as knockdown became more efficient (Fig. 4A). To study the effect of NIK knockdown over a longer period, we repeated the siRNA transfection 4 days after the first microporation. Strikingly, after 1 week of NIK depletion, nearly all cells had undergone apoptosis, showing the essential role of NIK in the viability of these tumor cells (Fig. 4B). The appearance of cleaved caspase-3 after NIK knockdown in both My-La and SR-786 indicates an induction of a caspase-dependent apoptotic pathway (Fig. 4C). Interestingly, NIK silencing in DEIL-7 or HuT 78 cell
lines, presenting low NIK levels, had no effect on cell survival (Fig. 4D), suggesting that NIK targeting has a selective effect only on the cells presenting elevated NIK levels. No obvious alterations of the cell-cycle distribution were observed after NIK knockdown, apart from there being more cells in sub-G1 (Supplementary Fig. S3).

To rule out whether the toxicity of NIK knockdown was due to a blockade of the classical or alternative NF-κB pathway, we knocked down either IKKa, IKKβ, or both, in these cell lines (Fig. 4E and Supplementary Fig. S4). Surprisingly, IKKa and IKKβ knockdown (separately or in combination) only led to a slight increase in apoptosis compared with NIK knockdown. Moreover, only the knockdown of NIK, but not the knockdown of IKK, was able to strongly reduce the levels of p52 and p50 (Fig. 4E and F). These results suggest that NIK might have, at least in part, IKK-independent roles that confer survival on these cells, and that targeting NIK could be a more effective therapeutic approach than IKK inhibition in these tumors.

NIK knockdown leads to decreased expression of NF-κB target genes and downregulation of prosurvival genes

To gain a better insight into the mechanisms involved in NIK-dependent survival, we analyzed the gene expression profile induced 48 hours after NIK knockdown in My-La and SR-786 cells. Knockdown efficiencies are shown in Supplementary Fig. S5. GSEA applying a limma t test comparing siNIK1 and siNIK2 with control cells was conducted. The gene sets significantly lost (FDR < 0.10) in the siNIK cells included the NF-κB target genes, the JAK–STAT pathway, and targets of XBP1, and are described in Supplementary Table S5. NF-κB target genes were significantly underrepresented after NIK knockdown, indicating again a pivotal role for NIK in NF-κB activation (Fig. 5A). A paired t test revealed 395 genes in My-La and 94 genes in SR-786, which were significantly and differentially expressed (FDR < 0.05 and log2 fold change > 0.6 in either direction) between NIK knockdown and control cells (Fig. 5B; see Supplementary Table S6 for the complete list of genes).
Reverse transcription quantitative PCR (RT-qPCR) was conducted on selected genes to validate the gene expression data (Fig. 5C and D). Several NF-κB target genes involved in cancer cell survival were downregulated upon NIK silencing, such as the antiapoptotic BCL2L1 [Bcl-x(L)] and CFLAR (c-FLIP) as well as several interleukins. Interleukin (IL)-6 and IL-21 are cytokines with known functions in cell proliferation and survival of cancer cells and were strongly downregulated after NIK depletion in both cell lines. Curiously, despite an activated NF-κB pathway in DERL-7 and HuT 78 as well, only the NIK-expressing My-La and SR-786 express high levels of these interleukins (Supplementary Fig. S6), indicating a different NF-κB transcriptional program in NIK-expressing versus NIK-nonexpressing cells. Apart from known NF-κB target genes, NIK depletion also modulated the expression of other genes involved in tumorogenesis, such as Yes-associated protein 1 (YAP1), paraoxonase 2 (PON2), and Kruppel-like factor 2 (KLF2). In summary, NIK knockdown leads to a decrease in the expression of NF-κB target genes and modulates the expression of many genes involved in tumor growth and survival.

Discussion

The molecular pathology of PTCLs has been poorly characterized, and the dismal prognosis of these neoplasms and the lack of efficient therapies demand further studies.
to clarify their molecular background and to identify new therapeutic targets. Previous data suggest that NF-κB activation is a key step in T-cell lymphoma pathogenesis (21, 23). NF-κB activation has previously been reported in a subset of human PTCLs using gene expression data and immunohistochemistry for classical NF-κB subunits.
(24, 27, 29, 31). However, only a few studies have described the alternative pathway status or the clinical impact of this activation. Here, we found markers of activation of the classical and alternative pathways in a subset of PTCL samples, characterized by the nuclear expression of p50, p52, RelB, and c-Rel, whereas nuclear expression of p65 was usually absent. Nuclear expression of classical or alternative components was significantly associated with worse OS in
patients with PTCL, suggesting that aberrant NF-κB activation may confer enhanced survival or treatment resistance on these tumors, and these data support the exploration of therapies that interfere with NF-κB activation. These findings mimic those already described in DLBCL, in which the more aggressive activated B cell–like (ABC) subtype is distinguished by increased NF-κB activation (5, 26). In contrast with our results, Martinez-Delgado and colleagues (27) associated the expression of NF-κB–related genes, using gene expression microarrays, with a favorable clinical outcome in PTCL. These differences might be explained by the genes included in the NF-κB signature (not restricted to NF-κB target genes) and the signals from the tumor stroma reported by Martinez-Delgado and colleagues versus the nuclear expression of NF-κB subunits as assessed by IHC in our study.

Even though there is evidence that NF-κB inhibition has an antitumor effect in some circumstances (5, 32), the need remains to identify therapeutic targets in the pathway and to develop specific NF-κB inhibitors. NF-κB inhibitors targeting mutated or aberrantly expressed molecular targets in a particular tumor might be preferable to broad NF-κB inhibition that also abolishes normal NF-κB activation. We showed that NIK was highly overexpressed in a subset of PTCL cell lines and tumor samples and that its expression was significantly associated with NF-κB activation. NIK has previously been found to be overexpressed at the RNA and/or protein level in other cancers, such as melanoma, multiple myeloma, DLBCL, mucosa-associated lymphoid tissue (MALT) lymphoma, and adult T-cell leukemia (14, 16, 21, 22, 33). In some cases, genetic alterations such as gene amplifications, translocations, or mutations in NIK, or alterations in genes regulating the stability of NIK protein, are described, emphasizing the role of NIK in tumorigenesis (14, 19, 34). From previous reports, the role of NIK in the alternative NF-κB pathway is clear, but the involvement of NIK in the regulation of the classical pathway seems to be signal and cell type dependent (13, 35). For example, in melanoma and pancreatic cancer, NIK only affects the alternative pathway (22, 36), whereas NIK regulates both pathways in DLBCL and multiple myeloma (14, 16). In PTCL, we showed that NIK is involved in both classical and alternative pathway activation, as NIK knockdown led to decreased expression and DNA-binding activity of both classical (p65, p50, and c-Rel) and alternative (p52 and Rel-B) NF-κB activity of both classical (p65, p50, and c-Rel) and alternative NF-κB activation (5, 26). In contrast with our results, Martinez-Delgado and colleagues (27) associated the expression of NF-κB–related genes, using gene expression microarrays, with a favorable clinical outcome in PTCL. These differences might be explained by the genes included in the NF-κB signature (not restricted to NF-κB target genes) and the signals from the tumor stroma reported by Martinez-Delgado and colleagues versus the nuclear expression of NF-κB subunits as assessed by IHC in our study.

Even though there is evidence that NF-κB inhibition has an antitumor effect in some circumstances (5, 32), the need remains to identify therapeutic targets in the pathway and to develop specific NF-κB inhibitors. NF-κB inhibitors targeting mutated or aberrantly expressed molecular targets in a particular tumor might be preferable to broad NF-κB inhibition that also abolishes normal NF-κB activation. We showed that NIK was highly overexpressed in a subset of PTCL cell lines and tumor samples and that its expression was significantly associated with NF-κB activation. NIK has previously been found to be overexpressed at the RNA and/or protein level in other cancers, such as melanoma, multiple myeloma, DLBCL, mucosa-associated lymphoid tissue (MALT) lymphoma, and adult T-cell leukemia (14, 16, 21, 22, 33). In some cases, genetic alterations such as gene amplifications, translocations, or mutations in NIK, or alterations in genes regulating the stability of NIK protein, are described, emphasizing the role of NIK in tumorigenesis (14, 19, 34). From previous reports, the role of NIK in the alternative NF-κB pathway is clear, but the involvement of NIK in the regulation of the classical pathway seems to be signal and cell type dependent (13, 35). For example, in melanoma and pancreatic cancer, NIK only affects the alternative pathway (22, 36), whereas NIK regulates both pathways in DLBCL and multiple myeloma (14, 16). In PTCL, we showed that NIK is involved in both classical and alternative pathway activation, as NIK knockdown led to decreased expression and DNA-binding activity of both classical (p65, p50, and c-Rel) and alternative (p52 and Rel-B) NF-κB transcription factors. Moreover, NIK knockdown also altered the expression of many genes commonly associated with classical NF-κB activation, such as IL6, IL10, and NFKBIA (37, 38). However, NIK does not seem to be strictly essential for NF-κB activation in all PTCL cells, as we found that nuclear NF-κB was not exclusively expressed in NIK-overexpressing cell lines. Thus, the pathway may be activated by different mechanisms in these cells, and a proper identification of upstream mechanisms is important for efficient NF-κB inhibition. The fact that NIK knockdown led to a more efficient reduction of p50 and p52, compared with IKKα or IKKβ knockdown, suggests that NIK can, at least in part, regulate the NF-κB pathway by IKK-independent mechanisms. Consistent with these results, direct phospho-

ylation of p100 in an IKKα-independent manner has been reported (11). It is not clear whether the effect on p105 processing is a direct effect of NIK or an indirect effect of reduced alternative activity.

To investigate the possible downstream effectors of NIK-regulated tumorigenesis, we conducted gene expression analyses of NIK-silenced T-cell lymphoma cells. As expected, many of the genes differentially expressed between NIK-silenced and control cells were NF-κB target genes known to be important in regulating tumor growth and survival. The expression of antiapoptotic proteins is one of the mechanisms by which tumor cells manage to survive in the environment and to resist chemotherapy (39). After NIK knockdown, we observed a downregulation of antiapoptotic genes such as CFLAR (Bcl-xl), BIRC3 (cIAP2), and BCL2L1 (c-FLIP), which might explain the strong induction of apoptosis observed in these cells after NIK inhibition. The interleukins IL6 and IL21, which were highly expressed in cell lines that were sensitive to NIK knockdown but not in resistant cell lines, were strongly downregulated after NIK depletion. These cytokines are important for B- and T-cell development and a proper regulation of the immune response but have also been widely studied in several tumors owing to their protumorigenic activity and their roles as targets for cancer therapy (40, 41). Both of these cytokines are NF-κB target genes but are also involved in JAK–STAT signaling, which also is consistent with our observation that NIK knockdown leads to downregulation of the JAK–STAT pathway. The expression of other genes involved in tumorigenesis, not described as NF-κB targets, was also modulated after NIK knockdown. For example, the expression of the oncogene YAP1 (42) was reduced and an upregulation of KLF2, a tumor suppressor with antiproliferative effects known to be silenced in tumor cells (43), was observed. This can indicate either NF-κB–independent functions of NIK or interaction between the NF-κB pathway and other pathways (44).

The upstream signaling events leading to NF-κB overexpression and/or NF-κB activation in T-cell lymphomas remain to be clarified. Several factors are known to trigger NF-κB activation in other tumors, including signals provided by the tumor microenvironment or mutations that give rise to a constitutive activation of the pathway. In PTCL, apart from the previously reported p100 truncations (7, 45), genetic lesions in NIK or other NF-κB pathway genes have still not been reported. Other possible contributions to NF-κB activation in T-cell lymphomas could be oncogenic viruses (46), signals from CD30 or the T-cell receptor (47, 48), or epigenetic mechanisms, such as the previously reported polycomb-mediated repression of mir31 (49). Even though we observed a lack of mir31 in our cell lines, this absence was independent of the levels of NIK (data not shown). It could also be hypothesized that the activation of NIK and NF-κB can be an effect of deregulated signaling of other pathways linked to T-cell lymphomagenesis, such as the phosphoinositide 3-kinase/AKT, Notch, or JAK–STAT pathway, which can all result in NF-κB activation (44).
NIK in T-cell Lymphoma

The present study reveals a pivotal role for NIK in the survival of T-cell lymphoma cells. NIK knockout strongly reduces the cell viability of PTCL cell lines and is shown to be more effective than IKK inhibition in these cells. Importantly, the fact that cells with a low level of expression of NIK were not affected by NIK knockout suggests a selective toxicity of NIK inhibition in NIK-overexpressing lymphoma cells. Moreover, although NIK-deficient mice exhibit defects in lymphoid organogenesis, they do not present any gross phenotypic changes (50), suggesting that pharmacologic inhibition of NIK might be safer than broad NF-κB inhibition. To develop NF-κB-based cancer therapies efficiently and safely, it is necessary to identify molecular targets as well as biomarkers with which to stratify patients who are likely to benefit from the therapy. PTCL are highly aggressive malignancies that currently lack efficient therapies. Our findings indicate that NIK is a promising molecular target in NIK-overexpressing PTCL, a conclusion that should be taken into account in further validation and development of specific NIK inhibitors.

Disclosure of Potential Conflicts of Interest

Pablo I. Ortiz-Romero has received honoraria from talking on the speakers’ bureau of Bristol-Myers Squibb and Eisai and is a consultant/advisory board member of AOP Orphan. No potential conflicts of interest were disclosed by the other authors.

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